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Attestation

Die angehefteten Unterlagen stimmen mit der ursprünglich eingereichten Fassung der auf dem nächsten Blatt bezeichneten europäischen Patentanmeldung überein.

The attached documents are exact copies of the European patent application described on the following page, as originally filed.

Les documents fixés à cette attestation sont conformes à la version initialement déposée de la demande de brevet européen spécifiée à la page suivante.

Patentanmeldung Nr. Patent application No. Demande de brevet n°

99870141.1

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Der Präsident des Europäischen Patentamts:
Im Auftrag

For the President of the European Patent Office

Le Président de l'Office européen des brevets
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I.L.C. HATTEN-HECKMAN

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Blatt 2 d r B scheinigung
Sheet 2 of the certificate
Page 2 de l'attestation

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JANSSEN PHARMACEUTICA N.V.
2340 Beerse
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Genetic sequences related to programmed cell death in yeast and fungi

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See for original title of the application
page 1 of the description



1

CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI

The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon
5 programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi.

Invasive fungal infections (e.g. *Candida* spp., *Aspergillus* spp., *Fusarium* spp., *Zygomycetes* spp.) (Walsh, 1992) have emerged during the past two
10 decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal infections have also increased in frequency in
15 several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with complications.

These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the
20 production of unwanted compounds (e.g. *Fusarium* spp., *Aspergillus* spp., *Botritis*, spp., *Cladosporium* spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses, expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal
25 agents is thus an essential element of any new antifungal therapy.

Classical approaches for identifying anti-fungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic, or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic
5 model organism. These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular target.

10 Cells from multicellular organisms can commit suicide in response to specific signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnecessary or damaged cells. To survive, all cells from multicellular organisms depend on the constant repression of this suicide program by signals from other cells (Raff, 1992). It has
15 been assumed that such an altruistic form of cell survival arose with multicellularity and would have been counterselected in unicellular organisms. Recent findings indicate, however, that a similar process of cell survival also operates in single-celled eukaryotes.

It has been found that expression of the mammalian *Bax* gene triggers cell
20 death in *Saccharomyces cerevisiae* and the fission yeast *Schizosaccharomyces pombe* with morphological changes similar to apoptosis (Jürgensmeier *et al.*, 1997). However, the mechanism of *Bax* lethality in *S. cerevisiae* remains unclear.

Since it has been discovered that the mammalian *Bax* gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the

molecular pathways eventually leading to programmed cell death may also be partially present in yeast cells and other unicellular eukaryotes.

It is an aim of the present invention to provide nucleic acid as well as polypeptide sequences which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungi infections.

It is a further aim of the present invention to provide uses of these nucleic acid and amino acid molecules for the preparation of a medicament for treating diseases associated with yeast or fungi.

10 It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

15 It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicine for treating diseases associated with yeast and fungi.

It is another aim of the invention to provide methods to selectively identify compounds capable of inhibiting or activating expression of such polypeptides in yeast or fungi infections. The nucleic acid and polypeptide molecules alternatively can be incorporated into an assay or kit to identify these compounds.

20 It is also an aim of the invention to provide a method of preventing infection with yeast or fungi.

It is also an aim of the invention to provide probes and primers derived from
25 the nucleic acid sequences of the invention.

All the aims of the present invention have been met by the embodiments as set out below.

The present inventors identified a range of specific nucleotide sequences which are involved in the molecular pathways eventually leading to programmed
5 cell death.

According to a first embodiment, the invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

- 10 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136,
15 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286,
20 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436,

438, 440, 442, 444, 446, 448, 450, 452, 454 or 456, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454 or 456;

- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID

- NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42,
44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84,
86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118,
120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148,
5 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178,
180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208,
210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238,
240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268,
270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298,
10 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328,
330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358,
360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388,
390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418,
420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448,
15 450, 452, 454 or 456; and
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ
ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39,
41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81,
83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117,
20 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147,
149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177,
179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207,
209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237,
239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267,
25 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297,

299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327,
329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357,
359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387,
389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417,
5 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447,
449, 451, 453 or 455;

(e) a nucleic acid sequence which is more than 70% identical, preferably more
than 75 or 80% identical, more preferably more than 85%, or 90% or 95%
identical and most preferably more than 97% identical to any of the nucleic acid
10 sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25,
27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67,
69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105,
107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135,
137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165,
15 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195,
197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225,
227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255,
257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285,
287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315,
20 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345,
347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375,
377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405,
407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435,
437, 439, 441, 443, 445, 447, 449, 451, 453 or 455; and

25 (f) the complement of any of the nucleic acid sequences as specified in a) to),

for the preparation of a medicament for treating diseases associated with yeast or fungi."

Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using
5 BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means the degree of sequence relatedness between
10 two polypeptide or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton,
15 1988). Methods commonly employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in
20 computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1984), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The nucleic acid sequences to be used according to this aspect of the

25 invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOS 1, 3, 5, 7, 9,

11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 5 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281 and 283. The invention also relates to nucleic acid sequences from *Candida albicans*, as represented by 10 the SEQ ID NOs 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 15 439, 441, 443, 445, 447, 449, 451, 453 and 455.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, and hydrogen peroxide.

20 The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in immunocompromised patients.

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic 25 reactions caused by said organisms, such as the so-called "professional diseases"

in, for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic".

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455, but isolated from other yeast and fungi which are also involved in a pathway eventually leading to programmed cell death.

According to the invention, these sequences and their homologues in other yeast and fungi as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides and their potential use in alleviating diseases or conditions associated with yeast or

~~fungi infections, such as diseases caused by Candida spp., Aspergillus spp.,~~

Microsporium spp., Trichophyton spp., Fusarium spp., Zygomycetes spp., Botritis, spp., Cladosporium spp., Malassezia spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix*
 5 *schenckii*.

The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*. As explained in Example 3, genes showing a difference of a factor 5 or more in expression as a result of Bax-induced
 10 cell death, were identified as differentially expressed candidate genes. Some of these genes are clearly down-regulated in a Bax-expressing strain, while other genes show an upregulated expression (Table 1).

According to another embodiment, the invention also relates to a nucleic acid sequence encoding a polypeptide which is involved in a pathway eventually
 15 leading to programmed cell death of yeast or fungi selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372,
 20 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a nucleic acid molecule encoding a protein having an amino acid sequence

25 ~~which is more than 70% similar, preferably more than 75% or 80% similar,~~

more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454;

(c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical,

more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454;

(d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;

(e) a nucleic acid sequence which is more than 70% identical, preferably more

than 75% or 80% identical, more preferably more than 85%, 90% or 95%

identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 5 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455; and,

(f) the complement of any of the nucleic acid sequences as specified in a) to e).

10 According to a more specific embodiment, these nucleic acid sequences are derived from *Saccharomyces cerevisiae*, *Candida albicans* or *Aspergillus fumigatus*.

A nucleic acid sequence according to the invention may comprise an mRNA sequence or alternatively a DNA sequence and preferably a cDNA sequence. A 15 nucleic acid sequence according to the invention may also comprise any modified nucleotide known in the art.

The present invention further relates to a nucleic acid molecule capable of specifically hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof, under high stringency conditions.

20 The term "nucleic acid sequence" also includes the complementary sequence to any single stranded sequence given, or the antisense version thereof.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid sequence capable of hybridizing to any of the above defined nucleic acid sequences.

Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

5 The present invention also advantageously provides nucleic acid sequences of at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according
10 to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically with any of the nucleic acid molecules of the invention. The primers will specifically amplify any of the nucleic acid molecules of the invention.

15 The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

20 According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different probes in discrete locations. Such arrays can be used to screen for compounds interacting with said
25 probes.

Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotides to a region of the gene
5 which is desired to be cloned, bringing the primers into contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as
10 described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P or ^{35}S , enzyme labels or other protein labels such as biotin or fluorescent markers. Such labels
15 may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable expression vector which may be transformed, transfected or
20 infected into a host cell. In such an expression vector the nucleic acid is operably linked to a control sequence, such as a suitable inducible promotor, or the like, to ensure expression of the proteins according to the invention in a suitable host cell. The expression vector may also comprise a reporter molecule. The expression vector may advantageously be a plasmid, cosmid, virus or other suitable vector
25 which is known to those skilled in the art. The expression vector and the host cell

defined herein also form part of the present invention. Preferably the host cell is a lower eukaryotic cell such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

The invention further relates to any nucleic acid as defined above for use as a medicament.

Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides, leading to impaired growth or death of yeast and fungi with reductions of associated illnesses or diseases.

According to another embodiment, the invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

(a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178,

- 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208,
210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238,
240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268,
270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298,
5 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328,
330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358,
360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388,
390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418,
420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448,
10 450, 452, 454 or 456, or encoding a functional equivalent, derivative or
bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar,
preferably more than 75% or 80% similar, more preferably more than 85%,
90% or 95% similar and most preferably more than 97% similar to any of the
15 amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20,
22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62,
64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102,
104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132,
134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162,
20 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192,
194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222,
224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252,
254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282,
284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312,
25 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342,

344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372,
374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402,
404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,
434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454 or 456;

- 5 (c) a protein having an amino acid sequence which is more than 70% identical,
preferably more than 75% or 80% identical, more preferably more than 85% ,
90% or 95% identical and most preferably more than 97% identical to any of
the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18,
20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60,
10 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100,
102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130,
132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160,
162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190,
192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220,
15 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250,
252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280,
282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310,
312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340,
342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370,
20 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400,
402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430,
432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454 or 456; and,
(d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

Functional fragments include those comprising an epitope which is specific for the proteins according to the invention. Epitopes may be determined using, for example, peptide scanning techniques as described in Geysen *et al.* (1996). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 100, 150 or 200 amino acids.

The polypeptides to be used according to this aspect of the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, and 284. Also according to the invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454 or 456.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative amino acid changes.

The nucleic acid molecule as defined in claim 1 or the polypeptide as
5 defined in claim 2 of the invention may be provided in a pharmaceutically acceptable carrier, diluent or excipient therefor.

The present invention also relates to a vaccine for immunizing a mammal against infections caused by yeast and fungi, comprising at least one (recombinant) nucleic acid molecule as defined in claim 1, or at least one
10 (recombinant) polypeptide as defined in claim 2, in a pharmaceutically acceptable carrier.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing
15 macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete. A vaccine
20 may also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions.

The term "therapeutic" refers to a composition capable of treating infections
25 caused by yeast or fungi.

According to another embodiment, the present invention provides a method of identifying compounds which selectively inhibit, induce or interfere with the expression of the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound, (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

According to the invention, the term "mutation" includes deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as

5 monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

The invention also relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway

10 eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1,

15 which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective

20 action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective

25 action of said compound on a polypeptide in the same or a parallel pathway, (d)

alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

The invention further relates to a method of identifying compounds which
5 bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2, (b) detecting the complex formed between the compound to be tested and said polypeptide, (c) alternatively, examining the
10 diminution of complex formation between said polypeptide and a receptor, caused by the addition of the compound being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.

The invention also relates to a method of identifying compounds which
15 selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene and (b) monitoring
20 increased or decreased expression of said reporter gene caused by the addition of the compound being tested.

According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus*
25 *fumigatus*.

The compounds identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of
5 endogenous yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

According to the invention, alternative methods for identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in
10 metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

The compounds identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell
15 death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenous yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

The compounds to be screened may be of extracellular, intracellular,
20 biologic or chemical origin. The protein or peptide fragments according to the invention employed in such a method may be for example in solution, affixed to a solid support, borne on a cell or phage surface or located intracellularly. One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine th

diminution of complex formation between the protein according to the invention and a receptor caused by the compound being tested.

Another technique for compound identification provides high throughput screening for compounds having suitable binding affinity to the polypeptides according to the invention. Hereby, large numbers of compounds are fixed to a solid substrate and tested for their binding affinity.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

10 This technique is based on functional reconstitution *in vivo* of a transcription factor which activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid
15 DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating
20 domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilizes the GAL4 protein in yeast. GAL4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of GAL4.

These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of GAL4.

These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL-4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as β -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes.

The invention also relates to a compound identified using any of the methods of the invention.

Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament, or in the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections, for instance *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii* infections. These

compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

A medicament according to the invention not only relates to fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

The invention also relates to genetically modified yeast or fungi in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or the polypeptides as defined in claim 2, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungi. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

Also according to the invention is the use of a compound according to claim 10 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

According to another embodiment, the invention also relates to an isolated protein which is involved in a pathway for programmed cell death of yeast or fungi selected from:

(a) a protein having an amino acid sequence as represented in any of SEQ ID

NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316,

318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354,

356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386,

388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90 or 95% similar and most preferably more than 90% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454;
- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454; and,

(d) a functional fragment of any of said proteins as defined in a) to c).

According to the invention, the polypeptides as defined above may be used as a medicament.

Also encompassed within the present invention are antibodies, monoclonal or polyclonal, capable of specifically binding to one or more epitopes of the proteins of the invention. The term "specific binding" implies that there is substantially no cross-reaction of the antibody with other proteins.

- 5 The antibodies according to the invention may be produced according to techniques which are known to those skilled in the art. Monoclonal antibodies may be prepared using conventional hybridoma technology as described by Kohler and Milstein (1979). Polyclonal antibodies may also be prepared using conventional technology well known to those skilled in the art, and which comprises inoculating
- 10 a host animal, such as a mouse, with a protein or epitope according to the invention and recovering the immune serum. The present invention also includes fragments of whole antibodies which maintain their binding activity, such as for example, Fv, F(ab') and F(ab')₂ fragments as well as single chain antibodies.

- Antibodies according to the invention may also be used in a method of
- 15 detecting the presence of a polypeptide according to the invention, which method comprises reacting the antibody with a sample and identifying any protein bound to said antibody. A kit may also be provided for performing said method which comprises an antibody according to the invention and means for reacting the antibody with said sample.

- 20 The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi such as, but not restricted to, *Candida albicans*, *Aspergillus* spp., *Fusarium* spp., *Botritis*, spp., *Cladosporium*

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response.

- 5 The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

Figure 1. *Saccharomyces cerevisiae* sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID Nos 1 to 284)

5 **Figure 2.** *Candida albicans* sequences (SEQ ID Nos 285 to 456).

Figure 3. Yeast genome macroarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters. The filters are cut in the upper right corner for orientation and the DNA is on the labelled side of the filter. Each filter contains 2 fields and each field is divided into 8 grids, organised in 24 rows and 8 columns.

The spots represent the genome wide expression profile without (A) and with (B) *Bax* modulated expression.

10 **Table 1.** Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed more than fivefold. The factor by which the transcript level was affected, is expressed as the Qt value. Upregulation or downregulation of a specific mRNA is stated when Qt had a value of at least five or at most 0.21, respectively.

20 **EXAMPLES**

Example 1. Differential gene expression analysis upon *Bax*-induced c II death

Materials and media

Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980)

25 — was used for the construction and the amplification of plasmids. Yeast strains were

grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* strain INVSc1 (Invitrogen®) was transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with YlpUTyL or YlpUTYLMuBax, after linearisation in the Ty δ element (Zhu, 1986).

5

Cloning of mouse BAX cDNA

Mouse *Bax* cDNA, encoding the mouse Bax- α protein, was cloned by Pfu DNA polymerase (Stratagene®) chain reaction amplification (PCR) from an EL4/13.18 thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the

10 primers:

5'-ATGGACGGGTCCGGGAGCAG-3' and

5'-TCAGCCCATCTTCTTCCAGATGGTGAG-3'.

The resulting PCR product was cloned in a *HincII*-openend pUC19 according to standard procedures (Sambrook J. *et al.*, 1989).

15

Plasmid constructions

The 2 μ ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *ClaI* and *BglII*. A *BamHI*-*HindIII* GAL1 promoter fragment was ligated into the *BglII*-*HindIII*-opened plasmid. A *XbaI*-*FspI* FLP terminator fragment was inserted into this *XbaI*-*HindIII*(blunted)-opened plasmid so that the plasmid YlpUT was obtained. Insertion of a blunted *EcoRI*-*BsaAI* Ty δ element in the *KpnI*-*AatII*-opened and blunted YlpUT resulted in the plasmid YlpUTy. Subsequent insertion of the *LEU2* marker gene, as a blunted *BsaAI*-*BsrGI* fragment, in the *BamHI*-openend and blunted YlpUTy resulted in the

25 plasmid YlpUTyL.

Mouse *Bax* cDNA was excised from pUC19 by digestion with *Xba*I and *Hind*III and subcloned into the *Xba*I-*Hind*III-opened plasmid YlpUTyL, obtaining the final expression plasmid YlpUTyLMuBax.

The plasmid YlpUTyLMuBax has been deposited in the BCCMTM/LMBP
5 culture collection as p5CTyGALmBax with accession number 3871 under restricted use.

GeneFilters

The Yeast GeneFiltersTM were purchased from Research Genetics Inc.
10 (Huntsville, AL, USA).

The Yeast GeneFiltersTM are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the
15 filter.

Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8 columns.

Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3
20 and 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

The yeast filters consist of over 6000 PCR products corresponding to 6144 yeast ORFs derived from the SGD. The PCR reactions used ORF specific primer

~~25 pairs designed to amplify the entire open reading frame. The primers were~~

generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per 5 microliter in a colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

10 Results

Induction of Bax-expression in yeast cells

Precultures of yeast strain INVSc1 containing YlpUTyLMuBax, wherein 5 Bax-cassettes under the control of the GAL1 promotor are integrated in the 15 genome near Ty δ elements, were grown overnight in parallel with the yeast strain INVSc1 containing YlpUTyL as a control. The precultures were diluted to an OD₆₀₀ of 0,25 in 100 ml minimal glucose-containing medium and grown for about 8 hours at 30°C until an OD₆₀₀ of 1 to 1,5 was reached. Subsequently, the yeast cells were transferred into minimal galactose-containing medium at an OD₆₀₀ of 1 (Bax- 20 expressing strains) or 0,4 (control strains) and grown for an additional 15 hours period.

RNA isolation

25 Total RNA was isolated using RNApure™ Reagent (Genhunter Corporation Nashville, TN, USA) according to the GenHunter protocol. $1.5 \cdot 10^9$ cells were

concentrated in a microcentrifuge tube and 1ml RNAPure™ Reagent was added together with 1 g of glass pearls. The yeast cells were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNase digestion. Chloroform (150 µl) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA pellet was resuspended in 50 µl RNase free dH₂O.

10

First strand cDNA synthesis in the presence of α -³²P dCTP

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1YlpUTyLMuBax or INVSc1YlpUTyL yeast cells and incorporation of α -³²P dCTP as follows: 2 µl (1 µg/ml) of Oligo dT was added to 20 µg of total RNA in a maximal volume of 8 µl RNase-free dH₂O and incubated at 70° for 10 min. After cooling down on ice for 1 min, the following components were added:

- 6 µl 5x concentrated First Strand Buffer (GIBCO-BRL)
 - 1 µl 0,1 M DTT
 - 1 µl RNase Block (40 units/µl) (Stratagene)
 - 1,5 µl 20 mM dXTP-solution (X = A, G and T) (Pharmacia)
 - 1,5 µl SuperScript™ Reverse Transcriptase (200 units/µl) (GIBCO-BRL)
 - 10 µl α -³²P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham)
- and incubated for 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Pharmacia). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was $3,1 \cdot 10^8$ cpm/ μ g and $3 \cdot 10^8$ cpm/ μ g for the INVSc1YipUTyL and the INVSc1YipUTyLMuBax probe, respectively.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection

The Yeast GeneFilters™ were successively hybridised with the α - 32 P dCTP labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during hybridisation. The MicroHyb solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250 mm) filled with 10 ml MicroHyb™ solution (42°C) containing 5 μ l polydA (0,5 μ g/ml) and incubated for 24 hours at 42°C whilst rotating. After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA probe ($3,1 \cdot 10^8$ cpm/ μ g, $6,5 \cdot 10^7$ cpm) was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating. Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third more stringent wash step was performed in a second wash buffer (0,5x SSC, 1% SDS) for an additional 15 min

at room temperature. The filters were flushed with dH₂O to avoid SDS precipitation. The Yeast GeneFilters™ were placed in a PhosphorImager™ cassette with storage phosphorscreen. After 4 days of development the screen was developed and scanned using the PhosphorImager™ 455 SI from Molecular Dynamics. The results of these can be seen in Figure 3.

In-between the hybridisation experiments, the filters were stripped off by incubation in 500 ml of a 0.5% SDS solution (prewarmed to near boiling temperature) during at least 1 hour at room temperature.

10 Example 2. Quantification of hybridisation Signals

Quantification of the hybridisation signals was done using the ImageQuant™ 4.1 software tool from Molecular Dynamics (Sunnyvale, CA). The quantification was performed per grid of the Yeast GeneFilters™, and by drawing a roster of 24 columns and 8 rows onto each grid of each filter. As such, each
15 rectangle of the roster corresponds to a spot on the Yeast GeneFilters™. Subsequently, from each grid a volume-report (quantification) was drawn up and the data were transferred to a Microsoft™ Excel sheet. Also for each grid a correction factor was calculated. Signals neighboring big and dark spots were separately quantified. For each grid, a background level was calculated.

Statistical processing of quantification results

The statistical processing of the results was accomplished in Microsoft™ Excel. For each grid, the following statistical functions were separately defined:

5 1. The frequency of occurrence of the values in a precisely defined intensity range(data range), established between 1000 and 61000, split up in intervals of 5000.

2. The frequency in terms of percentage.

3. The cumulated frequency in terms of percentage.

10 These numeric values were used for the graphical display of the cumulated frequency in terms of percentage.

Subsequently, the results of the two experiments (hybridization with cDNA from YlpUTyL containing INVSc1 cells and hybridization with cDNA from YlpUTyLMuBax containing INVSc1 cells) were integrated by determination of a

15 second range of statistical functions:

1. The average of the values of the two experiments for each spot on the filter.

2. The standard deviation on this average. This is a measure for the distribution of the values around this average.

20 3. The standard deviation in terms of percentage.

The quotient of the values of the second experiment (Bax expression) against the values from the first experiment (control) was determined. This immediately gives the factor by which the expression of a specific gene is changed upon Bax induction.

In order to process all these data and to be able to discriminate between differences in gene expression, a gene showing a standard deviation in terms of percentage of at least 90% and a difference of a factor 5 in expression as a result of Bax induction, was identified as a differentially expressed candidate gene.

- 5 (Table 1). Requantification of these candidates confirmed their selection.

When the expression pattern of all 6144 genes is compared in the two experiments, it could be concluded that the expression profile of 142 genes (this is 2,3 %) has been changed with at least of factor 5. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 1.

- 10 The sequences of these genes and the amino acid sequences which they encode are shown in Figure 1.

Example 3 . Search for homologues in *Candida albicans*

- Sequence similarity searches against public and commercial sequence
15 databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL
20 (Bairoch and Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minesota). The commercial sequence database used was the PathoSeqTM microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA).

- Sequence similarity searches were performed using the BLAST software
25 package version 2. The identity between 2 sequences was calculated as

percentage identical residues, the similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.

Example 4 . Screening for compounds modulating expression of polypeptides involved in induction of cell death of *C. albicans*

The method proposed is based on observations (Sandbaken *et al.*, 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to the wild type (WT) cell.

Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally sensitive to compounds with other mechanisms of action.

This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test compound.

The assay to be set up involves measurement of growth or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to

a wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti-sense or strains which carry disruptions in an essential gene. An in silico approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

Example 5. Assay for High Throughput screening for drugs.

10 35 μ l minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems). A 96-channel pipettor (Hydra, Robbins Scientific) transfers 2.5 μ l of R-compound at 10^{-3} M in DMSO from a stock plate into the assay plate.

15 The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at -70°C . The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C . For the parent strain, CAI-4, the medium is always supplemented with 20 $\mu\text{g/ml}$ uridine. A single colony is scooped up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250,000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20,000 to 50,000 cells/ml. Cultures are grown at 30°C while shaking
25 at 250 rpm until a final OD_{600} of 0.24 (\pm 0.04) is reached.

42

200 μ l of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 μ l total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

Optical densities are measured after 48 hours.

- 5 Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Tabl 1.

ORF	Qt	Sequence ID Number
YAR061W	7.80	SEQ ID NO 1
YAR073W	11.19	SEQ ID NO 3
YBL048W	5.07	SEQ ID NO 5
YBL051C	5.22	SEQ ID NO 7
YBL066C	6.04	SEQ ID NO 9
YBL078C	6.94	SEQ ID NO 11
YBR072W	26.56	SEQ ID NO 13
YBR073W	5.46	SEQ ID NO 15
YBR086C	7.14	SEQ ID NO 17
YBR093C	11.05	SEQ ID NO 19
YBR181C	0.15	SEQ ID NO 21
YCL007C	20.99	SEQ ID NO 23
YCL016C	23767.57	SEQ ID NO 25
YCR052W	10.51	SEQ ID NO 27
YCR064C	14.91	SEQ ID NO 29
YCR073WA	5.92	SEQ ID NO 31
YDL010W	5.31	SEQ ID NO 33
YDL036C	5.34	SEQ ID NO 35
YDL083C	0.16	SEQ ID NO 37
YDL125C	6.80	SEQ ID NO 39
YDL133CA	0.21	SEQ ID NO 41
YDL136W	0.20	SEQ ID NO 43
YDL167C	6.37	SEQ ID NO 45
YDL184C	0.21	SEQ ID NO 47
YDL191W	0.17	SEQ ID NO 49
YDR103W	6.26	SEQ ID NO 51
YDR238C	5.75	SEQ ID NO 53
YDR259C	9.68	SEQ ID NO 55
YDR294C	8.38	SEQ ID NO 57
YDR430C	5.66	SEQ ID NO 59
YDR438W	6.47	SEQ ID NO 61
YDR450W	0.16	SEQ ID NO 63
YDR471W	0.11	SEQ ID NO 65
YDR486C	5.27	SEQ ID NO 67
YDR499W	6.14	SEQ ID NO 69
YDR507C	6.34	SEQ ID NO 71
YDR515W	5.42	SEQ ID NO 73
YDR518W	6.15	SEQ ID NO 75
YDR519W	5.57	SEQ ID NO 77
YER102W	0.19	SEQ ID NO 79
YER153C	5.63	SEQ ID NO 83
YFL014W	41.08	SEQ ID NO 85
YFL015C	5.62	SEQ ID NO 87

Tabl 1. - continued -

ORF	Qt	Sequenc ID Numb r
YFR022W	9.44	SEQ ID NO 89
YGL011C	6.14	SEQ ID NO 91
YGL031C	0.11	SEQ ID NO 93
YGL032C	0.14	SEQ ID NO 95
YGL043W	10.74	SEQ ID NO 97
YGL102C	0.15	SEQ ID NO 99
YGL103W	0.17	SEQ ID NO 101
YGL130W	8.35	SEQ ID NO 103
YGL147C	0.08	SEQ ID NO 105
YGL213C	6.02	SEQ ID NO 107
YGL235W	6.23	SEQ ID NO 109
YGL260W	6.61	SEQ ID NO 111
YGR085C	0.16	SEQ ID NO 113
YGR118W	0.17	SEQ ID NO 115
YGR142W	8.91	SEQ ID NO 117
YGR236C	12.72	SEQ ID NO 119
YGR277C	6.27	SEQ ID NO 121
YGR284C	5.95	SEQ ID NO 123
YGR285C	5.84	SEQ ID NO 125
YHR010W	0.20	SEQ ID NO 127
YHR021C	0.16	SEQ ID NO 129
YHR141C	0.10	SEQ ID NO 131
YHR217C	7.6	SEQ ID NO 133
YIL112W	11.15	SEQ ID NO 135
YIL115C	7.67	SEQ ID NO 137
YIL148W	0.13	SEQ ID NO 139
YIL150C	6.83	SEQ ID NO 141
YIL167W	6.66	SEQ ID NO 143
YJL034W	11.61	SEQ ID NO 145
YJL035C	14.48	SEQ ID NO 147
YJL070C	5.29	SEQ ID NO 149
YJL078C	5.16	SEQ ID NO 151
YJL179W	0.19	SEQ ID NO 153
YJL180C	0.14	SEQ ID NO 155
YJL181W	0.21	SEQ ID NO 157
YJL187C	0.17	SEQ ID NO 159
YJL188C	0.1	SEQ ID NO 161
YJL189W	0.08	SEQ ID NO 163
YJL190C	0.09	SEQ ID NO 165
YJL197W	0.13	SEQ ID NO 167
YJL198W	0.2	SEQ ID NO 169
YJR049C	0.17	SEQ ID NO 171
YKR094C	0.14	SEQ ID NO 173

Tabl 1. - continu d -

ORF --	Qt	Sequence ID Number
YLR040C	10.13	SEQ ID NO 175
YLR048W	8.55	SEQ ID NO 177
YLR088W	6.09	SEQ ID NO 179
YLR159W	0.18	SEQ ID NO 181
YLR167W	0.06	SEQ ID NO 183
YLR232W	7.4	SEQ ID NO 185
YLR233C	7.63	SEQ ID NO 187
YLR234W	5.68	SEQ ID NO 189
YLR238W	6.74	SEQ ID NO 191
YLR241W	6.48	SEQ ID NO 193
YLR321C	12.17	SEQ ID NO 195
YLR322W	5.54	SEQ ID NO 197
YLR325C	0.06	SEQ ID NO 199
YLR344W	0.12	SEQ ID NO 201
YLR367W	0.19	SEQ ID NO 203
YLR393W	7.05	SEQ ID NO 205
YLR423C	8.61	SEQ ID NO 207
YML026C	0.11	SEQ ID NO 209
YML063W	0.16	SEQ ID NO 211
YML128C	5.1	SEQ ID NO 213
YML130C	5.41	SEQ ID NO 215
YMR022W	6.45	SEQ ID NO 217
YMR118C	5.13	SEQ ID NO 219
YMR143W	0.08	SEQ ID NO 221
YMR174C	6.75	SEQ ID NO 223
YMR191W	9.56	SEQ ID NO 225
YMR230W	0.13	SEQ ID NO 227
YNL054W	5.19	SEQ ID NO 229
YNL067W	0.12	SEQ ID NO 231
YNL075W	0.16	SEQ ID NO 233
YNL096C	0.14	SEQ ID NO 235
YNL162W	0.07	SEQ ID NO 237
YNL178W	0.11	SEQ ID NO 239
YNL182C	0.18	SEQ ID NO 241
YNL190W	0.07	SEQ ID NO 243
YNL208W	5.87	SEQ ID NO 245
YNL210W	0.02	SEQ ID NO 247
YOL031C	5.32	SEQ ID NO 249
YOL048C	14.34	SEQ ID NO 251
YOR010C	7.27	SEQ ID NO 253
YOR019W	5.19	SEQ ID NO 255
YOR027W	6.03	SEQ ID NO 257
YOR031W	5.35	SEQ ID NO 259
YOR096W	0.12	SEQ ID NO 261
YOR248W	0.18	SEQ ID NO 263

Tabl 1. - continu d -

ORF	Qt	Sequence ID Number
YOR293W	0.11	SEQ ID NO 265
YOR312C	0.12	SEQ ID NO 267
YOR369C	0.21	SEQ ID NO 269
YPL047W	5.09	SEQ ID NO 271
YPL090C	0.1	SEQ ID NO 273
YPL137C	10.41	SEQ ID NO 275
YPL159C	5.61	SEQ ID NO 277
YPL175W	5.95	SEQ ID NO 279
YPL180W	7.68	SEQ ID NO 281
YPL218W	6.26	SEQ ID NO 283
YPR102C	0.17	SEQ ID NO 285

REFERENCES

- Altschul, S.F. Gish, W., Miller, W., Myers, E.W. and Lipman, D.J. (1990). Basic local alignment search tool. *J. Mol. Biol.* **215**, 403-410.
- 5 Bairoch, A. and Apweiler, R. (1998). The SWISS-PROT protein sequence data bank and its supplement TrEMBL in 1998. *Nucleic Acids Res.* **26**, 38-42.
- Bishop, M.J., ed. (1994). Guide to Huge Computers, Academic Press, San Diego.
- Carillo, H. and Lipton, D. (1988). *SIAM J. Applied Math.* **48**, 1073.
- 10 Casadaban, M.J., and Cohen, S.N. (1980). Analysis of gene control signals by DNA fusion and cloning in *Escherichia coli*. *J. Mol. Biol.* **138**, 179-207.
- Chien, C. T., Bartel, P.L., Sternglanz, R., and Fields, S. (1991). The 2-hybrid system - a method to identify and clone genes for proteins that interact with a protein of interest. *Proc. Natl. Acad Sci USA* **88**, 9578-9582.
- 15 Devereux, J., Haeberli, P. and Smithies, O. (1984). A comprehensive set of sequence analysis programs for the VAX. *Nucleic Acids Research* **12**, 387-395.
- Gatignol, A., Dassin, M. and Tiraby, G. (1990). Cloning of *Saccharomyces cerevisiae* promoters using a probe vector based on phleomycin resistance. *Gene* **91**, 35-41.
- 20 Geysen, H.M., Rodda, S.J. and Mason, T.J. (1986). A priori delineation of a peptide which mimics a discontinuous antigenic determinant. *Mol. Immunol.* **23**, 709-715.
- Hinnebush, A.G. and Lieberman, S.W., in : The Molecular Biology of the Yeast *Saccharomyces* (1991). Broach, J.R., Pringle, J.R. and Jones, E.W., eds.,
- 25 CSH Laboratory Press, NY.

Jürgenmeiser, J.M., Krajewski, S., Armstrong, R., Wilson, G.M., Oltersdorf, T., Fritz, L.C., Red, J.C., and Otilie, S. (1997). Bax- and Bak-induced cell death in the fission yeast *Schizosaccharomyces pombe*. *Mol. Biol. Cell* **8**, 325-329.

- Kohler, F. and Milstein, C. (1975). Continuous cultures of fused cells
5 secreting antibody of predefined specificity. *Nature* **256**, 495-497.

Ligr, M., Madeo, F., Froehlich, E., Hilt, W., Froehlich, K.-U. and Wolf, D.H. (1998). Mammalian Bax triggers apoptotic changes in yeast. *FEBS Lett.* **438**, 61-65.

- Lockhart, D.J. Dong, H. Byrne, M.C., Follettie, M., Gallo, M.V., Chee, M.S.,
10 Mittenman, M., Wang, C., Kobayashi, M., Horton, H and Brown, E.L. (1996). Expression monitoring by hybridisation to high density oligonucleotide arrays. *Nature Biotechnology* **14**, 1675-1680.

Raff, M.C. (1992). Social controls on cell survival and cell death. *Nature* **356**, 397-400.

- 15 RiboGene Inc., Patent application (1995) PCT WO 95/11969.

Sambrook J., Fritsch E.F. and Maniatis, T. (1989). Molecular Cloning: A Laboratory Manual, 2nd Ed., CSH Laboratory Press, NY.

Sandbaken, M.G., Lupisella, J.A., DiDomenico, B., and Chakraburty, K. (1990). *J. Biol. Chem.* **265**, 15838-15844.

- 20 Sherman, F., Fink, G.R., and Hicks, J.B. (1979). Methods in yeast genetics, CSH Laboratory Press, NY.

Schiestl, R.H., and Gietz, D.R. (1989). High efficiency transformation of intact yeast cells using single stranded nucleic acids as a carrier. *Curr. Genet.* **16**, 339-346.

Stoesser, G., Moseley, M.A., Sleep, J., McGowran, M., Garcia-Pastor, M. and Sterk, P. (1998). *Nucleic Acids Res.* 26, 8-15.

Walsh, T.J. (1992). Invasive Fungal Infections: Problems and Challenges for Developing New Antifungal Compounds, in : "Emerging Targets in Antibacterial and Antifungal Chemotherapy" ,J. A. Sutcliffe and N.H. Georgopapadakou, eds, Chapman and Hall, NY, pp 349-373.

Zhu, J. (1986). One step selection of a multicopy integrant based on yeast genomic transformation. In "Heterologous gene expression in *Saccharomyces cerevisiae* using a dominant selection and amplification system". Ghent University, 10 doctoral dissertation, p 45.



CLAIMS

1. Use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or
5 fungi and which nucleic acid sequence is selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454 or 456, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a nucleic acid molecule encoding a protein having an amino acid
25 ~~sequence which is more than 70% similar, preferably more than 80%~~

similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454 or 456;

(c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106,

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388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414,
416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442,
444, 446, 448, 450, 452, 454 or 456;
(d) a nucleic acid molecule comprising a sequence as represented in any
15 of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31,
33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69,
71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105,
107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133,
135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161,
20 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189,
191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217,
219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245,
247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273,
275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301,
25 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329,

331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357,
359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385,
387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413,
415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441,
5 443, 445, 447, 449, 451, 453 or 455;

(e) a nucleic acid sequence which is more than 70% identical, preferably
more than 80% identical, more preferably more than 90% identical and
most preferably more than 97% identical to any of the nucleic acid
sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21,
10 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59,
61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97,
99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125,
127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153,
155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181,
15 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209,
211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237,
239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265,
267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293,
295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321,
20 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349,
351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377,
379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405,
407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433,
435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455; and

- (f) the complement of any of the nucleic acid sequences as specified in a) to e),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

5

2. Use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

- (a) a protein having an amino acid sequence as represented in any of SEQ

10 ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36,
38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74,
76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108,
110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136,
138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164,
15 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192,
194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220,
222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248,
250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276,
278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304,
20 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332,
334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360,
362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388,
390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416,
418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444,

446, 448, 450, 452, 454 or 456, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454 or 456;

- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16,

- 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54,
56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92,
94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122,
124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150,
5 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178,
180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206,
208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234,
236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262,
264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290,
10 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318,
320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346,
348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374,
376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402,
404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430,
15 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454 or 456; and,

(d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

- 20 3. A pharmaceutical or fungicidal composition comprising a nucleic acid molecule as defined in claim 1 or a polypeptide as defined in claim 2 together with a pharmaceutically acceptable carrier diluent or excipient therefor.

4. A vaccine for immunizing a mammal against yeast or fungal
25 infections, comprising at least one nucleic acid molecule as defined in claim 1, or

at least one polypeptide as defined in claim 2, in a pharmaceutically acceptable carrier.

- 5 5. A genetically modified yeast or fungus in which modification results
in the overexpression or underexpression of at least one of the nucleic acids as
defined in claim 1 or the polypeptides as defined in claim 2, which overexpression
or underexpression of said nucleic acid or polypeptide prevents or delays
apoptosis of said genetically modified yeast or fungus.
- 10 6. A method of identifying compounds which selectively modulat
expression or functionality of polypeptides involved in a pathway eventually
leading to programmed cell death of yeast or fungi or in metabolic pathways in
which said polypeptides are involved, which method comprises:
- 15 (a) contacting a compound to be tested with yeast or fungal cells having a
mutation which results in overexpression or underexpression of at least
one of the polypeptides as defined in claim 2, in addition to contacting
wild type cells with said compound,
- 20 (b) monitoring the growth, death rate or activity of said mutated cells
compared to said wild type cells; wherein differential growth or activity of
said mutated yeast or fungi cells is indicative of selective action of said
compound on a polypeptide in the same or a parallel pathway,
- (c) alternatively monitoring the growth, death rate or activity of said mutated
cells compared to mutated cells which were not contacted with the
compound to be tested, wherein differential growth or activity of said

mutated yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

5

7. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

10

- (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,

15

- (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

20

- (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the

25

compound to be tested, wherein differential growth or activity of said mutated yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

(d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

5

8. A method of identifying compounds which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:

10

(a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2,

(b) detecting the complex formed between the compound to be tested and said polypeptide,

15

(c) alternatively, examining the diminution of complex formation between said polypeptide and a receptor, caused by the addition of the compound being tested.

(d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.

20

9. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:

- (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene,
- (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested.

10. A method according to any of claims 6 to 9 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

11. A compound identifiable according to the method of any of claims 6 to 9.

12. A compound according to claim 11 for use as a medicament.

13. Use of a compound according to claim 12 for the preparation of a medicament for treating diseases associated with yeast and fungi.

14. Use of a compound according to claim 12 or a genetically modified organism as defined in claim 5 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

15. Use of a compound according to claim 12 where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidemophyton floccosum*, *Blastomyces dermatitidis*,

Coccidioides immitis, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*,
Cryptococcus neoformans, and *Sporothrix schenckii*.

16. A nucleic acid sequence encoding a polypeptide which is involved in
- 5 a pathway for programmed cell death of yeast or fungi selected from:
- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- 10
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454;
- 15
- 20
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97%
- 25

identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454;

(d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451 or 453;

(e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451 or 453; and,

(f) the complement of any of the nucleic acid sequences as specified in a) to e).

17. A nucleic acid according to claim 14, characterized in that it is derived from *Candida albicans*.
- 5 18. A nucleic acid sequence according to any of claims 14 to 16 which is mRNA
19. A nucleic acid sequence according to any of claims 14 to 16 which is DNA.
- 10 20. A nucleic acid sequence according to any of claims 14 to 16 which is cDNA.
21. A nucleic acid sequence capable of hybridizing to a nucleic acid
15 according to any of claims 14 to 20 under high stringency conditions, or the complement thereof.
22. An antisense molecule comprising a nucleic acid sequence capable of hybridizing to the nucleic acid sequences according to any of claims 14 to 20.
- 20 23. An isolated protein which is involved in a pathway for programmed cell death of yeast or fungi selected from:
- (a) a protein having an amino acid sequence as represented in any of SEQ ID
NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316,
25 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354,
356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386,
388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424,
426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or

454, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454;

- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454; and,
- (d) a functional fragment of any of said proteins as defined in a) to c)

24. An expression vector comprising a nucleic acid sequence according to any of claims 16 to 22.

65

25. An expression vector according to claim 24 which comprises an inducible promoter.
26. An expression vector according to any of claims 24 or 25 which
5 comprises a sequence encoding a reporter molecule.
27. A host cell transformed, transfected or infected with the vector of any of claims 24 to 26.
- 10 28. A nucleic acid molecule according to any of claims 16 to 22 for use as a medicament.
29. A polypeptide according to claim 23 for use as a medicament.
- 15 30. An antibody capable of binding to a polypeptide according to claim 23.
31. An antibody according to claim 30 for use as a medicament.
- 20 32. A pharmaceutical composition comprising an antibody according to claim 30.
33. Use of an antibody according to claim 30, or an antibody capable of binding to at least one of the polypeptides as defined in claim 2, for the preparation
25 of a medicament for treating diseases associated with yeast and fungi.
34. Use of an antibody according to claim 33 where the fungus is *Candida albicans*.

35. A nucleic acid probe which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 16 and which hybridises specifically with any of said nucleic acid molecules.
- 5 36. A nucleic acid primer which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 16 and which specifically amplifies any of said nucleic acid molecules.

ABSTRACT

The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi for the preparation of a medicament for treating diseases associated with yeast or fungi. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical or fungicidal compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

YAR061W, 704 bp, CDS: 501-704 (SEQ ID NO 1)
AAAATTTCGCACCTTCAGAGCTTATCGTATCTTCCCGGAGTTCCTCAAGACTTATACTT
CAGCCCGTATTAGGAATGCATAAAAGCAAAATAGGATTTCGTACAACCTGCTGCAGGACTCTT
TAGGACATGCATCAAGGTAAGCTCTCGCTGCACCTAAACGCCAAAATGTGGTTGTAACCTTTT
TAATTTTTTTCTTGAACCTGTGTAGTCGTAAATAATCGTTTCTGGGAAGTGGAAAGGTAAAT
AATGTAATGGAAATCGCGGCTTACTCGCATGTGCAGATATCAGCGACAAAAGGTGTGTAGG
GACGTTTCGATACCAAAATTTCTTAAATACAGCGCAGGAACATCACTACGCTAAACAAAT
CGTAGCGCATACATCTGATCGAAAAAAGACAGTTCCCAAAAACATGACATATGAAGAGAC
CAGCATCAAAATTTTCATCATTAAACAGCATGGCTAAAAGTTATTGTTTAAATATACCCATA
CCTGATTGACGAACCAAGAAATGCCTTATCACTATTATTATTTTGGCAGCTCTTCACCTTACC
TGCCACAGTCCAAATGTGTGTTTCAGGAAGTACACAAGCATGCCTGCCAGTGGGCCCGAGGA
AAAATGGGATGAATGCAACTTTTATAAAATACTCATTTACTGGATTCAACAACGTATTCCT
ACCCGCAATATAGCTTCTGGATATGCCTCGAATTGGAATTAG

YAR061W, 67 aa (SEQ ID NO 2)
MPYHYLFALFTYLATSNVVSSTQACLPGVRPKNGMNVNFYKYSLLDSTTYSYPQYMTS
GYASNNW

YAR073W, 1712 bp, CDS: 501-1712 (SEQ ID NO 3)
AGTGGCTCATGATCTGTAATATGATCGGTTGACCGCAGTATTATATAAATCAACTCCGTATA
AGTACATATATACCATGTCTGTTCTCTACATTCTTATTCAGAGTAAATTTGGTTTTC
CTAAGCCGCGCGCGCGCAGGTACCCCGCGCATCTCTTCTCTCGAAAGAACGGGAAAAA
ACAAAACAAAAGATATAAATAGTGGAGTCTTTTCCCATTTAAACATTTAGAAAACAAATTCG
AATGGAAATTTCTTCGCGAACATTTAACCGGAGACCTTGGCGGCTTTTCTTCAGTTTCG
TGGGCTAGTACTTTTACCTAGTATGCTGGGAACTTTTTCGGTATCTCTATTCTATCTCC
TTGGCTTACCTTTCTTATCAATTTTTATATAACCAATTTCAAATACTTTTAACTGTCT
ATAGACGCAATTTTGTATTATCAAAATTAAGAAGTCAAAATATAATATGTGCAATTAATAA
CTCCACAAGTAGCGAAAGCAATGGCCGCGCATTAGAGACTACAAGACCGCACTAGATCTTA
CCAAGAGCCTACCAAGACCGGATGGTTTGTGAGTGCAGGAACATGATGGACTCCAAGATCA
GAGGTGGGTGGCTTATAACGATTTTAAATCTTACCAGGTTTGTGCGATTTTGGCTGCT
CTGAAGTTAGGCTACAGACCAAGCTAACCGAGGAATATTACTTTAAACATTCCTATTAGTAT
CCTCTCCAATGGACACTGTGACGGAATCTGAAATGGCCACTTTATGGCTCTGTGGATG
GTATCGGTTTCAATTACCATAACTGTACTCCAGAGGACCAAGCTGACATGTGTCAGAAGAG
TCAAGAAGCTATGAAAATGGGTTTATTAACAACCTATAGTGATTCTCCAATACGACCG
TTGGTGAAGCTAAGAGCATGAAGGAAAGATGGATTTCGAGGCTTCCCTGTACCGCGAC
ATGGAAAGAGAAATGCAAGTGTGGTGGGTGCCATCACCTCTCGTGATATCAATTCGTTG
AGGACAACCTCTTACTCGTTACAGGATGTCTAGCAAAAAACCTGTTACCGGCGCACAAG
GTATCACATTATCAGAAGGTAACGAAATCTAAGAGAAATCAAAAAGGTTAGGCTACTGG
TTGTTGATGAAAGGGTAACCTAGTTTCTATGCTTTCCCGAACTGATTATTAATGAAAAATC
AGAAGTACCCATTAGCGTCCAAATCTGCCAACACCAAGCAACTGTTATGGGGTGCTCTTA
TTGGGACTATGGACGCTGATAAAGAAAGACTAAGATTATTGGTAAAAGCTGGCTTGGATG
TCGTCTATATTGGATTCTCTCAAGGTAACCTATTTTCCAATTGACATGATCAATGGA
TTAAAGAAACTTCCAGATTTCGAAATCATTTGCTGGTAACGTTGTACCAAGGAACAAG
CTGCCAATTGATTGCTGCGCGTGGCGGACGGTTGAGAAATGGTATGGGAACCTGGCTCTA
TTTGTAATTACCAAAAAGTTATGGCTTGTGGTAGGCCACAAGGTACAGCGCTCTACAACG
TGTTGAAATTTGCTAACCAATTCGGTGTTCATATGTGCTGATGGTGGTGTTCAAAAC
ATTGGTCATATTATACCAAGCTTTGGCTCTTGGTCTCTTACTGTTATGATGGTGGT
ATGTTGGCCGGTACTACCGAATCACCAGGTA

YAR073W, 403 aa (SEQ ID NO 4)
MAAIRDYKTAALDLTKSLPRPDGLSVQELMDSKIRGGGLAYNDLFLPLGLVDFASSEVSLQT
KLRTNLTNLPVSSPMDVTVESEMAFTMALLDGIIFIHNCCTPEDQADMMVRVKNYENG
FINNPVIVSPTTVGEAKSMKEYGFAGFPVTDGKRNKLVGAITSRDIQFVEDNSLLV
QDVMTKNPVTAAGQITLSEGNELKKIKKGRLLVVDKGNLVSMLSRDTLDMKNQKYLAS
KSANTKLNLWGAISITMDADKERLRLVLKAGLDVVLDSQGNISFQLNLMKIKWETFPD
LEIIAGNVVTKQEAANLIAAGADGLRIGMGTSGISITQKVMACGRPQGTAVYNVCFEPANQ
FGVPGMADGGVQKHWSYFYQSGFSWFFPYCDGMYVGGVRYRITR

FIG. 1 - 1

YBL048W, 812 bp, CDS: 501-812 (SEQ ID NO 5)
GGGAGAAAGCTTATCTTACTGTAGAAGAAAATGGGATTGCGTTACTCCATATATATGAAA
ATCCGTTATCTTCCCCATCATCATCGTATAAAATCAATAAACGACCCCGTTATTTCCACTCTC
AGCATCGATCGCAAAAAAAGCTGAGCTTCAACCTACGGTTGTAGACATTGCAAGACAC
ATCTTTCCGATCTCTTCCGATTATTTCTAGAGATTATAGGGGTAGGACCGGAACTGCTT
ATTTAATGAACAAAGTTGTTAATGTCGTTGAAGGAAAGGTCGAGCAACGAAGAATTTGA
CTGGCGACTACTTAGTCTCTGATATCTTTTGCATTTGGTGCAGAGGAACGTAGGTTGGA
AATACTTCGAGAGCAGCAATGATGATCAGCAGTATAAGGAAGGAAAGTTTATCTTAGAGC
TGAAAAACATTGTGAAATGTACTTGTATGTCCTTCCCTTTGCTGCTATCTAGCAGCTCTGT
CTTTTAGTGCTTTTATAGCGTATGATCTTTTAAAGAACTCGGTCTTTCTTCTCTCTATT
TGATTGGGTATATTTCTATTCTGTTCTTCAATCTAGTCTGGGTAAATGGGTTTGGTATT
GGTCCAGTTGTTTCAAGTAGCCCTTTATTTTTCATGTTGGTATTTTATCTTATCGATT
ATACTTTTTTTTATTCAGAAAGAAATTAACAGATAATCTCTTATGAGCCTAGCTACTTTG
TTTTTCTTACAGGCGCATGCTTATGCGCTCGAACGAGTCTTACTTTACTTTTTTTTGTGA
TTTTCAATAAGTGTGTTTCCCATGTTGTA

YBL048W, 103 aa (SEQ ID NO 6)
MLLFKNLVFLPSILIGYISIRVSLVWVNVWVWSSCFQVAFISFLWYFILSIYTFYFK
KIKQIISYEPSYFVFSYRAIDLCPERVLLYFFCIFNNVFPML

YBL051C, 2507 bp, CDS: 501-2507 (SEQ ID NO 7)
GGGAAATATCAATTCCCGTATTTTCAATGTTAGTAATTTGCCCTTCGTAATATACGGAATCA
CATAGCTTTTCAATTTTGTTCCTTTGATATATTTCCCTTACTTACATCTCTTTTCAATATCT
TACAGGGTCTGACATATTTTAACTTTCAGGTTAATGATGGTGTCTTACTATATATCTCGAG
TCGTACAGAAAGTTAGTTCAGATAAACTGCTTCGGTGCTGCCCACTTCTTATCATTTACTTC
AACTTTTACCTTCCCTTATACCTGTGTGCTTTATTAATTCAGTTAATTCGAGGTAATCAGTA
TTAGGGTAACCTTCAATGATGTCACGAAACACGGATGCTGCAACTTTGCGATTTTTCCT
GGAAAAGAATAACAATTAAGGCGAGCCTTTCAGCTGAGATTACAGCAGGCTTTTGGA
TTAGCGCAAGAAGAAGTGTGATATAGTACTCATAGAGGCGAGGCTACAGACTAGGGAAGC
GTGTTCAACAACAATAAGAAATGGAGAGCAGTTCTTTTGAGAATGCTCCTCTCGAGCCA
TCAATGATGCTCAGGATAATAATAATAACGAGACTAATGACCAGGAAACAAATCAGC
AATCTATCGAACTAGAGATGCAATTGACAAAGAAACCGGTGTGCAACCGGAACTGGTG
AGAACTCTGCAAAAAAATGCCGAACAAACGTTTCTTCTACAAATTTGAATAATGCCCCCA
CCAAATGGTGCCTTTGGACGATGATGTTATCCCAATGCTATTGTTATTAACCAATTCGCT
TGCTATTAAAAAAGGCAATTTGTAGACATTAATGAAGAAATGGATCTTCCCTTCCCTT
ATGCTTCCAATTACCACTTTTGATAACGGTATTTTCAGAGGACTAGCCTTTGCGAATTTGA
CCACTCTCTGAAGAACTACTCAAGTGATAACTTCTTTGAATGGAAGGAAATCAGCGGGA
GGAAATGGAAGTGGAAATATAAAAAAATGCTTCCCAAGCTGAAGGAGAAAGAATCAGCA
GGGAGAAGAGAGGAAAAAGAGGACAATTAGAAGAACAAACAGATCGTCACTTAATCTTT
CTTTGAGATCTTTATCTAAATGAGTGAAGCGGAAACAAATAACTCTTAACAATCAAT
CTTTCTGACTCTAATGAACGGCAATTAATGCTAATAGCATGATGAACAGTCCAATGAATA
ATACACTTAAACAATAACAGTTCTAATAACAAACATAGTGGTAACATCTTCTGAACCAAC
CTTCACTTTCTGCCCAACATACCTCTTCACTGTGTGTAACCAACAAACGTTAATAATCAAG
CCGAGATGTCCACTGAGAGATTTTATGCGCTTTTACCATCAACTCTCCACTTTGCTCTTCC
CAGCCCAACACTGGACTTCAATGACCCTGACACTTTGGAAATTTTATCCCAATTTATGTT
TATTAAAGGATAGAGAAAAGTATTATTACGAGTTGGCTTATCCCATGGGTATATCCGCTT
CCCAACAAGAAATATTCAATGTTTGTGCTCGTACTTAGGGCTAGTAGAAGTATATGATC
CAAGATTATTATTATCAGAGAAGAAAGATTCTGGATCATGCTAATTTACAATCTCATTTGC
AACACAAGGTCAAATGACATCTGCTCATCTTTGAGCCAACTCACTGGCGGGCTCA
TGAATAGGTCAACATCTTATACAAGTTGTTACAGGCCCATGACAGCAGCTGGAGCGAATA
GTATTAGCAATCAGGCGGTTAACAATTTCTTCCACAGCAATACTATTAAACAGTAATAACG
CTAACGGTAACAATGTCATCAATTAATAACAATAGCGCCAGCTCAACACCAAAATTTCTT
CACAGGCAATTTCTCATGCAACCAACACTAACCTCACTAAAATGAACATACACATA
GTTCTCAATACAATTCGCGACACCAACCGCAACAACTCAACCAACACACAGCAAAATG
TTCAGTCAGCTGCGCAACCAACAATCTTTTTTAAGACAACAGCTACTTTAACACCAT

FIG. 1 - 2

CCTCAGAAGATTCCATCCGGTTATTCTGCCAACCATATCAAAATCAATTCCGTTAATCCCTT
TACTGAGAAATTTCTCAAATTTACCTCCAAATTCACAAATCCCAATCAACAGCCAAACCC
TATCCCAAGCGCACACCAGCAGCAGTCCCAAACTCAACAACGGGTACAGTGGCATACC
AAAAATGCTTCAATGTCTTCCAGCAGTTGTACAACTTAAACGGCCCATCTTCAGCAAACT
CAGATGCCCACTGCTTCCACAGCACACAAATGGCTCAGTACATTCTAATTTCTCATATC
AGTCTTACAGATGAGTCCATGTTGTCCGCACACAATTTGAATAGTGCCGACTTGAATCT
ATAAATCTTTGAGTCACTCTGACTAGATGATGGCTTGAACAGGGCTTGAATCGTTCTT
TAAGCGGACTGGATTACAAAACCAACAAGAATCTATGGTAA

YBL051C, 668 aa (SEQ ID NO 8)

METSSFENAPPAINDAQDNNINTEQDQETNQQSIETRAIDKENGVTETGENSAKNA
EQNVSSNTLNNAFTNGALDDVDVIPAIVIKNIPFAIKKEQLLDIEEMDLPLPYAFNYHF
DNGIFRLGLAFANFTTPEETTQVITSLNKEISGRKLKVEYKMLPQAEIRIEREKREKR
GQLEEQRHSSSNLSLDSKMSGSGNNNTSNNQLFSTLMNGINANSMMNSPMNNTINNS
SNNNNNSGNIILNQPSLSAQHTSSSLYQTVNNNQAMSTERFYAPLSTSTLPLPQQDLDF
NDPDTLEIYSQLLLFKDRKYYEYLAYPMGISASHKRIINVLCSYLGLEVVEYDPRFIIIR
RKILDHANLQSHLQQQGMSTSAHPLQPNSTGGSMNRSQSYTSLQAHAAAAAANSINQAV
NNSNSNPTINSNNGNNGNNVIINNNSASSTPKISQQGFQSMQPTLTSPKNIHHSSQYNSA
DQOPQOPQOTQNVQSAAQOQSFRLQOATLTPSSRIPSGYSANHYQINSVNLPLRNSQI
SPPNSQIPINSQTLQAQPPAQSQTORQVPVAYQNASLSQQLYNLNGPSSANSQSQQLLP
QHTNGSVHSNFSYQSYHDESMLSAHLNLSADLIYKLSLSHGLDDGLEQLNRLSLGLDLQ
NQNKKNLW

YBL066C, 3674 bp, CDS: 501-3674 (SEQ ID NO 9)

ATCCCAAGAAGATTAGACTGATTTTACCTACCTCCACCGTCGGAAGAAACACTT
CTGAAGTGTTAAGGGTAATCGAGCCCTTGCATTTGACTGACAAGGAGGGCGTAGTAACCT
CAATTAATTTGGCAGCCAGCTGACGATGTCATTATTCCTCCCTCTGTCTCAATGATGAGG
CGAAGCTCAAAATTTGGTCAATTTAATGAAATTAACCCATTTTAAGATTACCAAGTCGA
AATAAGCTTTGAAATAAACGACTTTACTATATACAGGTATATGAAGTATCTCTCACTAAA
ACTTTATCTATCTTTCACTTCTATTATATCTCATCTCGTACGAAGGGCCGCTCATTTGGA
TCATTTTCTTTTACATACCGTAAAGGAATGGCGTTAAAAATATATATGAAAAATGCATG
TAATAAACTCTCTGCAGAAACCTTAATGTCAAAGTCCCGTATACAGATTATATTGGCTC
TGCATATACGCAATCTCTCGTCACTGGTGAAGGATAATCGAGATTCTGACCAAGACCAAGATT
TTAGTTCTGCTTACATGAAAAGACAAACCGGAGCAACAGTTGCAACAGCACCGACTTCC
CAAGTAAGAAACCAACGAATATCTCACCATGATGACAGTCATCAAAATCAACCATAGACGAC
TTACTCTATGATACACATTGTAGACAGCACAAAATCAAATGCGATCTAGTCAAAATTTCC
CTCATCTCTGCTCCAGATGCGAAAAAATTTGGTCTCCACTGTGAAATCAATCTCTCAATTC
GGCCTAAGAAGGGCTCACAGTTGCAACTACTGAGACAAGATGTGGATGAAATCAAATCTA
AATCGATACTCTTCTGGCCAATGACAGCGTTTTCGTTTCATCTTTTACAAACAGATTCCCA
TGGGCAATAGCCTTTGAATAAGCTCAATCTGCATCCAACTCCAACTCCGGGTACTATTA
TCCCTAACCCAGATCTCTCTCTCTCTCAGGTTCTCCAACCTCTCTCCGCGGCTCAACGAG
ATTCTAAGGTTTCAGTTCAAACCTTATTTGTCCAGGGAAACCCCACTCTTACAAGCAAACT
AGGGCAGCAATACGAATAAATTTAAGCAAAATATGAAGCATCTTCTCACTAGCAGTTGC
CGCATCTCTTTTATGCGCAAGATTGCAAGGCTTGGTTGCAACAGAGCAAAATGAAGCTGC
CCCCGTGCTTAATGACTCAGCATTTGCCATAATTAACAAAGAACTTTTCACTCTGCTGT
TGCAAAATGGCTTTTATAAGAACAACCTCTGCAGTAACTCGAACGACCCCTTCTCTC
CAATTCAAAAAACATTTCCCTCTACTACTGCTCGACCCCGTTACACGCAACCAAACT
AACCAACCTTTGCAGCAACCAAGCCACGTAGCAACAAATAAATGCAGATAGGCGAAGA
CGCCGGTAGTAGGCCACCACCAGACTATGCCATTATTGCGCTTCGCGCATGCAATGTAG
ATGAGTTTGTGATGGGCGATATTAGTATTTCCATTGAAAAGCGAATAGATTACCCATA
TTTTCGTGACTAGGTATCTGCGGTATTTTCCTATTATGTATCTCAATAGCCACCGGAAT
TATACTCCCAATCTCAGTTGCTTTTCTGGACCGGTATGTGACGGCATGTCTGTCTGATC
CTGAACGACGATGTATTGCAAGCTTAAGCTCTTTGATCAAGCAACTTGCCATAGAGACCT
GCTGGATAAGAACACCTAGATCCACACATATTTGCGAAGCTTTGTTAATATTGTGCATTT
GGCTTTGCTCAACCAAAAAGTCTAGATGATTGTTCTACCGTTTGTAGGATTAGCAA
AGTCACTGCTCTTATCAATAGGTTTGCACAGAGGTGAATTCATTTCTGAAATTCACAAGAA
CTCAAAACCTCAATGGCAAAATGCAGAAAAAGTGGAGAACTAGGACTTGGCTGGGAATATTTT
TTGCCGAACCTTTGTTGGGCGAGTATCCTTGGTTTGGCCACCAACTTCACAGACAGACTATT

FIG. 1 - 3

TATTAGAAAAAGCCTTATCTCTGGTGACGAAGAATCAGAAGAAGATAACAATGACAGTA
 TTGACAAATTAACCAATGATATAAGGAACAGAAGAAGACGACGCCAGCTTGAAGATAAT
 ACAAACTACCGGGCAGTTTATAGAAGATGTCTCAGCTGGCGAATTTCCAAGCAAAATTTGT
 CTCATATCATTTGGTTCTTCCACTTCCAGTCTGATGGTTTATTTGGAACCAAAGTATCTGTG
 CTGAGACACTGTCCATCTTGGGAAAAGAGTTAGATTTATTAGCAAAAACCTTTAAATTTCC
 AGAGTGACGATACGTGCAACATTTATTTCTTTATGTTAAATTAAGTGTCTGTGTTTGTG
 CATCTCTACCCGAAACACCTCTTACCAGTCAAAATCCCATATGTCCAGAGGCCATCTAA
 CAGCTACTAAAAATGTGCACTCTATGTAATATCTTTAGAAAACACCAATTAATTTGAAC
 TGCTTATTTATATTAGACAAGCTGCTACATTTCTGCAGCTGATTTCTCTTTAAATTCGAGT
 TGACTCCCTTACTTCTCTGACAAATATTTTGATTGACCAAGGCAATCCGTTGCTACATCC
 ATAGACTTTATAGAAATCAGTTAACTGCGTGGGCGCACTAGTGTGAGAATGATATTTGCA
 GAACGTCAAGTATGTTAGAAAACTGAACTTCGTACTGATCATGTCAATCAGAAAGTTTGTG
 TGGAAAGCAAGCGGATATTTCTTAGGATGAGATCACAATTAAACAGGCTCTCTATTTCTATG
 ATTTGGTTTGTGTGTTTACGAGGCGAGAAGAAGGAAATGGATCCCGAATATAACAAGC
 AAGCCTTAGAAAAAGCCGCTAAGAAAAAGAAAATTTTCTCAAATGGTATCTCAATGGCA
 CTTCGTCTACGGGTGGCATAACGGACAGAAAACTATATCCATTGCCACTATATAACCTATA
 TCTCCAGAGATGACTTTGAACTGTAACAAAAACAACCAAGTGGAAACCACTGTTTACCA
 CTTTATGTTCTTACTAAGAATGCTTAAAGCAGGACAGAAAAGCTAGCCAAGATAAATACG
 GAGATTTCTGACGGTTCTATAATGGAGATTAAACGGGATACCTCTTTCCATGCTCTGGGGAAA
 CAGGACGCGTAAAATTTCAAAGTTTATTCGCTAATACCTCGAATAGTACGATTATATA
 ATAAATAGGACGCTTATTTGGATCGGTCTAATGACATATCAATTCCTCTTAATTCAATTTATC
 CAGTGGCTTCTGTCCCGCTTCGAATAACAATCCACAAAGTACTAAGGTAGACTATTTATA
 GTAACGGACCTAGTGTAATTTCTGATCTCTCCATGAAAAGATCAGTAAGCACTCCCGTTA
 ATCATATTTCTCGGTCCTGTTCCAGGGTTAAGGAACACCCCGTTGGCAACTTCTATTAATA
 ATGTTACATTGCGGAATAGACCACCTTATCCAAAGGAGCACAGTAATTTACAAAATGTCA
 CCAATGAATTATAAATCAATTCAGCAACGCCAACCGGATTTGGAAGATCACAAGGTAGTA
 TGTCCCATTCACGTACACCTTTGTTTTCGGTCAATATATGACAGTTGGATTCCGCGTCGA
 CCCCAGTCTCTAA

YBL066C, 1057 aa (SEQ ID NO 10)

MYKNDNRSDQDQDFSSAHMKRQPEQQQLQHQFSPKKQRISHHDDSHQINHRPVTSCTHC
 RQHKIKCDASQNFPHPCSRCEKILGLHCEINFPQRPKKGSQLQLLRQDVDEIKSKLDTLA
 NDSVFVHLLQIIPMGNSLLNLKLNHPTPTPTGTIIIPNPDSSPSSGSPSSAAQDRSKVSQ
 TYLSREPOLQLQANQGSNTNFKKANNEASSHMTLRASSLAQDSKGLVATEPNKLPLLLNDS
 ALPNNSKESLPPALQMAFYKNNSAGNTPNGPFSPIQKTYSPHTTSTTVTTTNNQPPFAAT
 SHVATMNNADRTKTPVVATTTTMTPLLPSPHANVDEFVLGDISISIEKANRLHHIFVTRYL
 PYFFPIMYSNNATELYSQSOLLFWTVMLTACLSDPEPTMYCKLSSILKQLAIECTWIRTFR
 STHISQALLLCIWLPLPNQKVLDDCSYRFVGLAKSLSYQLGLHRGEFISEPTRTQTSMEFN
 AEKWRTRTWLGIFFAELCWASILGLPPTSQTDVLLLEKALSCGDEESEDNNDSIDNNND
 KRKKKDEPHVESKYKLPGRFRLLSLANFQAKLSHIGSSSTSSPDGLLEPKYRAETLSIL
 GKELDLAKTLNLFQSDDTVNTYFLYVKLTVCCFAFLPFPPTDQIPYVTEAYLTKATKIVT
 LLNNLLETHQLIELPTYIRQAATFSALILFKLQLTPLLPDKYFDSARQSVVTHRLYRNQ
 LLAATWSVENDISRTASMLEKLNFLVLMHPEVFVEEDGISIRMSRSLHTGSLFYLDVVCVH
 EARREMDPEYNQALEKAARKKRFSSNGLYNGTSSTGGTIDRKLYPEPLVYNIHSRDQVE
 TVTKTTPSGTPTVTVLVPKNAKQAEKLAKTNNGSDSGSIMEINGIPLSMLGETGSVKFQ
 FLANTSNSNDYNNRNLRLDASNDISIPNSNYPVASVPSNNNPQSTKVVDYVSNQPSV
 PDLMSKRVSPTVMNHFPASVPLRNHFEVGNLSNNVTLGIDHPIPREHSNLQNVTMNYYNQ
 FSNANATIRGSQSSMSHRTPLFRSIIYDSWIPRPTVPL

YBL078C, 854 bp, CDS: 501-854 (SEQ ID NO 11)

TAGTGGAGTACGAATAGTTAAAGATACTATCGACTTTGAAGCCATTGTCAAAGAACATT
 TGATATGTTAAGCAAGACCTGTAGATCCGACATTGCCAAATATGACGGCTCAAAGACAG
 ACCCAATTTGGTGATGAAGAACAATCTATTAATGACACCAATTTCAAATTTAAAGGTGTTC
 AATTATGAAACAACATCATATAAATACGTACAAATTTTCTCTCAAGTGTATAGATGATG
 TGATATGTGTAGTATTACGTTTAAGTTAGAGTCATGTAATGCTAATCTCTCCACCGAT
 AATGTTGTATAAATCCCGTGAATCATAGCACATGATATATCATCACCGGAGCGCGGTT
 ATTTTCGCGCGCGGCAAAAATATTTGGTATAAATTAGGAAATACAAAAGGGGAACCAAT
 AAAGGTTGAGGAGGGGATTGATAAGAGAATCTAATAATGTAAAGTTGAGAAAATCATAA

FIG. 1 - 4

TAAAAATAATTACTAGAGACATGAAGTCTACATTTAAGTCTGAATATCCATTTTGAAAAA
 GGAAAGCGGAGTCGGAGAGGATTGCTGACAGGTTCAAGAATAGGATACCTGTGATTTCGG
 AAAAAGCTGAAAAGTCAGATATTCAGAGATTGATAAGCGTAAATATCTAGTTCCCTGCTG
 ACCCTACCGTAGGGCAATTTGTTTATGTTATAAGAAAGAGAATTATGCTACCCCTCGAGA
 AGGCGATCTTCATTTTGTCAATGATACTTTGCCACCTACTCGGCGTTGATGTCTGCCA
 TATATCAAGAACACAAGGATAAGGACGGGTTTTTGTATGTCACCTACTCAGGAGAAAAATA
 CATTTCGAGGTAG

YBL078C, 117 aa (SEQ ID NO 12)
 MKSTFKSEYFPEKKAESEIRIDRFKNRIPVCEKAESKDPEIDKRYLVPADLTVGGF
 VVIRKIRMLPPEKAIFIVNDTLPTTAAALMSAIYQEHKDKGFLYVTVYSGENTFGR

YBR072W, 1145 bp, CDS: 501-1145 (SEQ ID NO 13)
 GCAGCAGCAACTCCGTGTGTACCCCTAACTCCGTGTGTACCCCTAAAGAACCTTGCCTGT
 CAAGTGCATTGTGTGATCGGAATAGTAACCGTCTTTACATGAACATCCAAACCAACGA
 AAGTGCCTTTTTCAAGCATTCGCTTGATTTCTAGAAAGATCGATGCTTATTCCTCCCCCTT
 ATGCTGTCAAAAATATAGGGTGCTCGTAACAGTAAGGTATTCGCACCTAGCGTGCTCGCA
 ACACAAAATTAAGTAAATATGCGAGTTTGTAGATGCTCTCGGATCATGTACAGCTTCTTGA
 GTGGTATTTCTATAACACACGGTTCTTTTACACCTTATTCTTAAACATATAATAGGACCT
 CCATTAGTTAGAGATCTGTTTTTAATCCATTACCTTTCAITCTACTCTCTTTATACTAAT
 AAAACCCCGATAAAGATATATCAGATCTCTATTAAACAGGTATCCAAAAAAGCAACAA
 AACAACTAAACAAAATTAACATGTCAATTAAACAGTCCATTTTTGATTCTTTTGACAACA
 CCAACAACGAAAGTTGATGCTCTTAAACAGATTGCTGGGTGAAGCGCGCTTAAGAGGGCTACG
 ACCAAGACGCTCAGTTAGCAAAACACCCCGCAAGGATTCTACTGGCAAGGAAGTTGCTA
 GACCAAAATACTATGCTGCGCTCTTTATGATCCAGAGATGAAACCTTAGATGATTGGT
 TCGACAATGACTTGTCCCTGTTCCCATCTGGTTTCGTTTCCCTAGAAAGTGTGCGAGTCA
 CAGTTGATATTTTGGACCATGACAACAACACTACGAGTTGAAAGTCGTGGTTTCTCGTGTCA
 AAAGCAAGAGGACATTGATATTGAGTACCATCAAAACAAAGAACCAAAATTTTGGTTTCTGT
 GTGAAATTCATCTACCTTGAATGAAGAGAGTAAGACAAAGGTCAAGGTCAAGGAGAGCA
 GCTCTGGTAAAGTTCAAGAGAGTCACTCACTTTGCCAGACTACCCAGGTGTGATGTCAGACA
 ACATTAAGACGACTACGCAAAATGGTGTTTTGACATTAACAGTTCCAAAATTTGAAGCCTC
 AGAAGGATGGTAAAGAACCCAGTCAAGAAGATTGAGGTTTCTTCTCAAGAAGTTGCGGGGTA
 ACTAA

YBR072W, 214 aa (SEQ ID NO 14)
 MSFNPFDFDFDINNEVDFAFNRLLEGGLRGYAPRRQLANTPAKIDSTGKEVARPNNYAG
 ALYDPRDETLDWFNDLFLPSFGFPRFVAVPVDILDHDNNYELKVUVVPGVSKKID
 IEYHQNKNQLLVSGEIPSTLNEESKDKVKVKESSGKPKRVITLDPYDGVADNIKADYA
 NGVLTITLVPKLPQKDGKNHVKKIEVSSQESWGN

YBR073W, 3377 bp, CDS: 501-3377 (SEQ ID NO 15)
 AGAAGGATGGTAAAGAACCGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA
 ACTAAAGTGACCTCGCTCTATAGTGTGTTCCCTCTCGCGAGGACCATTTGTTGCTTGCATA
 TGGCTTGAACATATGTCTATCAGTCTGAGCGATTTTACCTCTTAGAATATGTTTAGATA
 TATATGAGTTGATGAATAAATAGTTATATAAAACCTTGCTTTGGCTTCGATATATGACCGTT
 ATTTTGTACTAAGTTTTAACGAAGGAATCTAACCTCGTCTTGTGAATATACCAAAATCTTC
 AACACGCGCTGTGTGAGGTATCTCTATGGATGTGGCTTGAATATGGATGTCTTGCTCTA
 CTCTACTTCTGGGAAAGGCATTTTACTCGATCGCGTTAATATATGCATCAAGAAAAATA
 AAAAATAAAGCGGAAGAGCTAAAAAAGAAAAAGAAACCTACTATAAATAACCGGATTAG
 AATCGAGTTTGTGATTGAAATGGCGGTAAATAGCGGTAAACCTCGACGAGAGAGAAGA
 TCCCTAAGGAGGTAAAAAACAGCTCGGTATATCAACCGGTATTGATTCCCGGTACTACTC
 AAATCGCATATACGAAATATGAGAACAAGCCATTCAAGCCTCCAAGAAAGGTTGGATCAA
 ATAAGTACACACAACCTCAAAACCAACCGCCACTGCAGTCAACACAGCCCTATATCTAAAG
 CCAAGTTACTGTCAACTTGAAGAAAGAGCATTTTCGGCGGGACCTACTTTAAATCTTGCCA
 AGAAGCCGAATAATCTGTCTCAAAATGAAACACTAGATATTTTACTATCACTGTACAGGA
 AGCTACTACCAAAAAGCACAAGACTTGGAGTGGTGTGCTGACGCTACCTTTAAAGGCCA
 GTAGCGATAAGTTATGCTTTTATAACGAAGCAGGGAATTTCTTGGGTCAAGTATGCTAC
 CAAGTGATTACGATTCTCTCTCGAAACTCTTTTCAAGCAGGCTCCAATGAAGTACAAT

FIG. 1 - 5

TGGATTACGAATTGAAGGAAAATGCAGAAATACGTAGCGCCAAAGAAGCCTTATCACAAA
 ACATGGGAAATCCCAGCCCACCGACCACAAGCACACAGAAACAGTGCCTTCTACGAGA
 ATGACGGTGGCAAAATACCAAAATGCCTCTGTCTCAGCTGTTTTCACTAAACAGCTGAAAA
 GATTCAAATCAGTAACAAAGCAAAACAAATGACACATGACCACAGTACTTAAACACGATC
 AAAATTCCAAAGCCAAAAAATATTATCCAGTATTTGATGTCAACAAATCGATAATCTTA
 TAGTAATGCAACAAAAATGCAGCGCTGAAGTTGACGTAAATGTTGATCCATTACTGGGCA
 AATTCTTCGCGCCTCATCAGAGGGAAGGGGTGAAGTTTCAATGATATGCTTAATGGGCT
 TGGCAAGACCAACTATTGAAAATCCGATATCGAATGTACTACTAAAAGTTTAGTGTTAG
 AAAATGACTCAGATATTAGTGGATGCCCTTTTGGCTGATGATATGGGTTTAGGTAAAAAC
 TAATGAGTATAACTTTGATTTGGACATTAATTAGGCAAACTCCTTTTGCATCAAAAGTTT
 CATGTTTCGCAATCAGGCATACCAATTAACGGACTTTGTAAGAAGATTTTAGTCGTTTGTG
 CCGTTACTTTTAATAGGAAATTTGGAAAAGAGAATTTGGAAAAATGGTTAAATTTTGTCAAG
 TAGGTTGTTTGACATTAAGCTCAAGGAATTTCTCCTGATATGGATAAAATGCGTGTCAAG
 ATTTTGTAAAAGTGCACGAACTTATCAAGTCTTGATTTAGTGGCTACGAAAAAATCTTTGA
 GTGTTTCTGAAGAATTAGAGAAAAATAAACATTTGATTGACATGCTGGTGTGTGACGAAG
 GCCATCGACTAAAAACGGGGCTTCTAAAAATTTTAAATACGCTGAAGAGTTTAGACATAA
 GAAGGAAGCTTTTGCTTACGGGAACCTCTATACAAAAATGATCTTAATGAGTTTCTACTA
 TTATGACTTTTATAAACCCAGGAATCCTTGGAAAGCTTCGCTTCTTTCAAAAAGAAGATTCA
 TTTCCCTATAACTAGAGCCAGAGACACTGCAAACAGATACAAACGAAATTTGTGGAA
 AGGGGAAGAAAGGTTCAAAAGAGATGATAGAAATTACGAAAAGATTTTATTGAGACGAA
 CAAATCGATTTTAGAAAAAGTACCTTCTCCCAAGACGGATATAATTTTATCTGTAAAC
 CATACAGCCAACAGATATTGGCAATTCAAAGATATTTTGCAGGGCGACGTTTAGATTTTG
 GACAAATTGACGTTTCAAGTTCTTCTCGTAGGACTAATAACATTACTGAAAAGGTTTGTAACT
 CTCTCGGATTTGTTGGCTCAGATCCCATTACAAATTCACATATAAAGGATACCAAACTCT
 AGGACAGCTATAGTCTGTTCTTTGAACTCTGGTAAAGTTAAAGGTATTAATGACATTACTAG
 AAGGTATTAGGAAGGGTACCAAGGAGAAGGTGCGTGTAGTGTCTAACTACACTCAACAT
 TGGATATAATTGAAAAATTGATGAATATGGCTGGATTCACATTCGAGACTCGACGGTT
 CCATACCTGCTAAACAAAGGGACTCTATCGTCACATCTTTCAATCGGAATCCAGCCATAT
 TTGGAATCTTGTGTTAGTGCAAAAAATCGGGAGGTGTAGGATTTGAATCTAGTCGGTGTGCG
 GACTTATTTTATTTGATAATGATTGGAATCCTTCAGTAGATTGTCAAGCGATGTCACGAA
 TTCATAGAGATGGTCAAAAAAAGCCGTGCTTCATATAGACTTGTCACAACTGGGTGTA
 TCGATGAGAAAAATATTCGAAAAGGCAATTAATGAAGAACAGTTTGAGCCAAAAATTTCTAG
 GTGACTCGGAGATGAGAAATAAAGAACTTCTTAATGATGATCTTTTCAATAAAGAGGACT
 TGAAGGACCTGTTTCTGTCCATACAGATACCAAGAGTAACACACATGACTTAATTTGTT
 CTTGCGATGGTTTAGGTGAGGAAATGAATATCCTGAAACAAATCAACAGCAGAACACCG
 TAGAGCTGAGAAAGCGTAGCACTACGACATGGACAAGTGCCTGGATTTTCAAAAAGAAAA
 TGAATGAAGCAGCCACCAACGATGATGCCAAAAAGTCACAAATACATTAGGCAAAATGCTCG
 TTCATTATTAAGCATATCGATCCAGCAAGACAAGATGAATATTTGATGAGGTTATACAG
 ATTCTGTTTACCGAAATTGAAAGATAGTATTACCTTTGCGTTTGTAAAGCCCGCAGATAT
 GTCTCAGAGAACAAATGA

YBR073W, 958 aa (SEQ ID NO 16)

MAVISVKPRRREKILQEVKNSSVQTVFDSGTTQMQLPKYENKPKFPRRVGSNKYQTLK
 PTATAVTTAPIISKAKVTNLRKRSISAGPTLNLAKFPNNLSSNENTRYPTIMYRKPTTKKH
 KTWSDGYATLKAASDKLKFYNEAGKFLGSSMLPSDSLSLETFLKAGSNVQQLDYELKE
 NAEIRSKEALSQMNGNPSPTTSTTETVPSKNDGGKYQMLPSQLFSLNTPKRFKSVTK
 QTNHMTTVPKTSQNSKAKKYYPVFVNVKIDNPIMVKNAAAEEVDVIVDPLLGKFLRPHQ
 REGVFMFTCLMLARPTIENPDIDCTTKSLVLENDSDISGCLLADDMHGLKDTLMSITLI
 WTLIRQTFPASKVSCSQSIGIPLTGLCKKILVVCPTVLIGNWKREFGKWLNLRSITGLVTL
 SRNSPDMKMAVRNFKVQRTYQVLIIGYEKLLSVSEELKKNHILDMLVCDDEGHLKNG
 ASKILNTLSKSLDIRKLLLTGTPIONDLNEFFTIIIDFINPGILGFSFASKRFFIIPITRA
 DRFANRYNEELKEGEERSKEMIEITKRFILRRNTALKEKYLPPKTDIIILFCPKYSQIIL
 AFDKILQGARLDFGQLTFSSSLGLITLLKKVCNSPGLVGSDDPYKSHIKDTQSQDSYSRS
 LNSGKLKVLMTLLEGIRKGTKEKVVVSNYNTQLDIIENLMNMGMSHCRLDGSIAPAKQ
 DSIPTVFNNRPAIFGFLLSAKSGGVGNLVGRSRLILFDNWNPSVDLQAMSRIRHDSQK
 KCVFIYRLVTTGCIDEKILQRLMKNSLSQKFLGDSSEMRNKESSNDLKNFKEDLKDLSF
 HTDTKSNTHDLICSDGLGEEIEYPETNQOQNTVELRKSTTTWTSAALDLQKKMNEAATN
 DDAKKSQYIRQLVHYKHIDPARQDELFDVITDSFTELKDSITAFVKRGEICLREQ

FIG. 1 - 6

YBR086C, 3341 bp, CDS: 501-3341 (SEQ ID NO 17)

AGATCCTTAAACAGCAGCAAGCATATTATTGCGCATATAATTGTCCTTGTAGGACTCTTTTC
 TTGACATTTTTCCTACCTCTGCGAGAACTTCTCTTTTTCCTTCTAGGGACGAAAA
 CAACCAAGGGCCTTTTTCCTATCTTTTTCCTCTGTGTGTTTTCAAAACCAAAAGAT
 TCCACCACCTACATCAGTGTGAAGAGCTGTAAAGCTTCTGTATAAATAGCACTTTCCAT
 ATTTTTCACATGAAAAATAGTTTCTTTTTCGAGCTATTATTGACTTCAATTAGAAATAT
 CCCTTTTTCCCGGTGCAATATTTCCTATTAAGGGAAGCTGGAATAGGGGGCTGGAAA
 GATATTTGAACAGCTCGCTCCAATAACCGTTCTCACCATCAATTAACATTTTGAAGGTGAA
 TACTGTTTCGGTCTGATTTATGGCTAATTGTCAAATACATTTGAAAAAGATTAAACAAAG
 CAGACCGGTTGAGCATACTATGTGCGAGCAATTACATCTTAGATCCGAATTGTTGTA
 TTGTATTCAATAAAACCTTCGAGTGCAAACGAGAAGAGTTTGAATGTCGAATTCAAACGTT
 TGAATATACATTTCTATTATCGAACCTTGCCCATGATCTGCAAAACAGCTATGCGTTTATTA
 GAATCCATCAGGATAATGCGAAACCGCTTTTTCATTTTTCGAGAATCTGGACTTCATTG
 AATCCATCATACCATATCATGATCTGAAATTGTCGATGATTGTCATAAACCTGATTTCTTA
 TCAGCAAAATCAAAAATCTGAGGCTCCAAAACAGTATGAGTTGTACAACCTATCGAATT
 TGACCAATAATCCCAACAATCCTTATATTTTGCAATCTTACAGAACTATATAAAATGGT
 TGACTTCCCTCTCTCTTTTGGATTATCAATTAGATTTTATCTAATTTTACGTATGAAT
 TCAATTTCCACATCATCTCGCTGTTCGCCATCCTATGGACATTGTCATTTCACAGCCTTTTGGC
 TTTATAGATAAGAACCATTTTGGTCTGATAGACTGAGTAAATACTCATCATTTTTCAGCA
 TTGAGTTTCTTCAAGATAAACAGAAAGCCAAAAAAGCTAGTTGCGGTTATCATGTTGGA
 AGAAATGTTGTTTATTCTCTGTTGTTGTTGCGCAATATTACTATCATCTTCCAGC
 TATATTGTTTTCGCTTGGAAATTTTCTACAAGCAAAATTTATAACGGCCCAATGATTTCCA
 TCTTGTCTTTTTCCTTACTACTATTATTGCAAGTTTACTCCGGTTTAACTGTTGATTT
 ACAACAAATATTTTCGTAGAACCAATGACAAAGTGGGAAAATCTATGACAGTGTGTGAAT
 CAAAGAAATCTAAAGAGCTAAGAACTTGTATTATTTTTCTATCCAGTACGTTCCCTC
 TATTATTTACATATTTCCTTATCTGCGCAATGGGCAATTTGTGACCGCAGAAATTAAGAA
 CTAAGGTTTTCATAGCTCTTTCATATTGGCCCGTTTACCTACCCATGATTCAGATTTTA
 TTATTGATCAAAAGCGCTATGAAGATCAATTTTCTGATCTTATTGTTTATCAACCACTGA
 TTCATTTTACATGGAAGAACTTGTTCGAAGCTTGTGTAGCATTGCTCAGCAGAAAAATTA
 ATGGACCAAAATCCTTAACCTTGTCAAAGCTGAGAGTGAAATCGGTAAAGCTCAACTCAGCT
 CATCAGATATGAAAAATTTGGTCAAAGGTTAAGTCGTACCAACAGACCCCTGGGGAGCAA
 CATTTGATTTGGACGCCAACTTCAAAAAGCTTCTCTCAAAATTCGGGTATCTTGTATTGT
 TTTCTACAAATTTGGCCACTAGCTCCATTTATCTGTTTGTAGATCAATTTGATTGTTTACC
 AAGTCGATTTGAGGAAAGCTGTGCTTTTATAGTAAACCTGAGTATTTTCCATTTGAACTCT
 ACGTAAAGCCATCCTCTGTGCTAATACCCAAAACCTGACGGTTGGTCTATGGAACCTGT
 TCTTAGTTATGTTTCCATCTTAGGTTGTGTTATCACTGCTACTTTGACCTATATGTAGC
 AGAGCTGTAAATATACAGGTTGTGCGCGCTCATACTTCCATCCATACGAATAAAGCTTGGT
 ACCTTAGCAAAATCCAATAAACCACTCGTGGATAAAATATTGACTATATGCTGTTTATTG
 AGCATGTTAGTGTGTCTATTTTCTCTCTCTAGTATTTTGAATCTTCCCATGATG
 ACGTTGCAAAATGGCATTTGTCCAAAGCATGTAGTTAACGTGCAAAACCCCAAAACAAAG
 AAGTCTTTGAAAAAATTCCTCCCTGAAATTTAATTCGAATAACGAAAAAGAACTAGTTTC
 AAAGAAAAGGGTCTGCGAATGAGAAGTTGCAACAAAGAACTCGGTGAGAAACAGCTGCCT
 TCTCTGCCAATGATATGAGGCACATGCTGCCACTCATGCCAACATGATCGCTCTCTCT
 TATCTCAGCTCTCTCGCTTCAATTATCTTCTCTCTTCTAGCAGCAAAACCGGTGTAG
 TCAAAAGCTGTGATAACGATACAGCGGATCTGCTGGTAAAAAGCCATTTGGCCACAGAAA
 GTACTGAAAAAAGAAATTTCTTGTGTGAAGGTGCTACCGTTCATATGTTGTGTTGCGG
 GCGCCACTTTACCAGAAACAAATTTCAACATCTAAAAATTAATACTACTTAAGGTTTGTAGG
 ACGGTAAATCCATTAGGGATGCGAAATCCAGTCAGAACTTCCAAAGCCCAATAACA
 ACACCTTAGGCACGGAAAGTAAGCTTTTGGCAGATGGTGACGCGTTGATGCACTTAAGTA
 GAAAAATTTGATCAAAATACCAAAATTTGCTGTACTGTTGGCGAAAATACGAAAAATCCC
 AGCCCAAGAGCATGCTGCCACTTAAGACTCCACTTCAATTAAGATGCAAAATTTAAGCCTG
 TTGTCAACGCAAGCTGTTTACGATAACCAATCGAAGGTTTTCAGTGGCTACTGAACAAACAA
 AAAAGACTGAAATGAAGCAGAAAAATGGCCCATCAAGATCTATTTCCAGGAAGAACTA
 AGGATTTCTGCGAGACCATCTAATAACAATCTACTACTACTACTACTACAGATGCTACTC
 AGCCCAACCTCATCTATCACCACACCGCCATCGTGATGCTGAGGTGAAGAAATGTCACGA
 ACAATTTCAAGCAACCGAATCCTCTCTCTCTTCACTCGCGCGGCAAGGAAAAACCAAAAC
 ATAAAAAGGGGCTATTGCATAAGCTGAAAAAGAACTTTAA

FIG. 1 - 7

YBR086C, 946 aa (SEQ ID NO 18)
 MSQTTITSLDPNCVIVFNKTSSEANEKSLNVEFKRLNIHSIIIEPGHDLQTSYAFIRIHQDNA
 KPLFSPFLQNLDFIESIIIPVHDTLESDDLHLKILISISKSKILEAPKQYELVNLNLTNNPKQ
 SLYPAFLQNYIKWLIPFSFFGLSIRFLSNFTYEFNSTYSLFAILLWLSFTAFWLKYKEPF
 WSDRLSKYSSFTSTIEFLQDKQKAQKASSVIMLKKCCFIPVALLFGAILLSFLQLYCFAL
 IFYKQIYNGPMISLSLFLPTILICTFTFPVLTVIYNKYFVEPMTKWENHSSVVNAKKSKEA
 KNFVIIIFLSSVVPLLITLFLVPMGHLLTAERITKVFNAFSILARLPTHDSDFIIDTKRY
 EDQFPYFVIVINLIQFSMENFVPSLVLSIAQOKKINGPNPNFVKAESIEIGKAQLSSSDMKIW
 SKVKSQYQDPWCAFTDLNANFKLLQLQGYLVMFSTIWPAPFICLVNLIVYQVDLRKA
 VLYSKPEYFPPFIYDKPSSVSNTQKLVGLWNSVLVMSILGCVITATLTYMYQSCNIPG
 VGHATSITHNKAWLANPINHSWINIVLYAVFIEHVSVAIFLFFSSILKSSHDVANGIV
 PKHVNVQNPFPKQEVFEKIPSEFNSNNEKELVQRKGSANEKLHQELGEKQPASSANGYE
 AHAATHANNNDPSSLSASSSSPSLSSSSSSSKTGTVKAVDNDTAGSAGKKPLATESTEKRN
 LVKVPITGSGYGVAGATLPETIPTSKNYLRFDEDGKSIDAKSSAESNATNNNTLGTES
 KLLPDGDAVDALSRKIDQIKPIAVTGGENNENTQAKDDAATKPLIKDANIKPVVNAAVN
 DNQSKVSVATEQTKTEVSTKNGFSRSISTKETKDSARPSNNNTTTTTTDTATQPHHHHH
 HHRHRDAGVKNVNTNNSKTTESSSSSSAAKEKPKHKHGLLHLKLLKKL

YBR093C, 1904 bp, CDS: 501-1904 (SEQ ID NO 19)
 ACGTATTTGGAGGTCATCTTATGTGCGCTGCTTTAATGTTTCTCATGTAAGCGGACGTC
 GCTCTATAAACCTTCAACGAAGGTAAAGGTCATAGCGCTTTTCTTCTCTGCAACAAG
 AATATATATTAAATTAGCACGTTTTCGCATAGAACGCACTGCAACAATGCCAAAAAAG
 TAAAAGTGATTAAAAGAGTTAATTGAATAGGCCAATCTCTAAATGAATCGATACAACCTTG
 GCATCTACACAGTGGGACATGACAGACTAAATTTATGATCTTGGTCCCTGTTTTCGAAGA
 CATGCGCACTGCCAAATATCAAAATTGGTCACCTTACTTGGCAAGGCATATACCCATTGT
 GGATAGAAGGTAAACACTTTTGAATTGTGCAAAATGAAACGTATATAAGCGCTGATGTTTGG
 CTAAGTCGAGGTAGTATGGCTTCATCTCATGAGAATAAGAACCAACAACAAATAGAGC
 AAGCAAAATTCAGATTTACCAATGTTTAAATCTGTGTGTTTATTCAATTTTACGCGCTCTCT
 TGGCCAAATGCAAGTACCATTCCCTTAGGCACAACTAGCCGATGTCGACAAAGATTGGTACCC
 AAAAAGATATCTTCCACTTTTGGGTGGTCCCGGACCACTACTACTCTTCTTCCCTGGCGACT
 ATGGTATTCTCTCGTGATTTCGCTGAAGTTGTGAAATGAAGCAACTGCAAAATGTTGGTA
 GACATGGTGAAAGATACCCCTACTGTGAGTCTGGCTAAGACTATCAAGAGTACATGGTATA
 AGTTGAGCAATTACACTCGTCAATTCAACGGCTCATTTGTCTTCTTGAACGATGATTACG
 AGTTTTCATCCGTGATGACGATGATTGGAAATGGAACCACTTTTGCCAACTCGGACG
 ATGTTTGAACCCATACACTGGTGAAATGAACGCCAAGAGACATGCTCGTGACTTTCTGG
 CTCATACGGTTACATGGTCGAAACCAACCACTTTTCGCGCTTTTACCTCTAATTTCTTA
 AGAGATGTCATGACACTGCTCAATATTTTCAATGATGGTTTAGGTGACCAATCAACATCA
 CCTTGACAGCTGTCACTGAAGCTGAATCCCGTGGTGCCAACTTTGAGTGTCTGTAATCT
 CATGCTGTCTTGGGACTACGATGCCAATGATGACATTTGAATGAATGACACCAACCT
 ACTTGGATGACATTTGCCAAGAGATTGAACAAGGAAACCAAGGGTTTGAACTTGACCTCAA
 CTGACGCTAGTACTTTTATCTCTCGTGGTGTGCAATTTGAAGTGAACGCTAAAGTTTACAGTG
 ATGCTGTGATATTTTACCACAGGATGAATTAGTCCATTACTCTCTACTACCAAGACTTGC
 ACATTTATTACCTGAGGGTCCAGGTTACGACATTATCAAGTCTGTCCGTTTCCAATTTGT
 TCAATGCTCTAGTCAAAATTTATAAGCAAGAGTGAATCAAGACCAAAAGTTTGGTTGTA
 GTTTTACCACGATACCGATATCTTAACTTTTGACCAACGCTGGTATAGATTGACAGCA
 AAAACAACCTTAACCTGCCAATACGTTCCATTATGCGGCAACACTTTCCAGACATCTCGGT
 ACGTCTCTCAAGGTGCTCGTGTCTACAGCGAAAAATTTCAATTTCTTAACGACACCTTACG
 TCAGATACGTCATTAACGATGCTGTTGTTTCAATTTGAACCTGTCTTCACTGCTCCAGGT
 TCTCTTGTGAAATCAATGACTTCTACGACTATGCTGAAAGAGAGTAGGCCGCTACTGACT
 TCTTAAAGGCTGTGAACGTCAGCAGCGTCAAGTCTACTGAATTTGACCTTCTACTGGG
 ACTGGAACACTACTCATTTACAACGCCAGTCTATTGAGACAAATG

YBR093C, 467 aa (SEQ ID NO 20)
 MFKSVVYSILAAASLANAGTIPLGLADVDKIQTKDIFFLGGAGFYFSPFGDYGISRD
 LPEGCEMQLQMGVGRHGERYPVSLAKTIKSTWYKLSNVTQFNGSLSLNDDYEFFIRDD
 DDLEMETTFANSDVLNFPVTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNSKRCHDTA
 QYFIDGLGDQFNITLQTVSEASAGANTLSACNSCPAWDYDANDDINVEYDITLDDIAK
 RLNKENKGLNLTSTDASTLFSWCAFEVNAKGYSDVCDIFTKDELVHYSYQDLHTYHYHG

FIG. 1 - 8

PGYDIISKVGSNLFNPAVKLLKQSEIQDKVWLSFTHDIDLINFLTITAGIIDDKNLTAE
YVFFMGNTFHRWSVYPQGARVYTEKFCQSNDFYRVYINDAVVEIETCSGTGPGFSCSEIND
FYDYAEKRVRAGTDFLKVNCNVSSVSNSTELTFYWDWNTTHYNASLLRQ

YBR181C, 1563 bp, exon1: 501-506, intron1: 507-858, exon2:
1599-1563 (SEQ ID NO 21)

TAACTTCTCAACATAATATGTAAAAAATATCTCATTAAGCCAGATAGCAAAATATATCA
CATATTGTCATTGATTAATTTGAGAAAAATATACATGTATCTTTTCACTGAATTTTATATPAA
AAATAAAATTAATTCCTTACTTTTTTTTCTACAGTTTGCACCATTAACCTCTTTTCTTGCA
TCCATACATCTTTTGAACCTCCATACATCTTAATTTTTTGCCTGTTTTTTTTCAGTGTCTCGG
GCATACAGGCGCGCTTATCTTCATGCGCGCCCATCATCCTAGGAAACCTCTTTCCGGTATGGG
CCAAGGGCAGGCGAAAAATCCTATGTGCGTGGAGCTGATACAACTCTCGGCTGGCTTGGTGT
GTAGGGCAGCGTCAATGAATGCCCTGATGGGAGAAAAATTCATCTTTATGAAAAGTGATCT
TAATTTGAATAGTGTGCCCTTCAAAACATTTGGAAGTCATTAATTTGAAACTATCCAGTGT
GAATAGACGACTGAGCCATCATGAAGGTATGTAATATCACCCAAATCCTTAGAATTTCTAA
TGAATCAGCACGCGCTAACCGGCTGTCTCTGACTGTTTGATATAACGCTATACCCACAAAT
AGTGCACTATAATAAAAAATTCCTCAAGAACAAACGTTGTGTTAAACGAGATAATTCGCCCTAA
TATACACGTACCGCACCTTAGGAAAAATATCTCGCTAAGTTCAAATTAAGGAATGAAAAAG
GAATTTACGAAAAAGGGTTTGAATAATCAATGAAAAATAAGAAAAACCTGTAAACGGAAAG
AGGACAGCAGGAGTTCGTTGGAATTTGTGCGATTTGGCTTCGGACAACCTTTACTTAACAAA
TGGTATTTATTTATAACAGTTGAACATTTCTTACCAGTCAACGGGCTCTCAAAAGACCTTC
GAAATTTGATGATGAACACCGTATTCGTGTTTTCTTCGACAGAGAATTCGGTCAAGAAGTTC
GATGTGTAAGCGCTTGGTGATGAATTCACAGGCTACGCTCTTCAAGATCTCTCGTGGTAAAC
GACAAACAAGGTTTCCCAATCAAGCAAGGTGTTTTGTTGCCAATAGAAATCAAGTTTGTGTT
TTGACCAAGAACCTTTCTTGTGTTACAGACCAAGACGTGATGGTGAAGAAAGAGAAAGTCC
GTCAGAGGTGCCATTTGTTGGTCCAGATTTGGCTGTCTTGGCTTTGGTCAATTGTCAAGAAG
GGTGAACAGAAATTTGAAGGTCTAACTGACACTACTGTTCCAAAGAGATTTGGGTCCAAAG
AGAGCTAACACATCAGAAAGTTCTTCGGTTTTGTCAGGAAGATGACGTTGCTGATTTTC
GTCTCATGAAGAGAAAGTCAACCAAGGTTGAAAAGACTTACACCAAGGCTCCAAAGATCCAA
AGATTGCGTTAGCTCTCAAGGATTGCAAAAGAAAGAGACACCAAGAGCTTTGAAGGTTCAGA
AACGCTCAAGCTCAAAAGAGAAGCTGCTGCCGAATACGCTCAATTTGTTGGCTAGAGATGT
TCTGAAAGAAAGGCTGAAAAGGCCGAAATCAGAAAGAGAGAGCTCTCTTTTGAAGGCT
TAA

YBR181C, 236 aa (SEQ ID NO 22)

MKLNISYPVNGSQKTFEIDDEHRIRVFPDKRIGQEVDEAGVDEFKGYVFKISGGNDKQG
PFMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIVGPDLAVALVIVKKGEQE
LEGLDITTVPKRLGPKRANNIRKFFGLSKEDVDRDFVIRREVTKEGTYTKAFKIQRLVT
PQLRQKRHRQALVKVRNAQAREAAAEYAQLLAKRLSERKAKEAEIRKRASSLKA

YCL007C, 893 bp, CDS: 501-893 (SEQ ID NO 23)

ATTACTTTAAATTTGTTTGTCTATTCCAACATAATCAITAGCAGCACATGTGCGAGCAACAG
ATAAACAACAGCAGCGGCACGGTGAACACATAAGTGTATGTGCACACGCGTGTTTTGTGTC
AGTGATATTACCAACTTGCGCATGCAAGGATATACACATCTCGTTTCTGCCTCATGTCTTT
TAAACACGCTTCCACGGGACATGGGTCTTAATTTATGAGAGAAGATCAAGCTTTGAAATGGCC
CGTTTACACATTTTGATACAAACCGTAGACGGCGTCTCGTTTCAAAGACCGTGTGTTGTTG
TATCATGATATACTACTTGTGTTTTTCAAAAAATCTCTGGGTGTTTGTAGATGCCACTATA
TTTTCTATTCTGATTTTATTTTTATGTATACTTATTTTGCTTATTTTCTTATACTCAGGAA
ACGCTCATTTGGCTTGATATACTCGACGCTTTATTTCTGCAAAATTCAGTCTCAAAATCTGAA
CGCGTGGAGCCCAAGGGATGGAGCTGGCAAGGAACGTAATGGCCACATCAAAAAAC
ATCATGGCCAAATGTCAAAAATCACTGTACTTCTCAAAACACTGTACGACAAAAACAAACAA
ACAAACTCTTGTGTAGTAAAAAGAAAGGGAAACTAGTAATATGGAGACACATCGTAAAAA
AAATGTGACACATCGCTTGGTTGTTCTTTGGAGCCATTATCCAGAACAGCAGCAGCATG
GCATTAACCATATGAATACACCAACAACAGTATAGCTAAATTTGACGCGCAGAGAGATTA
GTAGAAGAGAGAGGAAGAAAGGGAAGCGGAGAGAGAGATATGACACATCAAAACTAC
TCATTACTCTTTGTTCTTTATTATTCTGTTGGACCTTTGTTTCTTAAAGTATAG

FIG. 1 - 9

YCL007C, 130 aa (SEQ ID NO 24)
 MELAKERNRPHQKHGQCQNHCTSPNTVRQNKTKLLLVKKKGKLVIRHVIKMLHRL
 VVLWSHYPEQHGHHGNTNHYEYTNNSIAKLDAQRVSRRRRKREARRDYDTYKLLITLCSL
 LFGVPLPLKV

YCL016C, 1430 bp, CDS: 501-1430 (SEQ ID NO 25)
 ACATGACCTAATTTATAGCTTAGGGTTCTTTTGTGCAATTCTATGCGTATGACAAAGA
 GCACACGATGGTGATCGAAATCTCTAGGAGTAGCATACCACAGCGATATATTTAGTAG
 TAGGCGGTTTATATCTTTGTCCCTTTATACTGTTGTGTTCTTGCCTATTGCTTTCAGTA
 GGCACGGTATAGTATAACCGAGAAAAAGGTGAAAAATAAACTAAAAAGCACTATGAGATG
 AACCGTAAAAATCCACAGAGATTGCTCACTAATAATCCTGTACCATGTCCATCAACT
 ACATTCCGACCCCGAGTATGATCCATCTTTAAGCTGTATCCAGTTGACACAGAGTTAAT
 GGATATAATACAGGATCCGGTTCAAATCACCAGTTAAGGTTTAAGTCACTTGGACAAAGA
 CAAGTCTGAAGTTGTACTGTGTTTCGCACGACAAGACTTGGGTGCTGCAAGCAGCCCAAC
 ATTCAACACAGTTCTACTAATGAGAGAAATTTGTTCTGAAACAACCTATTACTTTTCGACG
 AAACGCTCTTGTGTTGGACTGTCCAAGCCGTACATGGACGTCGTGGGATTCCGCAAGACTG
 AATCAGAATTCTGAGACCAGAGAGACATATGGCGAATTGAACTTGAATTCAGTCAACATAT
 ACAACCGGAGAACTGGATTCTCCGACAAAATCATGAAGAGGTCATCTACAAGGTTTATCG
 GACCCCTGGAAGCACTACTTGAGAACTCAACATGTTCTGCGCTAGAAGGTTATCAAAAT
 GCGATAAGATTGGTGGATCTGTGAAAGACGGGTGTTGTGTATTCTTTCACAAGACTTCC
 TTTTCAAGCACTGCATGTACTACTGTGAGCGCAATGGCAGAACTCACTCGATTACAGC
 ATCTGAATGTTGAGGATACACATCACGCTGTGGGGAAAGACATTGAGGACGAGTTCAATC
 CATACACAAGAGAAATCATTTGAAACAGTGCCTGAATAAATTTGCTGTTCAAGACCAAGAGG
 CTGAAAAACAATACGTGGCGCTTGAGAATACCGTTTATAGCTCAGTGGTACGGGATTCAAG
 CGCTAAGGAAATATGTTTCTGGAATAAGCATGCGCAATTGATGAGTTCTCTCATCAAGTGA
 AGTCCCTTTTCCCACTTTCTTCCCATGTGACATTGACATTGACATGCTGGGAGGCTATC
 ATTTCAAGCCTTACCGATAAGACTGTCCAGTATATAGCGAAAGCACATACCAATGGAC
 CCAAGAAACGGTTTAAAGTCTGTTTAGGCTACAGTCACAGTGGGACCTTTCAGGATATCA
 AGCCTCTAATTGAAGAACTAAATTCAGAGGTTGAATAAGACAGTTTCTCATGTAAGT
 ATGCCCGCGCTAAAAGACTGGGCAAAAGACCGTGGTCACGAGCAGGTAG

YCL016C, 309 aa (SEQ ID NO 26)
 MREFPVEQPIITFDETLFGLSKPYMDVVGFAKTESFEFETRETHGELNLSVPIYNGELDF
 SDKIMKRSSSTKVIPTGLEELNLSFCSALEGISKWHKIGSVKDGVLCLISQDFLFKALHV
 LLMSAMAESLQLQHLNVEDTHHVAVKDIEDEFNPTREIETVLNKFVQEQEENNTWR
 LRIPFIAQWYGIQALRYVSGISMPIDEFLIKWLSLPPFFPCDDIDIMLRGTHYHFKPTDK
 TVQYIAKSTLPMDPKERFKVLFRLQSQWLEDIKPLIEELNSRGMKIDISFIMKYARRKRL
 GKRTVVTSTR

YCR052W, 1952 bp, CDS: 501-1952 (SEQ ID NO 27)
 GTCATCGACAGCAAAATGCTGGAAGAGTTCAAGGACAACGTCAGATACACCTTGGAAAAAT
 GACCTTGAGGAAGGAGCCGATGAGGCCACTCTGCAACGCAAGGAGCGAGTTGGAACAGATC
 ATATACGGGAGACAACGCTGAGGAGGAGTTGGAAGGTTACATCCGTGCTATGGTCAGAGAG
 CAGATGCTTGGCGCAGGGCTCCATGGCGGGTTCCGGGACGAACAGATTCCAAGAGAAGA
 AATTAACGACCCGACGACAAAGGCTCTTACAGCTTGTCTAAAAGAAATTAAGCCGACGCTA
 CATGAACCTACTTCTTTCTCTTACATAGTCTTTTCCCTTATGTATCTTTCTGTACATTAA
 TAGACGTTCTTACAAAGTAAATTTACC CGCGCTTTTAAATAGAATGAAAAACGTTGT
 AGAGTGAAAGAAAAGCAACAAATATACAGTTCAAGGACGCTCTGTATGTAATACAGC
 ACGAAAAACAGCTCATAGAATGGTAACACAGACCAATCCGCTCCCTGTTACATATCCAA
 CGGATGCTTATATCCCCACGTATCTGCGCGATGATAAGGTTCTCAATCTGCGAGATTGA
 AAAAATTGATAGAATGGATTCCAGATAGATTGTATCTGACAAAGAGGAGGCTGGATA
 CGTCATCAATTTACCTACAAACACCAAGACCAAGGACCATCCCCCAATAAGAGGATGC
 TGAGGATTTTACGCTACAAACACTACGGAAGAGCGCCCTCGCAGCGGATTCTGGCACCCGAC
 CGGATCTCAGGCAAGACTACATGGACACTGAGAATAGAAGTAAGTCTTCGACAGTCCG
 CAAACGGAAGAACCCATTAGTGAAGTTTGGAAAGGTGTCGCGGTGCAGCTTTTAAAGAC
 TGAACCGCTGGGCTAGGGCAAGAAAGGAAACCGGATTCGTCTTGAAGCTTCCCTTTGA
 ATCTCGCAACACCCGAATACAAATGATCAAGATAGCACCATGGGCGGATACGACCAAGCGCG
 AGGATGAGGACAGTGCAGAGGCAGAATCCAGGGAGGAAATTTGATAGACGACTGGAATGGA

FIG. 1 - 10

ACTACGATGAAAAACAACGTTGTGGAGTTTGTATGGTATCGACATCAAGAGGCAAGGCAAGG
ATAATTTGCGATGCAGTATAACCATCCAAGTTGAGGGGTGTGACGGTGGAAAAGTACAGT
ACTCGCCCACTTAGCTACCTTTGATAGGTATGCAAAACGGGCTCCGTTAATGACGCGGTTT
TTTCGATCTACAAGTACATTTTGATCAACAATCTGTTTGTACGGGAACAAACAGAGGCTC
AAGATTGGTTCCAACGATGCGGAAGACAGCAGTAACGAGAATAACAATAAAAAACGGTGCTG
GTGACGATGATGGCGTCGAGGGAAGTACTCCAAGGATAAGCCCGAATTGGGTGGAGTGA
AGCTAGATTCACTCTTACAAAAGGTATTTGGATACAAACCGCCGCGCACTCCCTCTTGATGA
ATGTTGTGGAAACCGTGAACAAACCTGGTATCACCCCTACCGCCCATCATCTAGATTATA
CAATTGTATCTTTCCAAAGATACCACTATGGTGCTACCACTTGGATGATAGTGTGCGC
ACATCTCTCCACAGCCTCAACCCAGCCAAATTTACAAAAGAGGAAGAAACAGATGCTG
AAGACAGCAGCAAACTACGTGAAATCACAAAGCTTGCCTTGCAAGTGAATCTTAGTGGC
AAAAATACCAAGTTTTCACGAACTGTCTTTGCATCCAAGAGAAACGCTGACTCACTACT
TATGGTCTTCCAAGCAAAACGAGCTTTGTGCTGAGGGCGACCAATACTTCAATGAAGATG
CTGCAAGACGAGTGACATATACAGTAAACAACAATGACAGGTCATAATGGGCAATA
TCTCACTACTGTACTCCCAAGGAAGACTATA

YCR052W, 483 aa (SEQ ID NO 28)
MVTQTNPVFTVYPTDAYIPTFLPDDKVSNLADLKKLIEMDSRLDLYLTRRLDTSIMLPT
NTKTKDHPNPKEMLRIVYNTTESSPRSDSGTPADSGKTTWTLRIEGLKLLHESANGKHPF
SEFLGVAVDFKRLKPLGMGKKRRKRDSSLPLNLLQPEYNDQDSTMGDNDNGEDESAAE
AESREEVDALEWNYDENNVVEFDGIDIKRQKDNLRCSITILQRLGVDDGKVQVYSNPLAT
LIGMOTGSDVAVYSIYKYILINLNVFTEQTEAQDGSNDAEDSSNNNNKNGAGDDDGVE
GTFPKDKPELGEVKLDSLLQKVLDTNAAHPLMNVVQTVNKLVSPLPPIILDYITDLSKD
ITYGATTLVDVSHILHQPOPNLQKEETDAEDTAKLREITKLALQSSAQGYOFFH
ELSLHPRETLTHYLWSSKQNELVLQGDQYFNEDAARTSDIYSNNNNDRSLMGNISLLYSQ
GRL

YCR064C, 911 bp, CDS: 501-911 (SEQ ID NO 29)
AGGTTTTAAACGCGTTATCTTTGTTCCGAAAAAAGGAAAAATATATTTTTTTC
GCGTCGCGTCTCGGCTCTGTTTTGTTTTCGCGTTCCAATGACCAAAATGGGAAAAGTG
GTCGCTTTTGACGAAGGAGACGAAAACTCTCTTAAACCGTTGGGAGAGAGATAATATCA
TGGCCAGAACAATACTGCAACGTGCATATAGTCGTTAGTCTGTGCTTGACATCCACGGC
AGCCGACGTGGACGCACTGATGGAAGGACACCTGTGTGCCCTTTTTCGCTGCTTCTCTCT
CTAATCTGTGCACGAGGCACCTGTCAGATGCAAGTGCTACCGTTGTTAGTTTTCGTTCTTT
GAATGACGCGCAGACAGCACAGTTTTCATACCCGGTTTTCGCCATTGGCAATATAGCA
ATTTTATCAGCATCTTTTCTTTATCAACCAATCGTAAAGGCTTTGGAGATGGCCCTTTC
TCTGTGATCAGAGTATATATGTATCTAGAGCGCTGGTGGTGGAGTTTGGCATATCTCCCC
AGAGCTGCTCATCTGACTTTTGTGCGAGCTTAGACGACCTTGTCTTTTGGGCACTCTGTA
TGTGGATTTCGAAATCTGTGAGGGTTGGCTTGATTTTTCGAACCCGTCAGGTCGAGGCT
TGAGCTTCTGTGCTTTATGCGCGGCATGTGCTTTTGTGAGGTGAGCTTCTGATGCTTG
ACGCGCTCAGAGGTGTTTACATGTATGATGAGTCCCTAAGAAAAATTTTCTTTTTC
AGGTTTCACTTTCCGTTGTGAACGACAAATGTACTATGCGCTTCAAGAGAAATGTGATTAGA
TATCGTCAAGTTCCTACCACAACGCGGTGTGATTGATCTTGTACTGGTTGTAATGTGC
TAAGTCTGTGA

YCR064C, 136 aa (SEQ ID NO 30)
MYLERWWSCTIISQCSLDFASLDDLFSWASLSWISKSVRVGLIFSNPNSGAGLDDLVMF
RMSFCEVFSASLDGCRGVYIDDESRLKFFFFQYFTFCRERQMYAFKQRSITIVKVP
TTRVLDLVLVNVNLSL

YCR073W-A, 1448 bp, CDS: 501-1448 (SEQ ID NO 31)
GTTTATGGCTGGAATGACTTGATAATCTCTTACGAGCTTACTTGAGATGGTATGAGGAG
CCAGAACTCTCCCGCTTCAGCCGCTTTTGTGTGTTTTCAGTATTCATCATCATCA
TTTTCACTTACAGGAATACCTTTTATAGCCACCTAAGTAAAAACAACATTAGCTTAGC
ATCTCAATTTCTTTCGTATGTGTGTGCTGCTATTTTATCCTATTTGTCTCTGGCATCGC
TTTTTTACATAAGGTACCAAGGCAAGAGAAAGACCCCGGAAATTTTCAATTGCGAGCAT
AGGGTTAATACGAAATATGTTAAGGTCTAGTTTCCAAAAATGAAGAAAAATGTGATTAGA
CATCTCGGGAAATTAGGTTTAAATAGGGCGGGCGCTACAGGGGTTTTCCTAACAAATTT

FIG. 1 - 11

CAATGATAATAGTGGCATCATCATCGTCATATCCAGTGTAGGTATGGACTAGAACAGAAA
 GCAAATTTCGACGAAGCAAAATGACTACGACGGTACCCAAAGATATTCGCGTTTCACGAGT
 TTTCAGACGTGGCAGAGGCCGTAGCTGACCATGTAGTCCACGCGCAAGACGGGTGCATTGG
 CTCCTCAAAGAACGAGGAGGAAACACTCTGTTCCCAACATCAGCATGAAATGCATGGATATGA
 CGAGAGGCGCCCTCTTGCAAAGCAGACGATCTGCGCGGGAAGGAAAGTGGTAGCAGTGT
 GTAGTGGCAGTGGTAGCAGTAAGCCCAAAGGAGAAACGGTTCAAGATTGCTCTCTCCG
 GTGGGTCTATTGATCGAAGTGTCTACACGAAGTCTCTAAAACGAGACGATGACGGTGGG
 GAGACTGGGACATTTACTTTGTCAGACGAGAGACTTGTACCCTTCAGCTCGAATGAAAGCA
 ATTATGCGATCGCCAAAGGAAGATTTTGGACCTGATAGACACGCGCAAGATTGCGAACTC
 CGAAGGTGTACCATTCGACGAGTCTATTGATTGACGACCCGCAAGATTGCGTTGATAACT
 ATGAAAAGGTGCTAATCCGCGGGTTTGCCGGTAGAGATTTCGGTCAAACTTCGGATGTTCG
 ACTTGTCTCTGCTTGGTGTGCCCCGATGGTTCATATCGCATCACTCTCCCTAACCTTCC
 AGGACAACTCTACGTGAGAACTTGCATGGGTGGTGGCCGTGGAGAAACGCTCCTTAGTGGGC
 CCTCGACAGAAATTTCGCTGACTATACCTGTAACTCGCAATTCTCACAGGGTTACTTTCG
 TTGTGGAAGGTGCAACCAAGCGCCCATCATCAAGACCAATTATGGAAGGCGCTGAAAAGG
 GCCTACCTAGCAGTATTGTCAACGAAGGTGCTGCTGGTGTATCATGTTTGGTTCAGC
 ACGATGCTCTTACGGAAGTCTCTGTCACCAAAAAAAGTATAAATTCCACCAAGGTTTGT
 CTATTATA

YCR073W-A, 315 aa (SEQ ID NO 32)

MTTVPKIFAFHEPFDVAEAVDHVHQAQDGLAPKNERKHSVPNISMNALDMTREASCK
 STTAAAEKSGSSGSSGSKPKKEKRPKIALSGGSLIEVLHGLLRKDDVRWGDWDIYF
 ADERLVFPSSNESNYGCAKRIIDLIDTAKYQTPKVIYHDESLIDDPQECVDNYEKLIR
 FVAGRDVSKLPMFDLLGCPDGHIALSPFNQDNREKLAWVVPENAPSGESTRISL
 TTPVICHSHRVTFVVEGATKAPIIKTITERPEKGLPSSIVNEGAAGRVSWFVDDDALTDV
 LVTKKKYKFHQGLSI

YDL010W, 1196 bp, CDS: 501-1196 (SEQ ID NO 33)

TAGTAATTAGTTTCTTATGATGGATTTAATGGCGTAGTTCATCCGCGTTTAATTAACTA
 GAGGATAATCTACTTCGAGCATGAATGAAATAGTAAGCCAGTAAGGATGCAGTGACAGA
 CACTGTGCTACCGATTAGTGTGTTGACTTTTCGCAAGATCCTTTCTCCCTCTTTGGACC
 TAGTCATCCCTCCACACAAGATTTCGCTCTTAAGTAGTGGCGAGGCTGTTTCGCTTTTAAG
 CATAGTGTCTAATGTGCAAGGCTTTATAGATCCCAAACTACTACGCTTTGAGAAATGGAAT
 GCACCTAGCAGTTAGTTAACTTTCTGGAACGCGCATGACGCGTCCCGGGCGCCTGAGGCG
 GAGCGTTTCGCGAAATCGGGAACATTTACTGGGAAGATCACTATCTATTCTCTAAAT
 GAACTTTTAAGCAAAATTATCGTAAGATAGAAAGACGAAACCTTAGCAACCTAGCGGTTT
 AATATAGAAACAATTTTATTATGATACCTTCCAATAAGAGAAATGCTAGAAATTTAAGCA
 TTACAACGCTATTATTGTTGTTAGTGTTTTCGTAGCGCAAAATGCGAACCTTCTTGACGG
 TAGAGATAAAGAGGAAACTTCTAAAGCATTAGTACTAATATGGACAATATGGCTGGAG
 GATCTTCCAGGGAATATGCTGCTATGCCGACTTCTACCACGAATAAGGGGAGCTCTGAAG
 TAGACGAAGAATAATTAAGAAATAAACAGAAAGTGGGACTCCAACAGGCCATAGCATCGG
 TGTGATGATAGTTTTCGCGCCATTAAAAACGATAAAGGGTTCGCAATAACCAAGCTTTTA
 ATGTTCAAAAAGAACTACTCCTCATATACTAGACTTGTCTCCGATTATAATATTAGTAAAA
 GCACCTTGTTCATATAGCAAGGGCATGAAGGAATGCTTGAAAATGAGTATCGAGTTTATCC
 CAACTACTATATATATAGAACTTGACAACATGGACATGGGAAGAGCTGCAAGAATATA
 TCAAGTTGGTGACCGGTAGACGAACTGTTCCAACCTTTTGGTTAATGGAGTATCAAGAG
 GAGGTAATGAAGAAATCAAGAACTGCACACTCAAGGGAACCTTTTGAATCATTTACAAG
 TCTGGAGTGATGGTAAATTTCTCGTTGACCAACGTCAGCACTGAAAAACCTTCCAATTAATTGA

YDL010W, 231 aa (SEQ ID NO 34)

MTPSNKRNARILSTITLLLLLVFFVQANFLTVEIKEETSKAFSTNMNDMAGGSSREYA
 AMPTSTVNDKSSSEVDDEINELKQKVLQQPIASVDDLSAINKDKGSRITKAFNVQREYS
 LLLDLSPIIIFSKSTCSYSGMKELLENEYQFIPNYIYIELDKHGHGEELEQYIKLVTRG
 GTVPNLLVNGVSRGNEEIKKLHTQGLLESLQVWSDGKFSVEQREKPSNN

YDL036C, 1889 bp, CDS: 501-1889 (SEQ ID NO 35)

TCAAAATCAGCTCTTTTCAAGCAATATTGTCACAAACGATGATGAGAATAGCATTGAAG
 AGGATAAGAAATTCAGCTATTTCAGATGCTAGTGCATCTGAAAAATTATCTGGTCAAGCCCCA

FIG. 1 - 12

CAATACCAGGTACGACTCTGATCCAATAATTGAGGCGCAGAACGATAATGATAGTAGTG
 ATAGTAGCGGCATAGATTGTATAGCCTTCTTAAGAAATGGACCATTATAAAGTTTTTGTA
 TCGCGAGTTTGAAGAAATGGAAGTAGGAACGTAATACAAATTGACAAGTAGCCGACATG
 AATGACCTCACTTCTCTTATATATGTGTAGTAGTATATGCATTATAGAATTTTTCATT
 GAAGCAATGTGATTCTCGATAAGTAAGCTTTTTTTCTGCTGGCGCGCAACCATAGAG
 AAAAAAGACCGAGTTAAGAAAAAGTTCATAAAAAAATTTTGAAAAATGGATGAGTGCTCG
 TATAATGGAATAGGAACCTATGCAAAAGAAATAATAGGTTAAGAAATTTGTTTACAGTGC
 CAGTAATAATGGTTCGACAACTCAAAAGGAATGCATTATCTGCAGGTCTGCTTTTGCAG
 GTAATGCAACCTCAATGAGTTTGTATGAACATTTGCAAAATGAGGTGAAAAGAGAGAGGG
 AAAATCAAAAGAAAAAATAAAGCGAACTCAATCAAAAAAATCGCCAGATTGATTGATTA
 ATAAATCTACTTTTCAATCAGAACGATAGGCAGCAAAAAAGAGAAAAATAGACAACATG
 ATCCAGAGTATGAAATGTCTGATGGCCCTCTAAGGAAAAATCAAGCCCTACCATTTTA
 CTGACAGGACCTTTTGCAAAGAGCGTTGGAGAGATAAAAAATTTGGTTGATGTCTTTATAT
 CTGAATTTTCAGATCGTGAATCTGAATATTATAAAGAAACAATCGAAAACGGGGACGTTCC
 ATATAAACGATGAAACTGCGGACTTATCTACTGTAATTCGCAATGGTGACCTGATTACGC
 ATCAGGTACATAGACATGAACCTCCAGTCACTTCCAGGCCTATCAAGTTATTTTGAAG
 ATGATACTCAATGGTTATTGATAAACCGAGCGGTATACCTGTTTCAACCAACTGGCCGAT
 ATCGGTTCAATCAATACGAAAAATGCTTCAAAATATCTCGGATTGTTGTGAAACCAT
 GTAATAGGTTAGATAGGCTTACAAGTGGATTATGTGTTTTTGCAAAAACTCGAAGGAG
 CCGATAATATCGCGCATCAACTAAAAGCTCGAGAAGTCACTAAGGAATACGTGGCCAAGG
 TAGTTGGAGAAATTTCCAGAAACCGAAGTAATTTGTGAAAAACCTCTAAAACCTGATCGAGC
 CAAGCTTGTCTTTAATGCGAGTTTGTCAAATGGACGAGAAAGGAGCCAAACATGCAAAAA
 CTGTTTTTAACGAATCAGCTACGACCGTAAAACGAGTATTGTAAGTGCAAAACCGCTTA
 CGCGCGGATCAGATCAAAATAGAGTACATTTACAGTACTTAGGCCACCAATTTGCTTAACG
 ATCTATTTATTTTCCAATGATGAAGTATGGGGTAACAATCTCGGAAAAGGCGCCAGAGCTG
 ACTTCGATATAGTTATTACTAAGCTAGACGAAATAGGGAAGAAAACTGCTCAAGGTT
 GGTTCATAGTAATGGCGGGTACGGTGAGGTATTAAGGCAAGAAAAATGTTCTATTGTTG
 AATCTGATTTGTATATCTGATCTCGGCCCAATGATCTTGATCTGTTGCTACATGCTTATC
 TATACGAATCACTGAGACTGAAGAAGAACCGAAAAGAAAAAGTGGTGCTACAAAACAG
 AGTATCCAGAATGGGCTCTGAGAAGATAG

YDL036C, 462 aa (SEQ ID NO 36)

MQRNRLRLNFTVPVIMARQLKRNALSGALAFAGNATSNEFDEHLQNEVEREREIQKKKK
 IKRTQSKSSPDLINKSTFQSRITIGSKKEKHRQLDPEYEIVIDGPLRKIKPHYFTYRTFCK
 ERWRDKKLVDVFISEFRDRESEYKYRTIENGVDHINDEADLSTVIRNGDLITHQVHRHE
 PPVTSRPIKIVIFEDDNIMVIDKPSGIPVHPTGRYRFNTITKMLQNNLGFVVPNCNRLDRL
 TSGMLFLAKTPKGADNIGDQLKAREVTKEYVAKVVGGEFPETEVIPEKPLKLEPRLALNA
 VCOMDEKGAHKHAKTVFNRLISYDGTSTIVKCKPLTGRSHQIRVHLQYLGHPINDPIYSND
 EVWGNLNGKGGQADFIVITKLDEIGKRKPAKSWFHSNGGYGEVLRLQEKCSICESDLYTD
 PGPNDLWLHAYLYESTETEBGTEKKWKYKTEYPEWALRR

YDL083C, 1364 bp, exon1: 501-909, intron1: 910-1341, exon2:
 1342-1364 (SEQ ID NO 37)

TATTCCGACTAGAAAAAATAAATTTTCTAAGTACAAAAAATGCCTGCATATATGTAA
 GGAATGTAACAGGAAATGTATGGTCAACATATTAAATAGCTGTGTTTACTTCCATAAAAGAGT
 CTGATAATTCAGAAAAAACCCATACATGTGAAAAAATAATGCATTGTGAAAAAAGAGTGG
 TTGAAAAATGTATGCGATCTAGGAAAAAAGTGAATTTTCTGTAGGTTGTGCTCTCTCTCT
 AGAAGGATGCTGTGGCCTTTGACCTGGGCGGAAATTTCTCTGTGTTTCCCTCTAGCTGAGG
 GAAACAGAATCTGTAGCAGTTTCGTTCCGCCAGGCGCGTGAGCCTATATACCACCGAATAT
 TATCTTACGCGCAGAGAGTAACACTGGCAAAGTCAAAAGTAAATGCCATGTAAAAATGTATA
 GGTTCAGCAGTACAGCTATTTAATATATACCTTTTATTATAGCAGTGTGTTTCAAAAAATGAC
 GCAAGAGAATAAGCAACAAGATGTCTGCCGTCCTCAAGTGTCCAAGTATGTTAAATATTT
 AAACGATGTACAGAAATTTGTGAGGGATATTGAACCATGCAGTGAGATTAATTTCAATTTA
 AGAACCATATCACTGAATAAGACGGGTGGGGCAAGCACTAGATGCGAATCATAGTTTGA
 GAACAACCGGATCAACATTTACACAGTTTAAAGACCGAGTAGAAAAATACCAATAAATGTGTG
 GGGAAAAATATTATCTAATTTCTCTGTGGAGTAAAGTAAATGAGCGCTCTTTTGGGGTCTT
 ATTTATTCAATTCGCTCCCTCTGCAATGAATTTTGAACAGAAATGCTCCAAAGAGGAAGTGC
 CAGGTAACCTCACTGTGTTTCAACCTTTTACACAGTTTCAATAATTTTGTAGAGTTTGTAA

FIG. 1 - 13

TTTCTGTTTTACTAACATGTGACACGAAATGTTTTTCATTTTTTGGTTTTATAACAGACTT
 TTGGTAAGAAGAAATCAGCTACCGCTGTTGCCACGCTCAAGGCCGCTAAGGGTTTGATTA
 AGGTTCAACGGTTCTCCAAATCACTTTGGTTGAAACGAGAAATCCTAAGATTCAAGGTTCTACG
 AACCATTTATTTGTTGGTTGGTTTGGACAAGTTCTCCAAACATCGATATCAGAGTTAGAGTCA
 CTGGTGGTGGTCACTGTTTCTCAAGTCTACGCCATCAGACAAGCTATTGCTAAGGGTTTAG
 TCGCTTACCACCAAAAGTACGTTGACGAACAATCCAAAGACGAATTGAAGAAGGCCTTCA
 CCTCTACGACGAACTTTGTTGATCGCTGATTCTAGAAGACCAGAACCAAGAAATTCG
 GTGGTAAGGGTGCTCGTTCTAGATTCCAAAAATCTTACCGTTAA

YDL083C, 143 aa (SEQ ID NO 38)

MSAVPSVQTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF
 SNIDIRVRVTGGGHVSQVYAIRQAIAGLVAHYHKYVDEQSKNELKKAFTSYDRTLILLAD
 SRRPEPKFKFGKGARSRFQKSYR

YDL125C, 1088 bp, exon1: 501-597, intron1: 598-708, exon2:
 709-1088 (SEQ ID NO 39)

TTCAAAATACGAGTAAAGGAGATCCTAGGTGTGGATTAGTAAGGGGAGTGTGGCAACTTC
 CTTTTCCGGTTAATTCTCCGCGCTTTCGTAGACTATTTGCAAGGACCCAAATAGGAG
 ACGCATGGAGGCTTCTACAAAACAGCGTGCCGTTTGTAGTGGCATGAGCAGGGGGCGCAAA
 GGAAACACCGGTAAATCGCGCAAGACCTTGTGGCCACGTAGCCCTCAAAGGTTGAATTGA
 CACTTGTCTACAGAACTTGAAGAAGTACAAAAGGAGGTCACATPAAAACAGTAAGCTTGA
 AGCTTTAAGATATCGTGGCAATCGTTACAGAATATTCTTGCAGAAATAATGGCGGGTCC
 GTTCTCTTCTGAAGAAGTTACCGCCCTACTGAAGCATTTGCTGACGATCGTGAATGTGA
 TGTGTTGTTTCGACTGGAAAGCGGAGAACATTATGAAGTAAAGGACAATCAGCACGCCCTTC
 CAGACTTTTAAAGAACATTGTATGGAGCCATTGATATCGGCACCCGTACCTTAACAACAACA
 AAATGTCGTCTCTGCTACGCTTGATGCTGCCTGTATTTTTGCAGATATATAAAAGTA
 TGTCACATTACTAATAAAGAGCTTACACTCACACCAATGATGGCGATAGTCTCTATGTAG
 TACATATACATAAAGCAGAATACTAACAAATCGATCCGCTATGCAACAGCGCGAAATTCAT
 CCTTCAAATTGATTGAAACAAAGTACTCGTATGCTTTCTTGGACATCCAACCTACTGCTG
 AAGGTCATGCTTTAATCATTCCTAAGTACCATCGGTGCGAAGTTGATGACATCCCGGACG
 AATTCCCTTACCGATGCTATGCCGATGGCCAAGAGACTGGCCAAGGCAATGAAGTTGGACA
 CTTATAATGTGTGTCAGAAATAATGGTAAAATTGGCGCATCAAGAAGTTCGACCACGTCCT
 TCCATTGATTCTTAAGAGAGATGAGAAAAGTGGTTTGATTGTAGGGTGGAGCAAGCCCAAG
 AAACGGACTTCGATAAGTTGGGCAAGCTACACAAGGAATGCTTGCCAACTAGAAGGCT
 CCGATTAG

YDL125C, 158 aa (SEQ ID NO 40)

MEPLISAPYLTTTKMSAPATLDAACIFCKIKIASEIPSFKLIETKYSYAFLDIQPTAEGHA
 LIIPKHYGAKLHDIPDEFLTDAMPIAKRLAKAMKLDYINVLNQNGKIAHQEVHDVHFHLI
 PKRDEKSLIVGWPAQETDFDKLGLKHELLAKLEGSD

YDL133C-A, 578 bp, CDS: 501-578 (SEQ ID NO 41)

AAAGGTGGTTCGAGACTTTGTGTGTAGCTTAGAATTTCTTCCACTATATGAAGCCAAAG
 ACCCTCTCTCTCTCTTCGACACTTCGTTTATTTCCACTTTCCTTATTAGTATTTCATCG
 TCTCAGAATGCTTTCTTATTTCACGACGGTTACCACACCCGTACACCCTTATCTCATTTTC
 ACCAGTACCTTCTCTTATTAGATTCTATCTTATTTATTATTAGGATTATTAGGTCAATTGA
 CGAGCGGTGTCGCAACCATGGAAGAGTGTGCGAGCTGCGATGCTATTCATTATACCCTGTA
 CTAATTGCTGGCAGAAATCCCATCTTCTCTGCTGGGGTGATTATATATATAGGAGATTGA
 ACGAATATGAATATTTCTGAATGTTAAATAATGTTATCCGTCATTATTGTTTCACTCTCT
 TCTTTGAAATTTTCGCTTGTCTGTTTTCATCTTATATTTCCTTCAATCCCTAAGATAG
 TCATATCGACTTAATCCAAATGAGAGCTAAGTGTGAGAAAGAAGAGAAGTCTAGAGACTTA
 AGAGAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL133C-A, 25 aa (SEQ ID NO 42)

MRARWRKKRTRRLKRKRKRVARSK

FIG. 1 - 14

YDL136W, 1268 bp, exon1: 501-503, intron1: 504-908, exon2: 909-1268 (SEQ ID NO 43)

CATGCGGACCTGTGTGTTTTGTTCTAGATTGTTTTATTTTATGATTGTTGAAGATAT
AAACCACCTGTATAGTTGTATAGATAGGATAATGATGGTGCACCTGAAAATAAACTTACTA
GCTCTTTAATATTGCAACGGCTTGTAACGGCGCCATGATGACATTGAGAATTTATACCAC
TACTATATGAAAAAATGAAAAAGAGGCCCTGCTTTGAACCCGTACATTTTTATCTATAATA
TTGCATCTGTGGTTTGCCTGACGGCAGCGAGTCCAACACAAAGTCTGGCATATGCTACGA
ATTTTCCACCATGGATTGACGACCCAAACATTGAAATTTTTTTTTCATGTGCAATTGTGAAA
TTTTTCTGAAGATGAGGGTAAATAGAGCCCTGCAATCGTCATCATATGAGAAATGGATAT
ATTGAAAATCTACTCACATCTCTTTTTTGGGGGTTTGGTAGTACAGTACAGTGAGAACATGAA
AGAACCAATAGGACTAAAAATGGTATGTAGAGATGAATATACATGAAACGGACGCGTATA
TAATGTGCTATGGAAGAAAAAAGTCTCCTTTAATGTCTGCAGGATAAATTAATCAAGTGGT
CTGAAGAAAAATTTACAGCTACAGTATTACTGCAAACTTGCAGGCAAAATATACAGAGAT
CTCACCAGCTACAACTTGGTAACAGAAATTTATAAGTTTATGGCACTTGTAAAAATTTGTT
TGGAAAGTTTTCGAAATTTAATAATTTGGTCTTCAGAAACCTGGAACCACTATGAACTATT
TTTTTTGGATAATGCAATGCACAGAGCGTATTAGTGTATACGAGAATTCAAAAATTTGAA
ATCGGCTCATAAAAACAGGAACCTTTTACTAACAGTTATGATTTTTTGTTCCTATTTCTTT
ATCAATAGGCGCGGCTTAAAGCTTACGAACTAAGAACCAAAATCCAAGGAACATTAAGCTT
CTCAATGGTGTGATTGAAAAAGGAGTTGGCTGAATTGAAGGTCCAAAAGTTGTTCAGAC
CATCTTTGGCAAAGATCAAGACCGTCAAGAAAGATATCGCCTGTGTCTTGACCGTGCATCA
ACGAACAAGGAGAGAGCTGTAGACAATTTATACAAAGGTAAGAAGTACCAACGCAAGG
ACTTGAGAGCCAAGAAGACGAGCTTTGAGAAGAGCTTTGACCAAAATTCGAAGCTTCCC
AAGTTACCGAAAAGCAAGAAAGCAAAATCGCTTTCCCAAGAAAGTACGCTATCA
AGGCTTAA

YDL136W, 120 aa (SEQ ID NO 44)

MAGVKAYELRKTSSKQLASQLVDLKKELAEKVQKLSRPSLPKIKTVRKSIACVLTVINE
QQREAVRQLYKKKYQPKDLRAKTRALRRALTKEASQVTEQRKKQIAFPQRKYAIIKA

YDL167C, 2660 bp, CDS: 501-2660 (SEQ ID NO 45)

TGGGTGTGCTCAACAGGATGCCGTGGAATCATACGAACCGACATTGTGGTAGAGCTAC
AAAGCGATACGAAAGAAGATATGGTATCTAACGTAATCCCGTATTGTGTCTTGGCAAAAGA
TGTGGTTAGAACCAACATCCAGATGGAGTCACAAAATGAATATCAAGGGCCCTCGTAGCGATG
ACGAAGACGATGAAGACAGTGGTAGGCGTTCCATAAATTTGTGTATCTCATATATACA
TATATAATTGTAAATTAGTAACAGTAGTAATAGTAGTGCCTATTATATAAAGGGTTTCTTT
AAGTAATGTGCTACTTGTTTAATGTGACTTTGGTAATATATTTTCATTCTCCGATGCC
GATGCCAGTGGAAAGTTTAAAGTGAAAAATTTTCAACACATACAAGTTTAAATAAGTT
GGTTTTGTAGCAAAATAGCATTTACTAAAGAAGAGCGCTAGGATAATTGTGCATTGTATTG
TGAATTTTGATACAGAAATTTATGCACTATGTGGTACTAGAGCTGCAAGTTGCGCATTTGCG
CAGATACCCCCAAGGATCAATGTGCGATTGCGAATATAGCAATTTCAAAATGTGAATGCTG
AAACATTAGTATGCCATTATGGGACCAATTTTACCAGGACATTGAAGTAAACGGGACGA
CAAAAGATTGTGGAGAGTGCAATGGTGCAATTGGACAAGGATATTCAATGACGTTATTGGTA
ACGACGACTTTGTCTGTGTTTCCCTGTATTCAACATGGCATATCCGTTGTACCTTACCAC
GTCAAGCGAGAGATGATGGTTTATTTCTTACTTCTTATTTACAACATCCGAAAGTATTGTG
ACTTATGGAAGGAATTCGATAGATGGTGTGTCAACCATCCGGAGATTTTGGGACAAAAGA
AAGCAATCTCCAACAACAATTTGTAATACTAAAAGTATTAGTATTAATGCAAGCCAAAATA
CGAAGGATTTGGACGAAATAGTTAGAATATTGGAAGTTTCAATCCCACTGAAGAGGACG
GCTCTGTTCGAGACTATACTCTCTTTTAAAGAAGACAACGGATATATTAATCAATTTGC
ACAAAAGTGTAGTTCTCCCTGGAAGATATGGAATCTGTCTTAAACAAAACCATATGACTCAC
ACACCGATATTAGAGCGTTTTCGAAAGAGAAATCTAAGATTTTGTACATGAACAAATTTAC
CGCCCGACACAACCTCAAAGTGAGTTGGAATCATGGTTTACCCAATATGGTGTAGACCCAG
TTGGGTTTTGGACTGTCAAAAACATCGTAGAAGATACGTCCTAACGTTAAATTAATACATGGA
GTCTAAATAACAGTCCCTATGTGGAAGATCAAGATATCTCAGGATTTGTGTGCTTCC
AAACACATGAAGAAGCAACTGAAGTACTAGCGTTGAATGGGAGATCACTCTCTATCTAATC
TGGGCAACATCTAAGCAACCAAGGGTGGTGGAAACATGCTCTTGAGCTTCAACCTTTCTCCA
CCGAGTAGTACGTAAGGCTCAAGAAATTTATCGCCTTTCCCTCAAAGTAAAAACCAAC
CAAGACAGGTGACTCGAATTTGCCATCTTGTGGTTTTCACAACTTTCAAAGACGCTACTG
CATGTTTTAGATGTTCTTTTCCGGCACCATCAAAATAGTCAAATACATACTCGCAACTCAA

FIG. 1 - 15

ACAATAATGTTAAACAGTAGTAAATAATTTAAACAATCGCGTGAACTCGGGATCTTCAA
GCAATATTAGTAACACTGCAGCGAATCACCCTATGGTGCCCTGAGTTCAACATGATGT
CTAACACACGCCAGCAGCTTTAAACATACAATAGAGCTCATTTCCTGCAATTACGCCAT
TGTGCGGACAAAATTCATTGAACATGGCACCATTGAAACAGTGGGTCCGCCGATATATATAG
CGGATCATTTCGCGAAATAATAATATAGCCCCAAATTCGTGTTAATAAATGATTA
ACAATAACAACAATAATATTAACAATATGACCAATAATAGATATAACATTAAATAACAACA
TCAACGGTAAATGGGAATGGTAATGGGAACAACAGTAATAACAATAACAATCAATAAACA
ATCATATAACAATCATCATATAATGGTAGTATCAATAGTAATAGTAATACCAATAATAATA
ATAATAATAACAATGGTAACAATAGTAATAATTTGTAATCCAATTCGGTATGGGAGAT
GTGGCTCCAACTGCCATTAGAGCAGGAGATGGGAAGTGTCCACGTGCACGTATCATA
ACTTTGCTAAAAACGTAGTGTGCTTACGCTGTGGTGGTCCAAAATCAATAAGCGCGGATG
CAAGTGAACCAATCATTTACATAGATTTCATCAACATTTGGACCAGCGTCGCGTATCTCCA
GTAATAACAATATTTCTGTTAATACTAATGGTGGTAGCAATGCTGGTCCGACCGCATGGGA
ACGATAACAAGAGTCTGTATATAGTTTGTAGTGAATTTATGTCAACCCGTTATTCGATGG
CAACAAAGTCAATGAAGGAGGAGATGGGAATGGTAGCTCGTTTAAACAGGTTCAAAAGTG
ACAAAGCTAACGTTAATTTTCCAAATGTTGGTGATAATAGCGCTTTCGGTAATGGTTTAA
ATAGTTCAATACGTTGGTAG

YDL167C, 719 aa (SEQ ID NO 46)

MHYVLELQVAHLEDPFKDQCRANIAFQIVNAETLVCHYGTNSLPSIEVNGTTKSLESA
MVQLDKDIDHIVGNDDFVLVSLYSTWHIRVTLPRQARDGFIILSYLQHPKVPFLWKEFDP
RWCWNHPEILGQKKAISSNNNCNTKSISINAAKNTKDLDEIVRILEVSIPTTEAGGSVPEIY
SLLRKTTDILQLHKKCTSPEDMESVLTKPYDSHTDIRAFLEQKSKTALYMNLPDPDTQS
ELSEWFTQYGVVRVPGFWTKNIVEDTSNWNNSLNNSPYVEDQDSISGPFVVFQTHEEAT
EVLALNGRSLLSNLANTKQPRVVEHLELQPSSTGLVDKAQEILSPFPQSKNKP RP GDWN
CPSCGFSNFQRRTACFRCSFPAPSNSQIHANTSNNNVNSRRNLNNRVNSGSSSNI SNTA
ANHYPGAPFPNMIANNTPAALTYNRAHFPALTPLSRQNSLNMAFSPNSGSPHIIADHFSGN
NNIAPNYRYNN
NGSINSNSNTNN
CLRCGFPKSTSGDASETHYI DSSTFGPASRTPSNNNISVNTVNGNSNAGRDTGNDNKRGR
I LMFSPPLSMATKSMKEGDNSSGSPNEFKSDKANVSFNSVNGDNSAFNGNFSIRW

YDL184C, 578 bp, CDS: 501-578 (SEQ ID NO 47)

AACAAGAAAACCCCTCCGTTGATCTTAGATTTCTTAGAGGTTTCATGAACTAGAAAGCGAC
TTGAACAAAGTCATCCTTCAAGAATCGAAATCTCAAGAGAAAAACAAATTTAATGTAGA
TTGTCCCACTATCTCATGTAAATATACATAACAGGTATTCCTGAGCGGTCGAAATTAGAC
TGTACTTTCTGATGGCCTCCGTCACACCTTTGACATATACAACACTCCGCACATTTTAT
AGCTTTCTTTCTAGAAATTTTTCCTCCAGCGCTCTCGATCAATGAACCTTTTAAAGTAAGTG
ACCCTAACCTTTTCCAGGCAAGGCTGGCCTCATACCCTACCAGAAAGTTTTCATTTTA
CCCCATGGCAGATGGAGCATATTTTAAACAGACGAACTGACCTCGTCTTCTATAAAATC
GGACTCTTAAGCAACTCTCATTTATCTTATATCCGTTCCATTTTGTACTATAAAGAACCG
ACCACTCGATTCAATCGAAATGAGAGCCAAGTGGAGAAAGAAGAGACTGAAGACTTA
AGAGAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL184C, 25 aa (SEQ ID NO 48)

MRARWRKRTRRLRKRKRVRARSK

YDL191W, 1354 bp, exon1: 501-503, intron1: 504-994, exon2:
995-1354 (SEQ ID NO 49)

TATTGACGTTTCGCTCTCAGGTCACCGTGTCTCAAAAGATACCTTTTAAACCTAAAAAC
ACACGAAATCATATTATGATAATTCAGAATGATAGTGTGGTACTGTGCAATTGACTGTT
CAAGACTGAAGAGGATCTTTGATTGTGTGTACTCAACAAATAATCTTTCAGCAAAACCTT
CTCAATCTCGGGACTGTATTAATCTCAGACCCATACATATCTACACCCATCACTTTTATAC
ATTTAATTTTGTATACATATAATAGGTAGCTTAAATTTGAAAGTCGCAAAAAAATATGGCA
CGCGAGCTCTCCGGGTGAACCCACGCAACTTACCTGGCACTCCATGCACTAACCGGGC
GGGTTTGGGACGAGATCCAGCATCAATTTGCAAAATTCACACCTGAGTATTCATATAT
GTAATATAATGTTAAGCATACGCTGTGCGATTAGCACTATATTGACCGGTAGAATAGGTAC
AGTGAGACAGTATATTGCAAAATGGTATGTTGAGATGAACAAAAATAAAGACTGCACAA

FIG. 1 - 16

CTGCAGAACGAGAGGAGTATAGCAACCTAGTGCAGAAAGACGCTCGAAGCGTTAAACT
TTTGGAAACGTAATTCATCCGTTGGCTATGTCTATTCATACAGTTAGAATACGAAAGCTG
TAATCAAGTATATCGGATATTTCGCAAGCAAGAAATCAAGGAAAGAAAGTGAATACG
ATACATCTTTAAATTCAGAGGTTTGCCTGAATTTAATAGGGAAGTTTACGTTATGATTG
TTGGCCGTATAGCTCGCTACGCTTTGACCAAATTTAAATTCCTCAATTTTATTATGATAA
AAAGCGCTTCAACGAAATAAAATTAGTTATTGGTTTTTCTCTGTTCAGGAGGATATAT
GATCGCTTGCTGTGTAGTTCATTATAAGTGCTAATAAAATCTAACGTTAATAAAAAAT
TGAATATTATTTCATTTTTATCCTATTAAATAGGCCGGTGTAAAGCTTACGACAATAAG
AACCAAATCCAAGGAACAATTGGCTTCTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGA
ATTGAAGGTCAAAAGTTGTCCAGACCATCTTTGCCAAGATCAAGACCGCTCAGAAAGAG
TATCGCTGTGTCTTGACCGTCATCAACGAACAACAGAGAAGCTGTAGACAATTTATA
CAAGGGTAAAGAAGTACCAACCAAAGGACTTGAGACCAAGAAGACCAAGCTTTGAGAAG
AGCTTTGACCAAAATTCGAAGCTTCCCAAGTTACCGAAAAGCAAAGAAGACCAATTCGC
TTTCCCAAGAAAGTACGCTATTAAAGCGTTAA

YDL191W, 120 aa (SEQ ID NO 50)

MAGVKAYELRTKSEQLASQLVDLKKELAEKVKQLSRPSLPKIKTVRKSIACVLTVINE
QQR EAVRQLYKGGKYQPKDLRAKKTRALRRALTKEFASQVTEKQRKKQIAFPQRYAIIKA

YDR103W, 3254 bp, CDS: 501-3254 (SEQ ID NO 51)

ATCAAGTTTCCCTTTAAAGGGATATATAACAGATTCTAAAACGACGAAATATTTTCGAGT
GAAGAAGAAGCGTTAAATATTGGATCTTCCGCGAGTTCTACTCTGATACATTTTGAAGT
AGGAGAGTCTATTAGAAAGCGTATTGCTCAATAGTAGAAAGCAGGCCCTGTGCACATGAAT
TAATTTAAATAATATAAAGGTAGTGATTAGACGACACATGTCCATGAGTAACCTGATGAAT
TTTTGAACAATTTTCCCTTCTTTTCTTTTGGGTGCGGCGATAGTAGCTGTGT
AATTTACACATCATGTACTTTTCTGCATCAAAATATGAAGGCGATAGTAGCTAAAGAAA
ATACCGAGAATTTCTCGAAAAGTTGACGACAAAAGAAAGCATAAAAAGTAAATTGAAA
ATAATTTTAAACTGTTTTAACCCATCTAGCATCCGCGCTAAAAAGAGAGATACAGAGT
ACAGCGGAAACCACTTTTAAATGATGGAACCTCTACAGACAATATAGTTTCCCTTTTC
ACAATTTTGGTAGCTCGACACAATATAGTGGTACCTTCTCGAGAACTCCCAAGCAATAA
TAGAGCTTAGAGAAGCCCGACTCTATCCCAATGTGCAAGGAGAAAAAATGTGACGCGAAA
AGTTAGCCAGGTTCCAAAGAAGTAGTGTCTAAAAGAAAAGATTCTCACCTTCTCTTATTT
CCTCCTCTACATTTTCTGTCTCACCCAAATCTAGGGTCACTTCTTCAAACTCTTCTGCGA
ATGAAGACCGTAACCTTAATGAATACACCTTCTACGGTTTCCACTGATTTATTGGCACAAC
ACCCTCACAGAACATCGTCTTTGCCAAGACCTAATTCCAATCTCTTTCACGCAAGTAATA
GTAACCTTATCCCGAGCAAAATGAGCCCCCAAGGGCCGAAAAATTTATCAGATAATATACCC
CAAAGGTGCGTCCATTGGCTATCCCAATACAAAGAACCTCTATTAAAAAATCCTTTTGA
ATGCTTCTTGTACGTTATGTGACGAGCCTATTCTTAACAGAAGAAAGGGAGAGAAAAATTA
TAGAGCTTGATAGTGCCCACTTAAGTCACCAAGAATGTCTATTATCTCTTTTGGCACCA
CTTCAAAGGCGATCTCAATGATTCAGAAAATGATGAACTAAAGGATATTCTAATTTCTGATT
TTTTGATTCTAAGATTTCTGATTTCTGAGTTATCAATCACACCTTCAGTCCCGCTTTCCTC
CTTATTCAACACTCTTGCCTTCTTTTGGGTATTCTATACACCTGTGTGAAGACAAACGA
TATATTCTCAAGCTCCAAGTCTAAACCCAAATCTCATATTGGCTTACAGCTCCCAAGGAAA
GAAACCAATTTCCAAAAAATAATCAAACTATACATTTTACATTTCAACCCTGGGGCACA
GAGAATTTCCGTCGAGCAAACTCTATCTTAGCAGACACCTGTAGCGTGTGACGCTA
ATGATTCTATTCTCTGCTTTTCCAAATTCGGTAAGAGCAAGGATGAGCAAAACCAACAA
CGTTGCGCTGTAAAGGTCAATTTTATTCAAAATCTTTTGAACAATTTCCAGGAAGAT
TGCAGGATTGGAGAAATAGACGGGACTATGGAATTACTAAGTTTGGTAGACAAATTGATGA
TTTCCAAAGATGTGACAGATATATACAAATGCTGTGTTTCTATTTTGAAGACGCATTTTG
TAATGACAGAAAGTGGATTAACGATGTTGATGTTTGGAAATTAGACTATAAGAAATTTAGAAG
TATTTACACCTATTGCGCACTTGAGAATGACTACACTCGAAGCTTCAGTACTCAAAATGCA
CCTTAAATAAACAACATTGCGCGGATTTATCAGATCTTTACATTGTTTCAGAAATATAATT
CTGACGAAAGCAACACTGTACAGAAATGGATATCAGGTAATTGAATCAGGATTTTGTAT
TCAATGAGGACAATATCACTTCGACCTGCTTCTTCCATATAAAGAACTTTTCCAA
AAGATGTGTGTAATGGTAGGCACGAGACGAGTACCTTCTAGGTTTAATCAATCAATCAACA
AAGTTGTTGAAGTTGAAATGTGCAACGATAATGATACGTAAATCAATGAAGGGGGATTTCA
CCTTAAATTCAGAGAATGTTCTAGGCAGAGTACTGTGACAGTATACAACTCTGTTCTAA

FIG. 1 - 17

CCACGATAAGCTCAATTCTTTCCCTTAAACGAGAAAAACCTGATAAATTGGCAATAATCT
TACAGATCGATTTTACGAAATTTGAAGGAAGAAGACAGTTTAAATGTTGTTTATACAGCTC
TAAAAGCTTTTAAACATTAAATTTGCGCGTTTGACGTTTGTGTTTCGTGATCGGAAATAAAT
ATGTTCTGGACTATGGATCGGTATTACACAAGATAGATTCACTAGATTCCATCTCAAATC
TCAAATCAAAGAGTTCTCGACACAATTTTACCTATTGTTGGTTGAAAAATACTCTATATC
CCGAAAAATATTCAATGAACATTTGGGTATTGTTGCTGTATCAAAATAGTAATATGGAAGCCAA
AAAAATCCATACTATTTCAAGATTACAGATGCTTTTACAAGTTTGGGAAGAAGAAGGCCAA
ATGAATTGAAGATTAAAGTGGCGTATTTGAACGTTGACTACAGTGAATAAAATTTGATGAAC
TAGTTCGAGGCCAGCTCTCGACTTTGTTTGTAGAACTCTTGCTACAGTTTTCGCTTAA
GTTTGTATGAACATGATGACGATGACGAGAGGATAATGATGATTTCGACCGATAATGAAC
TTGATAATAGTTACAGGATCACTGTTCGGATGCTGAATCTACAACACTATTCATATTGATT
TCTCAATTTGATAATGAAAAATGCTACCGCAAAATATGGTGAATGACAGAAACCTTTCACTCG
AGGGTGAACATAGCAATATAGAAAACTTAGAAACTGTCGCTTCTTCAGTAGACGCCAGCTC
TGATTTCTTAATATTAGATTCTTACTTCACTCTGAGGAGGAAGGTCAATAGAAATGAAA
ATGAAAAATGATATGCCAGTATTATTACTTAGTGATATGGATAAAGGAATCGATGGCCATAA
CCAGACGAGTTTCAATCTCGAGTCTTATAGAGAGCGGTAATAACAACTGTCCCTCCATA
TGGATTATATATAG

YDR103W, 917 aa (SEQ ID NO 52)

MMETPTDNIVSPFFHFGSSSTQYSGTLRTPNQIIIELEKPTLSPLSRGKKWTEKLARFOR
SSAKKKRFPSPSPISSTTSFSPKSRVTSNSSGNGDGNLMTPTSTVSDYLPQHPRHTSS
LFRPNSNLPHFASNSNLSRANEPRAENLSDNIPPVAFPGYPIQRTSIKKSFLNASC
TLCDEPISNNRRKGEKIIELACGHLHQECLIIISFGTTSKADVRALFFPCTCKKKTINKAVQCI
PENDELKDILISDFLIHKIPDSELSITPQSRFPYSPPLPPGLSYTTPVERQITTYISQAPS
LNPNLILAAPKERNQIPQKKSNTYFLHSLPHGRRIPSGANSILADTSVALSANDSISAV
SNSVRKADDETKTTLPLLRSYFIQIILNNFQEEQLDQRIDGDYGLLRVLVKMLISKDQQR
YIQWCVFDFEDAFVIAEVDNDVDVLEIRLKNLEVFPIANLRMTTLEASVLKCTLNKQHC
ADLSLYLVQNNINDESTTVQVKMISGLNQDFVFNEDNITSTPLPIIKNFSKDVGNGR
HETSTFLGLINPNKVVEVGNVHNDNTVIRRGFTLNSGECRSQVDSIQSVLTTISSIL
SLKREKPDNLAIILQIDFTKLKEEDSLIVVYNSLKALTIKFARLQFCFVDRNNYVLDYGS
VLHKIDSLDSISNLKSSSTQFSPWLKNTLYPENIHEHLGIVAVSNSNMEEKSILFQ
DYRCFTSFGRRRPNELKIKVGYLNVYDSDKIDELVEASSWTFVLETLCTYSGFLSFDHDD
DDEENDDDTDELNDNSGSLSDAESTTTIHDSPFDNENATANMVNDRNLLTEGEHSNI
ENLETVAASSVQPALIPNIRFSLHSEEGTNENENENDMPVLLLSMDKIDGITRRSSFS
SLIESGNNNCPHMDYI

YDR238C, 3422 bp, CDS: 501-3422 (SEQ ID NO 53)

CCGTGCTCAAGATTAAACACGGTAGTCACTACTACACAAGGTCTCAGAACAGAAATGAGAA
TGGAACTCACTGGATAATGATTACGTAGAGTAATATATCGCGTCAGGACTCTGCTCCACAA
AGGATTATCGTGATGCTAATGCTAGAGTAATATATCGCGTCAGGACTCTGCTCCACAA
CGAATCTGATGTGGTAGACCTCAGCTATTCTCTGGGGCATGGCTGCGTGTGGCAAAACC
CTGATTACGACCCCAAGATGATATCCTTCTCTGTAGTTTGTAGATGCTATATGTACGT
TTATGGAACAGCATTTTAGAAAAAGTATTACCCAGCTTATCACTCTCGTTTTTTTTCTTT
CCGTGACTCGCTACAGGTAGAAGAAATCAGAAAAACACAGCTCGACAAGTGAATTTG
ACGTTTCATTAAAGACTCAGTTAAGATTGCCTTGAGAATAAAACAAAGTAATACAGTTAACT
TATTGAACAAGAGTGCACCTTATGACTTCACTTTCTTCAAGCCAGCGTACACGTTGGTTT
TCGATCCTTCTCCAGATATGGAGACTTACTCGAGTACCGATTTCAGAAAGCTCTTGAAA
AGGGAATCGATTGAACAAAAAATGACACGATGAAATCAATTTTGTAGTTACAATGCTGGAAG
GAAATCCAATGCCGTGAATTGTTGATGCACATAAAGATTGTCTAGTGCCTCTTAAAAATTA
AGGAATTAAGAAAGCTTTTGTACTTCTACTGGGAAATTTGTTCCAAACTAGCTGCAAGATG
GAAATTTAGACATGAAATGATTCTGTCTGTAATGCCATTCAACACGATTTGCAACATC
CTAATGAATATATATAGAGTTAACACATTAAAGTTTAAACGAAATTGAGAGAGGCCGAAC
TCTTAGAACAGATGGTTCCTCTGTCTTAGCGTGTCTGGAATACCGGTACATGATATGTTT
GTAAGTATGCCAATCTAGCAGTTTCTTCCATTTTCAAGGTACAGCGAACATTTACTTCCCG
ATGCTTAAAGAAATCATCAATTCGTTCACTAGTACTGAAACTGATCAATATGTAAAGAA
ATGATTGCTGATATAGAAAACCTAGACCTTTTATTACAAGCTGTCTTTGTTCAATTTATCA
GACAAAGATGCAAAACGAGACCCCTGCTTTGAAAGCCCAATATATCGAATTTATTGATGGAAC

FIG. 1 - 18

TGCTTTTCGACCAGCACTTCCGATGAAGTCATCTTCGAGACCGCATTAGCCCTAACTGTGT
 TGCTTCGCCAATCCAAATGTCTTGGTTCCTCGCGGTAAACAAATGATTGACTTGGCCGCTCA
 AGGTTTCTGATAATAACATTAAAGTTAAATTGTTCTAGACCGTATTCAAGACATCAATGCTTA
 ATAAACGTAGGTGCTTTTGAAGAGAGTTAACCCCTGGATATTTTGAGAGTCTTGAATGCGAGAAG
 ATTTTAGACGTTTCGTTCAAAGGCGCTTGATATTTCAATGGACTTGGCCACATCCAGAAATG
 CTGAAGAGTTTGGTTTCAGCTTTTGAAGAAGAGCGTCAACAAACCGTAAATAACCCAGATC
 AAGACAAGGCAATGCGATACAGACAATTTGTAATAAAAACTATTTCGTACCGTGGCTGTAA
 ACTTTGTAGAAAATGGCAGCAAGTGTGTTTTCGCTATTATTAGATTTCATCGGTGATTTAA
 ACTCGGTTGCGCCGAGTGGTATCATTTGCCCTTTATCAAAGAAGTGATCGAAAATATCCCAAC
 AACTTAGAGCCAATATTCCTTGAAAACATGGTTCAAACGCTAGACAAGTGAGATCTGGCTA
 AAGCTTACCGCGGTGCATTATGGATTATGGGTGAGTATGCTGAAGAGAGAAAGTGAGATAC
 AAGCTTTGTGAAGACACATTCGTAACAGCGTGAGTGAAGTTCTATCTTCAATTCAGAAA
 TCAAAAAGTTTAAACACAAAACCAAGAACACACCGAAGAAAATGAGGTTGACGGCTACCGGCA
 AGCCACACTGGTCTCAGTTATTCTACAGACGGTACGTATGCCACTGAAAGCGCTTTTCGTATG
 TGAAGACTTCTCAAAAGTCAGTTACCGATGAAGAACGTGATTCTAGACACTCCAATTCCGCC
 GGTTTGTTTTAAAGTGGTGATTTCTACACAGCTGCCATTCTGGCCAACACCATCATTAAC
 TTGTTTTAAATTCGAAAACGTTTCCAAGAACAAACTGTCATCAATGCTCTAAAGGCGG
 AAGCTTTACTAATTTTAGTTAGTATTGTAAGAGTGGGTCAAGACTCTTTGGTGGAGAAA
 AATTTGATGAAGATTCTTTAGAGAGATTATGACATCTATTCTAATTTATTGATGAAG
 TTAATCTCTGAGGAAAAGAAGGAAGATTAAACTTTCTGGAGGTTGCATTCTGGGACCA
 CCAAACTCTCATTAAGAGACAAATTTGAAATTTGCAAGAAGAACCAAGCATTAAGAGCAT
 TAAAGAACAGTTTCAAAAACATCGAACCAATTTGATACGCCGATTTCTTTTCGAGCAATTTG
 CTGGTGTGGATTCTACTAATGTGCAAAAAGATAGATTGTAAGAAGATTTACAACCTGGCAA
 TGAAGAGGAGATGCAATCCACGCTACTAGCAGCTCTAGTATTTCGAAGCTGAAGAAGATAG
 TACCTTTATGTGGCTTTTCTGATCCAGTTTACGCCGAGGCTTGTTATTACAACAACTCAAT
 TTGACGTCGTATTAGATGTTCTTCTTTGTTAATCAAACGAAAGAAACATTGAAAACCTCAT
 ATGTGCAATTTGCAACTCTTGGTGATTGGAAGATTATTGACACACACAGAACAGCAAGC
 TGATTCTCATGGCTCCACAAATTCAGTGTACTGTCAAAGTTTCTCTGCTGACACAG
 GTGTCAATTTTCGTAATATTATTATGATGGTGGCGCATGGTGAAGATGCTCGTTATGTTA
 TTTTAAACGACGTTTATGTTGACATTATGGATTATATCAAACGACCATGCTGACGATG
 AACATTTCCGTACCATGGAATGCAATTTGAGTGGGAGAACAAATATCGGTCAAATCAC
 AACTACCAACATTCGATGCTTATTGAGAGAACTGGTCAAGGGAACATAATTATGGGTATTC
 TCAACCATCAGATCGTGGAGAAAGATGATTGTAGGTTCTTAAAGTTGTAATCTGTATG
 CGAAGTCGTCCTTTGGTGAAGATGCCCTAGCCCACTTGTGTATCGAAAGGATTTCCAAA
 CCAATGATGTCATAGGTTATGTTCTGTATCCGATCAAAGGGACAAGCTTTTGGCTCTGCC
 TAGGTGACAGTAGGGCATTTGATTGCTAAGAAGACCAATAAATCTGCTCTCACTCATGTTT
 GA

YDR238C, 973 aa (SEQ ID NO 54)

MTSLSSQPAYTLVFPDPSMETYSSTDFQKALEKSGDEQKIDTMKSLIVTMLEGNMPPEL
 LMHIIRFVMPSPKNEKLKLLYFYWEIVPKLAEDGKLRHEMLVNCATQHDLQHPNEYIRG
 NTLRLFLTKLREAELLEQMVPVSLACLEVRHAYVRKYAILAVFSIFKVSEHLLPDAKEIIR
 SFIVAETDPICKRNFIFGLAELDRENALHYLENNIADIENLDPLLQAVFVQFIRQDANRT
 PALKAQYIELLMELLSTTSDSEVIFETALALTVL SANPNVLVPVAVNKLIDLAVKVSNNI
 KLIVLDRIQDINANNVGALEELTDLIDLVLNAEDLDVRSKALDISMDLATSRNAEDVVQL
 LKKELOQTTVNNPDQKAMQYRQLLIKTIRTVAVNFVEMAASVVSLLLDFTGDLNSVAASG
 IIAFIEKEVIEKYPOLRANILENNMVQTLDKVRSKAYRGALWIMGEYAESEIQCWKHI
 RNSVGEVPIIQSEIKKLTONQEHTENEVDATAKPTGPVILPDGTATYATESAFDVKTSQKS
 VTDEERDSRPPIKRFVLSGDFYTAALLANTIIKLVLFENVSKNKTVINALKAEALLILV
 SIVRVGSGSLVEKKIDEDSLERVMTSISILLDEVNPEEKKEEVFLDLLEAFGLDTTKSSFKR
 QIEIAKKNKHKRALKDSCKNIETDTPISFRQFAGVDSINVQKDSIEDQLAMKGDAIH
 ATSSSSISKLKLVPLCGFSDPYABACITNNQPDVLDVLLVNQTKETIKLNLVQFATL
 GDLLKIIDTPQKTNVIPHGFHKFTVTVKVSSADTGVIIGNIYDGAHGEDARYVILLNDVHV
 DIMDYIKPATADDEHFRMTWNAFENWKISVKSQPLTTHAYLRVLKGTNMGILTPSESL
 GEDDCRFLSCNLAKSSFGEDALANLCEKDSQNTDVIYGRIRSKGGQLGLALSGLDRVAL
 IAKTNNKLALTHV

FIG. 1 - 19

YDR259C, 1652 bp, CDS: 501-1652 (SEQ ID NO 55)
AAACTTTTGTTCAAGATTATGCTTCTTTGTAATTTTAAACATAGTCTTGCACCTTATTTTT
ACTCGCATGTGGATAAAAAGTTTTCGAATCGTTTGCAGGCAAAATGTAACATTAATCTTTTT
AATGATTTCTGATACTCTTTGATTCATTCTGTCTACATCTTTTCTGCATTGTAAACGCTT
AATTAAGTATTTCTTGGCCCTGCTTCTTTCCCTTTGATTCTCTTTTATTTCTCAAGTT
TTTAAATTTCTGGAGAACTCTCTTTTTTGTATTATTGTGTTAACACAGTTAGTGGAGCCTTG
TAGTATCGAGAGTAGACTATCTTTGGAAAGCAATGCGAGTTGAGAGATTGTGGAGTGAC
TACAGAACCAATATTAAACCAATCTTTCTCAAACCTGTAACACCGAGTTTTTTTCCCCA
CCAATCGTGAATCCGATAGCATATACCTTTGTCTAGAAATTTCAATTAACACAGATAA
CGAAGAGTGTCTAAGGGACAATGCAAAACCCCTCCGTTGATTGCTGCCGATATGTAATAAC
AGGGAAGCAGCTCAATGGCTACTTATAATGGCTCTGAGAAAGAACTCAATGAGCATCCCTT
CTCCGCAAAATGCAACGCCAGCAGCTCCCAAAAGTTACCTTATAGAAATAAATCCTCAAC
CCACTAATGGGGACACCGACATATCTGTTAAACAGCAATCCTATCCAGCCTCCTTTGCCAA
ACTTGTATGCACTCTATCTGGTCCGCTCTGACTATAGATCGATGCAATCAAGTCCCTATACATC
CATCTTATATCATCCCTCCGCAATTCAAATGAAAGAAAAAATCAGCTTCTTACACAGAC
CTCAAAATGCTCATGTTAGTATTCAACCTTCCGTGGTATTCCCCCTTAAAGTTATTTCCA
TATCTTATGCACTTTATCAAATAAATCCCTTTACCAATGGACTCCCAACCGAGCA
TATCTTTAAGTAAAGAGTATATTGACAGAGGAGCACTATCAACCTCCCAATCTCGCAAT
CCAGTGTGTACTACTGCACCTCCTTCTTTTCAAACAGTGTGTATACCGCTCAAAATTCAG
CTGATAATAATGATAATAATGATAATGTAAACCAACCTGCTTCTGATAAGACACCCAAC
TCATAAGTAGTTTTCAGGCAAACTTTAAGAAATACTAGAAGAGCTGCTCAAAATAGAACCG
CTCAAAAGGCAATTTAGACAAAGGAAAGAAAAATACATCAAGAACTCTCGAACAAAAATCAA
AGATATTTTGACGATTTTACTAGCAGAAAAATAAATCACTCAAAATCATTAACCGATTCAATTA
GAAATGACAACAACATTTTAAATAGCTCAGCATGAAGCTATAGGAATGCAATTACTATGT
TAAGAAGGTGAGTATGATGTCTTTATGTAACGAAAAACAACATGTGTGAAGAAATGAGAAATGTA
TAATTAATAAATGAAACAACATGTCAAGAAATGAAATGAAACCTTAAACCTTGAGAAAT
AACGCTTCCACGTGGAATATATACGAATGATCGAGGATATTGAAATCTATAAAGAAAGG
AACAGAACAACGAGATGAATAGACAACATAAAAAAAAATAAGATCCCTGGAGGAAA
TAGTAGGGAGACATCTCGGATAGTGCCACGTA

YDR259C, 383 aa (SEQ ID NO 56)
MQNPPLIRPDMYNGSSSMATYNASEKNLNEHPSQIAQPSTSQKLPIRINPTTNGDITD
ISVNSNPIQPPLPNLMLHSGPSPDYRSMHQSPHPSYIIPPHSNERKQASYNRPQNAHVS
IQPSVVFPPKYSISYAPYQINPPLPNGLPNQSI SLNKEYIAEELSTLPSRNTSVTTAP
PSFQNSADTAKNSADNNDNNDNVTKVPDKDTQLISSSGKTLRNTTRAAQNRTAQKAFRQ
RKEYIKNLEQKSKI FDDLAEENNFKSLNDSLNRDNNILIAQHEAIRNATMLRSEYDV
LCNENMLKNENSIKNEHNSRNNENENLKENKRFHAEYIRMIEDIENTKRKEQEQRDE
IEQLKKKIRSLLEEVGRHSDAT

YDR294C, 2270 bp, CDS: 501-2270 (SEQ ID NO 57)
CCGACAGTACGACTTAAAAAACAAAAACACGTCACAGGTGGAAGGCTGCCGCAAAATGG
TACACGGTTTAGATCAACAAGATCCAATACCCCTAATTACACATGAATGTGACGTTTCCT
AAAAGAAGTAGCCCTGTATATATAGAGAGATTTTATATACTTCTTAATGAAATAGAGCT
TTTCTCAAGTATTTTGACACTGGAAAAAAGAGAAAGTACATAGAGATTGGCCAAATATT
TAACTCTACACAGTTGCCTATCGTTTATCGCCTTATTCTTCAGAAACATTTTCATCAACTA
CTCTGGTGCAATTATTTCAATGTTAGTTACCATATATACCGGCCGCCGATCGGGGTTTTT
TGATTGAAAAAATTTGGTATATTTTTCAGTACACATATAATAAAACCCCTCAATTTGCCCTCT
CCAACCGTTATATCTATTCCAGATCCTCTTTACCGGACCAAGTAGGCTAGCTTCTGTAAG
GGATTTTTCATCTTAATACAATGAGTGGAGTACAAATAAAACAGTATCAATTAATGGTT
GGATATGGCAATGCCAATTCATTTACTAAGGGAAGAAGGCCACTTTGCCAGCTTATGAATTC
TAACCATCAACGAATTAATAATAGCCATACATGGTTACCTCAGAATAACCCCATGGTCA
ACATGTTGAAGGATTTATTGTTTGTGATCTTTTGTTACAAGCTAATAAGTAATTTTTTTT
ATCTGTTGAAGGTTTATGGGCCGTGAGGTTAGCAGTGAGAACATACGAGCATAGTTCCA
GAAGATTGTTTTCGTTGGTTATTGGACTTCCAGTACCGTAGAAGAAAGGAA
TACAAAGGCTCAAAACATCGATCGAAGACGAACTAATTAGATCGGACTCTCAGTTAATGA
ATTTCCCAAGCTTGCCATCCAATGGGATACCTCAGGATGATGTTATGGAAGGCTAAATA
AATTGAACAGCTTGATACCATACCCAATGGAAGGAAGGAAGGTCTCTGGTGGCGTTT
ACCACGGTGGTGATGATTGATCCACTTACAAACATCGCATACGAAAAATATTGCGTTG

FIG. 1 - 20

CCAATCAATTACATCCCGATGCTTTCTCTGCCGTACGTAATAATGGAATCCGAAGTGGTTT
 CTATGGTTTTAAGAATGTTTTAATGCCCTTCTGATACAGGTTGTGGTACCACAACTTCAG
 GTGGTACAGAATCCTTGTCTTTTAGCATGCTGAGCGCTAAAATGTATGCCCTTCATCATC
 GTGGAATCACCGAACCAGAAATAATTGCTCCCGTAACGCACATGCTGGGTTTGACAAG
 CTGCTTATTACTTTTGGCATGAAGCTACGCCACGTGGAGCTAGATCCAACGCATATCAAG
 TGGACCTGGGAAAAGTGAAAAATTCATCAATAAGAACACAATTTTACTGGTCGGTCCCG
 CTCCAAACTTTCTCATGGTATTGCCGATGATATTGAAGGATTGGGTAATAATGACCAAA
 AATATAACTTCTTTTACACGTCGACAGTTGTCTAGGTTCTTTATTGTTTCAATTTATGG
 AAAAGCGTCGGTTACAAAAATTCGCCATTACTTGACTTTAGAGTCCCGGGGAGTCACTCAA
 TATCATGTGACACTATAAATATGGATTGACCAAAAAGGCTCTGCAGTTATTAATGTATTA
 GAAACAGCGACTTCAGCAATGCATCAGTATTACGTAAATCCTGCTTGGACGTGGCGGGTTAT
 ATGGCTCTCTACATATTAGCAGGCTCCAGGCTGGTGCTATTGTCGTAGGTTGTTGGGGCA
 CTATGGTCAACTATGGGTGAAAATGGGTACATTGAGTCTGCCAAGAAATAGTCTGGTGAG
 CAATGAAGTTTAAAAAATACATCCAGGAAAAACCTTCAGACCTGAATATAATTGGGCAACC
 CTAGATATTCACTCATTTTCATTTTCTTCAAAGACCTTGAACATACACGAATCTATCGACA
 GGTGTGCCAAGAAAGGCTGGCATTTCATGCCCTTACAAAAGCCGGTTGCATACACATGG
 CCTTCACGAGATTGAGCGCTCATGTTGTGGATGAGACTGCGACATTTTACGTACTACCG
 TGCAGAGTGTGAAGAGCGAATCAAATCTTAAACCATCCCAGACGGAACTAGCGCTCTAT
 ATGGTGTGCGGAGCGCTTAAAACTGCTGGCGTTGCAGACAATAATGATTGTGGGATTCC
 TAGACGCATTATACAAGTTGGGTCCAGGAGAGGATACCGCCACCAAGTAG

YDR294C, 589 aa (SEQ ID NO 58)

MSGVSNKTVSINGWYGMPHILLREEGDFAQFMILTINELKIAIHGYLRNTPWYNMLKDYLL
 VFVIFCYKLLISNFFYLLKVYGPVRLAVRTYEHSSRRLLFRWLLDSPFLRGTVKEVTKVKQS
 IEDELIRSDSCLMLNFPQLPSNGIPQDDVIEELNKLNDLIPIHTQWKEGKVSAGAVYHGDDDL
 IHLQTIAYEKYCVANQLHPDVPFAVRKMESEVVSMLVRMNFAPSDTGCCTTSSGGTESLL
 LACLAKSMYALHHRHGTIPEPIAPVTHAGDFDKAAAYFGMKLRHVELDPTTYQVLDLKVK
 KFLINKNTILLVGSAPNFPFHGIADDIEGLGKIAQKYKLPVHVDSCLSFVVSFMEKAGYKN
 LPLLDLFRVPGVTSISCDTHKYGFAPKQSSVIMYRNSDLRMHQYVNVNPTGGLYGSPYLA
 GSRPGAIVVGCWATMVNMGNGYIESCQEIVGAAAMKFKKYIOENIPDLNIMGNPRYSVIS
 PFSKTLNIELSDRLSKKGWHFNALQKFLVHMAFTRLSAHVDEIDCLILRTTVQELKSE
 SNSKPSPDGLSALYGVAGSVKTAGVADKLVGFLDALYKLGPGEDTATK

YDR430C, 3470 bp, CDS: 501-3470 (SEQ ID NO 59)

ACGTCATTTTGTTCCTGTGGAGCTGGTGGTTCTTGTGGAGCAGATTCCCTGTGGAGCAGAT
 TCCGTGTGGAATCTGTGGTTCTTGTGGAGCATCTGGAGCCTGTGGTGGTTCTTGGTGTCTGT
 TCTTCGACTGGGGCATCGACAACAGATTCTGGTAGTTGCTCTACGTGAGTTTCTTGAGCT
 TCAGACATTTATCCTTATGGTTTTAGCGTAATTGCTTAATTTGATTCTTCAAAAAGTATA
 TATATTTAGAAGAGAGGAAATATTTTCTCATGTCTTTTAAATCCCTTTGGGTGGCG
 AAAAAAAGAAGTATAAAAAATTTGCCCTTCGTTTACAGTGATAAATATACGGAGGGGCT
 CTATGATAAAGGTAGTAGTAATCATTTGAATTGTTGAACAAGCATTGACAGATATGATAA
 CAAGCAATTGTAAATCAATAAGCCACCAATTAGAAGGCTACTCAAAAAGATAAAGTTTAA
 TAAAAATACTCGGATATATATGTTGCGGTTTACGCGATTTCGCTCCTCGATGCCCCAAG
 CACGCGCGCTTGAAAAATATCCAGTTGGAAGTATATTCATGGTTATGAAGTGAGAAGAA
 TTCTACCGGTTCCGGAGCTGAGACTCAGTCGGGTAGATTGGTGCACTCCGACAGAGGAG
 CCGAGCCTTGCATATTGATAGAGACGACAAGATAATGTGTTTACAGATTGCTTTTAAAA
 CCAACCCCTCCAGATTCCACTGGGGTCCCTCATATTCTAGAGCATACAAGCTGTGTGGGT
 CTGTTTAAATATCCAGTTAGGACCCCTTTTTCAAAATGCTAAATAAATCTCTAGTAAAT
 TCATGAACGCTATGACAGGTCAGATTATACATTTTTCCTCTTTCACACTACGAACCTC
 AAGATTTCGCTAATTTAAGAGGTGTTTATTAGACTCCACCTTGAATCCGCTACTTAAAC
 AAGAAGATTTTGATCAGGAGGGTTGGAGGTTGGAGCATAAAAACATCACAGACCCGGAGA
 GTAACATTGTTTCAAAGGTGTTGTCTATAACGAAATGAAAGGTCAAATATCAATGCGCA
 ATTACTATTCTCGAGTAATAATTACAGCTCTATTATCCTTCCCTGAATAACTTCGCGG
 GAGATCCCTATGAAAAATTACAGACTTGAGATACGGCGATCTCTGGATTTCCTACAAAA
 ATTACACTCCCTCAATGCAAAAACTTTCACGTACGGTAACCTTGCCATTGGTGATACGT
 TAAAGCAATTAAATGAGCAGTTTCACTGGTTACGGGAAGAGAGCTCGAAAGGATTAAGTTGT
 TAATGCTCATTTGATTTAAAAAAGACATAGATGTCAAGTTACTGGCTCAAATAGATACTA
 TGCTTCCACCGGAGAAGCAGACAAAAGCCTCAATGACGTGGATTGTGGAGCGCCACAG

FIG. 1 - 21

ACACATATGATACCTTTTGTGTTAAAGTACTGGGGAAATTATTAATGGATGGCCATTCTT
 CTGTAATGTATCAAAAATTAATAGAACTAGGAATTGGTTGGAGTCTTCGCTAAATTCAG
 GTGTTGAACCACTACAGCAGTAAATTTGCTAACTGTTGGTATACAGGCGGTGAGTGATA
 TTGAAATATTTAAAGACACTGTAATAATATTTTCAAAACCTGTTGGAAACAGAAACATC
 CTTTITGACCGCAAGCGTATCGATGCCATAATTGAACAATTGGAATTATCTTAAGAAAGGATC
 AAAAGGCTGACCTTTGGACTTCAATTACTCTATCTATATACTACCTGGTTGGACAAACAAAA
 TCGATCCCTTTTGAGAGCTTGTGTTTGGAGGAGCTTTGCAAGATTGAGAGGTGATCTTAG
 AAACCAAGAGGTGATACTTTATCCAAGATTAAATCCGTAATATATCTGGTTCATAAAACCTT
 GTTTCACGTTTTCATTACAGGGATCTGAAGAGTCTCTAAATCTTTGGTATGATGAAGAAC
 AAACAAGACTGAGAGAAAAAATTACTGCCTTGGATGAACAAGACAAGAAAAACATCTTTA
 AACGTGGTATACCTGTTTACAGGAGAAAAAATGAAGAAGAGATTATCTCTGTTTACTTA
 CCTTACAAATAAAGACATCCCAAGAGCTGGTGATAAATATTCATATCGAACCAAGAAATA
 ATACAATGCTTAGAGATTACTGATACCAATGGTATCAATATCTCAGAGGTAAACGTTTAC
 TAAATGACATAATACCTTTGAACTCTTCCCATACTTACCTTTATTTGCTGAATCGTTAA
 CTAACCTAGGGACAACAACAGAAATCCTTCAGTGAATAGAAGTCAGATAAAATTCATATA
 CGGGTGGTATATCAACACATGTAGAGGTTACATCTGACCCCTAACACCACAGAGCTCGCC
 TGATTTTCCGGGTTTGACGGATGGTCTTTAAATTCGAAGACCGACCATTTTGTAAATTCT
 GGTCTTAAGATCTTACTAGAACTGATTTCCTATAAAACACGCGATAAATGAAAGTTCTTA
 TCCGCTTATTAGCATCTTCAACACATCTCTGTAGCAGATGCCGGTTCAGTATTTGCAAC
 GGGGCTATTCTGCGCACATTATAGATCAAGTGGAGCTATAAATGAGACCCCTCAATGGTA
 TTGAGCAACTCAATTTATAAATAGATTGCACAGCTTGTGTAGACAAATGAGAAACTTTCC
 AAAAGAGAAGTTGTGCAAGCTTAACCTGAATTTGCAAAAGTACATTTGTATACCAATAACA
 TGAATTTTTCATCACTCAGACTCTGATGTTTCAAGCGAAAACAGTAGAAGAACCAAAATTT
 CAAAATCTGAGAGAGATTACCTCATGGCAGCTGCTTGCCCAATGGACCAAAGACTTCAG
 ATTTATCTCTTATTTGGATCCAAATGTAAACATACITTTGATAAAATTTTCCCTTTCCAGGTC
 ATTAGACATCCCAAGCTTTTATGGGTGTGCGGTATACACATAAGTAGGGCTCTGACACTTC
 AAGTTATGTCAAATATGCTAACATTTCAACACTTTGCACAGAGAAGTCAGAGAAAGAGGTT
 GTGCTGTGTGGTGGTGTCTTCTTATAGCGCTTATAGCGGGTATTTTCAGTTTCTATTCTCT
 ATAGGGATCCTCAGCCTTTGAAGAGTTTGAAGAACTTCAAGAAATAGCGGGCGTTATATAC
 TGAACGATGCCAAGTGGGGCGTCACAGACCTTGATGAAGCTAAATTCACATATTTTCAAC
 AAGTAGCGCCACTTAAAGTCCCAAAGGAGAAGCGGTGACGTATTTTCATGAGCGGTGTTA
 CAGACGATATGAACAAGCAAGAAAGGGAACAACCTCTAGACGTATCTCTCTCGGACGTTCT
 ATAGAGTCGCCGAAAAATATCTACTAAACAAGAGGGGTGAGTACGGTCTTAGGACCTG
 GAATCGAGGGGAAGACTGTTTACCACAAATTTGGGAGGTGAAGGAAGCTGTAG

YDR430C, 989 aa (SEQ ID NO 60)

MLRFQRFASSYAQAQVRKYPVGGIFHGVEVRRILFVPELRLTAVDLVHSQTAGAHLHID
 RDDKNNVFSIAFKTNPPDSTGVPHILEHTTLCGSVKYPVRDPFFKMLNKSILANFMNMTG
 PDYTFPPFSTTNPDQFANLRGVYLDSTLNLPLKQEDFDQEGWRLEHKNITDPESNIVFKG
 VVYNEMKQGISNANYFYFWSKFQQSIYPSLNNSGGDFPMKITDLRYGDLDDPHKKNYHPSNA
 KFTFYGNLPLVDLTKQLNEQFSGYGRARKDKLLMPIDLKDDIDVKLLGQDITMLPPEKQ
 TKASMTWICGAPQDTYDTFLLKVLGNLLMDGHSSVMYQKLESGIGLEFSVNSGVEPTTA
 VNLLTVGTQGVSDTIEIFKDTVNINIFQNLLETHEFPDRKRIDAITEQLSKKDKQADFGL
 QLLYSILPGWINKIDPFESLLFEDVLQRFGRDLETFKGDTLFDQLLRKYIVHKPCFTFSIQ
 GSEFSSKLDDDEBQTRLREKITALDEQDKKNIKRGILLQEKQNEKEDLSCLPTLQIKDI
 PRAGDKYSIEQKNNTMSRITDNTNGITYVRGRKLLNDIIPFELFVYLPLFAESLNLNLGTTT
 ESPSEIEDQIKLHTGGISTHVEVTSDFNTEPRILFGFDGWSLNSKTDHILFEFWSKILLE
 TDFHKNSDKLVLRLLASSNTSSVADAGHAFARGYSAAHYRSSGANETHLNGIEQLQFI
 NRLHSLLDNEETQREVRVDKLTQLKYIVDTNNMNFITSDSDVQAKTVESQISKFMERL
 PHGSGLEPNKFTSDYPLIGSKCKHTLIKFPQVHYTSQLLGVPTHKDGSGLQVMSNML
 TFKHLHREVREKGGVGGGASYSALAGISFYSYRDPQLPSLETFKNSGRYLLINDAKWG
 VTDLDEAKLTIFFQVDAPKSPKGEVTFYMSGVTDDMKQRRLEQLLDVLRHVAEKY
 LLNKEGVSTVIGPIEGKTVSPNWEVKEL

YDR438W, 1613 bp, CDS: 501-1613 (SEQ ID NO 61)

CTTTTCTCAGCACTGTCCAGAGACATAACATCAACAATCACATCGCCCCAGTAAATGCA
 TACGCAAGATAAGATACAACCTGGCTACGGGAACACTACGCCAACGCTGATTGGCAATTGT
 GCTCTAATAGTTACTCTATTATTGCTGTTAAATTGACAATGTTTAGTCACGTGCAACACAA

FIG. 1 - 22

TTCAAGTCACGTGGAAGGCCCTTCACATGGTGTATCCATCTTCTACATCTTCATCGGTCTT
GCATAAAGTCATAATATGGGGCTACTCGGAATGTATGCACCTTAACAGTACTATTATATGGT
GAGGCGTGAATGCTTACCGTCTTTGTGGCTATTCTCGTATTCTGTAGGCCCCCCCATACAC
ATTTTTCGGTAAGTCGCGCATAGATGAAAGTTGAAATGAATATTCAAAGAATATATA
TAATAATGCAGGAGATCAAGGAAGAATAGATATGTATAAGAGTGTATGCTAGAGCAAAA
AATAAAAAGTAAGCAGGAGAAATGAATCGTGTGGTATAGACGTAGATCATATGATAGGGG
TCTCGTCTTCGGCCCTAGTGGTGGTGTTTGGGTTGGCGCTTCGTGTTTGACATTAATGAAT
TGCTCGAGACAAAACCGCATACAATAAACCTTCTTCCTTACTTATCTTAAACATTAATCGT
TTGCTCTTTATTTGACGCCAGATCTATGGAGGATAATCCAAATCAAGAAGGAGAGCTTGC
AGGAACAGCAGCAAGAACATTAACCTATTACACACAGAATCTTTTTCAGAGTCCCTTAC
CTTTACTATCTTCAACTCCTTCTACTTCTCAAATTTGCTCTCGATAGCGGACAGGAAG
TGAAGATACAAATGAGGTTGAGTCTGCTATTTTGCGTCTTGTGGTTTCGTGGCAAAATTTGG
CGGCTAACGCTGCTTTTGTGCTATACCACAGTGGCTTCGTCAACAAATCTTCTTACATGCAT
CCTCATTTTTTACCTTATTCTTTCGCACTAGCTTAGGAATAGAAATCTTTTCGACAAAAA
AAGTCTCGGGTATTATTGTGCTTTGTTTGAATTTATCTTAATTGTGATGCAATCTCGA
AGCAACAGGATTCTGTGAGTGTCTTCTCTCTTTTGGTAGGTAACACTTTAGCACTGCTGG
GGTCAATGCGTTACAGTGTCTATACAAACCTTTTGAATACGAAATATCATCCAAAGGTC
TCAGACTAGACATTCAGATGTTTCTTGGTTATGTTGGTATCTTCAGCTTTCTGTGTTT
GGCCAAATTTAATAATCTCGGATATAACACATATGGAACACTTTGAACTACCAAGTAATCT
TCCACATTTCTTTCTTGTGATGTTAAATGTATCATTATCTTTGTTAGTGACTATTTT
GGTGAAGCCCTCATTTTGAATCACCCTTGGTGGTTACCGTTGACATCTTTTACTA
TCCCGTTAGCCATGTTTCGTGATTTTGTATGGCAGAGGCAATTTTACGCTTTGGTATA
TCATTGGTGTATTTTTCACTTTTGTTCATTCTTTCTAGTTAACCTCGGGGAGAAATCTG
CTGTTGAAAAGGACTGTGCTGCGGTGAAAAGGACCTATCTTGGATGCTCAA

YDR438W, 370 aa (SEQ ID NO 62)

MNRVGIIDVHMIQVLLVAVVVVFWGASCLTNELLEYNAYNKPFFLYTLNIISSFALYLP
DLWRIIQSRKSLQERTERTLPHTQESFEFLPLLSPTSPSSNLSSIIDTKVDLMRL
SLLFCVLWFVANLAANAALSYTTVASSLTSSSFFTLFLATSLGIEFTSTKLLGLFLV
SLFGIILVMQSSKQDVSASSFLVGNLALLGLSLGYSVYTLKLEYISKKGLRLDIQM
FLGYVGIFFTLFWPLILIIDITHMETFELPSNFHISFLVMLNCIIIFVSDYFWCKALLL
TSPLVVTVALTFTIPLAMFADFVWREAFFTPWYIIGVIFIVSFFLVNHRGESAVEKDCA
AVEKGPILDA

YDR450W, 1376 bp, exon1: 501-547, intron1: 548-982, exon2:
993-1376 (SEQ ID NO 63)

CGGCCCATGAGCATAAAATGAGAAGATATTATTAATCTAGTATATTTTAGGAACAGCA
GGCCATTATATCCAAAACCTTTTAAATAGCATCCACATCACTTACTGGCGTACAGTTT
CGTGTCTGGCAACAAAAAGTACATTTAATTTCAATGATTAAGAACATTAACATCCG
TACATTACGCACCCATGCATGCTATCTGAAAATATTCTACATGCTGCTTTTGAAGATTTG
AAGCGGCATATGGTGTCTTCTTGGCGAGACGCGCGCTCAGGGGAACGCGGATTCCGAAAG
ATGCGCTTCCCATGCCATATGCCATCCCAAGATCATGCCCGGAGAGCAAAATGTCCGC
CGAGCCAGGTCGGACACATCTGTCATTCGACCCTAAGTATTTGTCAAAGCTAGGGTTAAT
TGAAGATTAGCTCTTACATGTTATTAGTAGAGTTTAAACGTTGAGATTAAGTGAACGTA
TACACAAGAGCGGATAAAAGATGCTTTAGTTGTCCAAGAACAGGTTCTTCCAACACA
TTTTTACGGTATGTTTATTATTAAGTAGTGAGCTATGACAAAATCGGCTTAAACCTTAAAA
TATGACAGACAAGAAAGAAATTCATTCACTCTTTAATCGTGGCGATTATTCGCTAACG
ACGTGATTAATATAATGATGTTTCCGGGCTGGACTAAGAAGCTAATAATTAAGGCTG
ATGAACAAATTTATGTTTATGTCATCAAAAGGAACATGAATTTGGCATTAAGCGCACATA
ATTACGGAACATTGCAATAGCGGTCCGAGGTAAAGTACCGGAATGCTTTTCAATGAATC
AGCTATTGGCGGATATTGACCAACCAACTAAAAATTTATATCTCTGCTCCGATTTTGT
CTTGGCGGTGAAATCCATTATGCACATTTTACTAAGCTTTTACCACTTGGTCTGTGTAAG
CCGTCTAAATTTTTCACGCAGTTTGTGGAACACTAACGTTGACCGTAACATTAAAGATCG
ATTCGCTTTGACCACATCAAGGGTGTGGTGTGCTTACCTCAACTTGGTCTGTGTAAG
AGGCTGATGTTGATTTTACACAAGAGAGCTGGTGAATGACCCCAAGAAGAAATGGAAGAA
TTGTTCAAATTAAGCAAAACCAACTCACTACAAAATCCAGCTTGGTCTTGAACCGCT
AAATGACATCACTGATGGTAAGGACTACCACATTTGGCTAACACAGCTGCAATCCAAAT

FIG. 1 - 23

TGAGAGATGACTTGGAAAGATTAAAGAAAATCAGAGCTCATCGTGGTATCAGACACTTCT
GGGGTTTCGGGTGTAGAGGTCAACACACCAAGACCCTGGTAGAAGAAGAGCTTAA

YDR450W, 146 aa (SEQ ID NO 64)

MSLVVQEGGSFQHILRLNLNTNVDGNIKIVYALTITKVGRRYSNLVCKADVDLHKRAGE
LTQEELEIRIVQIMONPHYKI PAWFLNRQNDITDGKDYHTLANNVESKL RDDLRLKKIR
AHRGIRHFHWGLRVRGQHTKTGRRRA

YDR486C, 1289 bp, CDS: 501-1289 (SEQ ID NO 65)

ACTGCATACACAATAACGTAGATGTAGCCCAAGGCCTACCACAGGTATTCTGCTCAC
GACAGGTCGATGACTTTGAGGGCTCTTGCAGACTCTTCTCTACGCCAAAATCATTTTTTA
AAACCAGGGCACATCTGTCCCTTGAGAGCCGCTGATGGCGGTGTTTTCGAGAGAAGAGGC
CACACTGAGGCGCGTGTGCTATTTGTGTAAACTAAGTGGACTAAGTCCCGCTGCTGTTATT
GGCGAATTGGTTAACGATGACGAACAAGGAACATGATGAGATTAAATGACTGCCAAGCG
TTTGGTAAGAAACATGGCATTCCTTTGATCTCCATCGAAGAATTGGCCCAATATTTTGAAG
AAATAATCTGGTGAACATTTTCTCCATTCATCTATCACAACAGACTCACACATATATAC
ATGATATATATTGTAACTTTGTATATATCTTTTGTGTTTTTGACCTTTTCTTCTCTATG
TTTTTCAGCCATAAAAAATATGGGATTTTAGCAAGAGAAAAAGTACATCTAAAAAAG
TAGTAAATAGGAGGAAGCAAGATTTGGTTGAAACACAGTTATAAACTCTTCAAGGCAATTA
TGAACAGGATTTTCGGATATGGGAACAAGAGGCCATGATCAGCTCTTACAGAGATCGA
ATCAGTCCATGAATCAGGCCCAACAATCACTATCGAACAAGATATCCAGTGTAGATATC
AAATCGCCCACTTAAACTTCCAGCTGCAAAATATTCAAAGAATTTCGAAGATCAACAA
ACAAGCAACCCCTCGTTAAGAAAAACAGGCTTTGAAGATTTTAAATAAAGCTAAACAGTTAG
AAAATATGAAGGATTTCTTTAGATTCTCAATCTCTGGTCCATGACGCCAAGCCAGTTAAACAA
ATGATAACTTACAGAACACATATGATCACTATAAAGCGCACTAAGCAACAAACAAATGCCA
TGAAGGCTCAATACGGCAAGATATAATATCGACAACTACAGGACATGCAGGATGAGATGC
TGGATTTAATAGAACAAAGGGGATGAGCTGCAAGAAGCTTTGGCAATGAATAAAGACTG
GCGAGCTCGACGACATAGTGTATGACAGAGCTGGATGACAGAGCTGGATCTCTGGCACAAG
AGGATTTTCACTTTTGCCCAACGAGCAAAAACCTATTAGGTAAACGATATGCCAGTTACTTAC
TAGGTGCGAATGCGCCACCGGCTTTTATTGATGAAGAGCCAACTTAGATACTGAAGACA
AAATAAAGCTTTTGAAGAGCGCTCAGTGA

YDR486C, 262 aa (SEQ ID NO 66)

MGFLAREKVHLKKVVIGGSQDWLKHYSYKLFKAIMNRIIFYGNKKSHDQLQESNQSMNQA
QQSLSNRI SLDLTQIAQLNFQLQNIQKLNQRSNNKQPSLRKQALKILNKRKQLENMKDLS
DSQSWSMTQALQTLNDNLQNTMITINALKQTNNAMKAQYKINIDRLQDMQDEMLDLIEQG
DELQEVLAMNNNSGELDDISDAELDAELDALAQEDFTLFTSENSLGNMPSYLLGANAPP
AFIDEENPLDIEDKNKALESQ

YDR471W, 1295 bp, exon1: 501-531, intron1: 532-915, exon2:
916-1295 (SEQ ID NO 67)

GGCAAAATCAATTAAAAATTCCTTTTCTCTCTACCTTTTGCTAATATAAAAACCATAGTTGT
AAGGGGTACTTAAGTCTATATTTCTGTAAAGTTTCTTATTTCCACTTGTTTTTCCAAATT
CTTACCAATTTGAAGACTATGTTTTTAAACACCCAAATCATTTTCCACCACGACATATATT
ACCCTTTTTTTGGGTGAAGAGAAGTAGTATTTTGTGTTTTCATGGGAGTGGAAGTCTTCTT
AAAACATAACCGAGCAGTAGTGCTGTCTAGGCGGAGATATTGAAAGTTCGGCATCGGCTC
CAGCTAGCGTTTTTGGTACTACCTGTCAAACCCGGCGTCTGCCTAGATTGCGCGG
AGGTTACGTTGAAACTTTTGCCCTTTCCAGCTCAGTTTATAATATCAAAGAGCAGCAATATA
CACATTTAATGGTTTGGCCCTTAGTGACTATTAGGCGGTTTTGGTGAAGAGAAAGAGCTCGC
TCAAAGAAATCAATATAACCATGGCTAAATTTTGAAGCAGGTAAAGTTGGTAGCTAA
TTTAAACAGAGCAACCGCTCTAATTAAGATATCGAATAAAGGGGACTTTTACGGTGCATAA
TAGGGAAATTTGTACAATCTGAGGGACAACAAATATGGAAGCAGTACATGATTGTTATTG
TCATTGTAGGAGGTACCAATTTGTGCCAGTAAAAAAGAGAGGCCCGGGGAGCACCACAT
CAGCAACAATCGTGTGCTGATCTGCAAAAAAGGCACATGGAATATGTAATTTTACAGTTTC
AACACTGAGTTGAACAGATAGCTATCTAATCAATGTTAACTTTCCAGGGAACAAAAGCT
AATCCAATCTCTCTTTTATTTCAAAATATCATGAAATAGAAAAATTTACTAACAAAT
TTCTGATATCTGATAGCTGTCTGTTGTTCTGGTCTGTACGCTGGTGAAGAGGTTGTGATCG
TTAAGCCACACGATGAGGGTTCTAAATCTCATCCATTGGTTCACGCTTTTGGTTGCCGGTA

FIG. 1 - 24

TTGAAAGGTACCCATCAAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTCGTAAGAGAA
CTAAATTCAGCCATTCATCAAAGTCGTCAACTACAACCACTTATTGGCAACCAGATACA
CCTTGGATGTTGAAGCTTTCAAGAGCGTTGTATCTACAGAGACTTTTGAACCAACCATCCC
AACGTGAAGAAGCCAAGAAGGTTGTAAAGAAGGCATTTGAAGAAGACATCAAGCTGGTA
AAACCAATGGTTCCTCTCCAAGTTGAGATTCTAA

YDR471W, 136 aa (SEQ ID NO 68)

MAKFLKAGKVAVVVRGRYAGKKVVIVKPHDEKSKSHPFHVALVAGIERYPKSVTKKHGAK
KVAKRTKIKFFIKVNVNHLPLTRYTLDEAFKSVVSTETFEQPSQREEAKKVVKKAFEE
RHQAGKNQWFFSKLRF

YDR499W, 2744 bp, CDS: 501-2744 (SEQ ID NO 69)

TAACAAATAGAAAAATACACACATTAGATTGGAATTAGAGCTTAAGTGGTACAAACT
AGGCGTAATTAAGAGGTTAACGGTTCGTCTCTACTAAGGTTGCTATTGTGTGGCACCAGAT
GTTAAGCACCTTTTAAGCGGAATAACTTCAGTGGAAAATTTTATGTTTAGTTAGGTTTACC
TTGAAATTTTTTAAAAAAAAGAGTCAGACAGGCTCGCTCTTCCCTACTAAATATTAGG
AGCAAAAGCAGTAAAAAGTCTCTGAATAAGGATAGTAACCTGTAGTAACCTCAAATTTTAT
CTTCAAAAGAGCTATTAGTATCTTGGTCTCTCTATTTTCTTCGATTATTGGTGTATTTTC
CCGCTCTAGCCAAATCCGAGCGTTCCATCGATTTTTGGGGAAAACGAGCACATGCAATA
AAATAAAAAGCAACAAATACGCGATAGTGCAGAAACGTCACACCAATCATCAAACTCT
TTTGCATATTTCTATTATAGATGAGACGAGAAGACGGTGGGTGAATTTTCTTCAGATGAGC
ATGATGATATTTCTTTTGGAAATTAGGCACCGCCCTCCAAGGTTTACTCAAATACCGCCAT
CATCAGCAGCATTAACAAACACAAATTTCCCACTACTTTGGAGGTTACAAACGACCACATTA
ACATAAAGCAGATAAAAATGATAACCAACTGGTTAAACCACTGAATAAAGCTCAAGGTT
AAGCAAGCATGCTTCGTGATAAAATAAACTTTTGAACATTTGAAAGGGAAAAAGGAAAGA
ATATTCTAAGCCGTCAAAGTTAATGAATTGCAAGTCAAGCATCTTCAAGAGTTGGCTAAAT
TAAACCAAGAATTACAGAACTGGAAGATGAGAAGAAGTTCTTACAGATGGAAGCGAGAG
GAAATCGAAAAGGGGAAGTTATTACGAATGTAAACACCGCTCAACCAACATTATCAACAA
ACACAAACACTATAACGCCAGATTTCGTCTCAGTTGCAATCGAAGCAAAACCTCAATCAC
CACATCAAAAAACCTAGATGAAGTGAATAATTTACTGAAAAAAATATGGTTCCCTCAT
ACCCAAATACGATTTATTTCCGATGAAACGAGTTTATTTCTAGAGTCAATATTACTTCTAA
AAATAATAGGCGCTGACCTGAGCACAATAGAAATATTAAATAGATTGAAGCTTGACATACA
TCACAGGTTTAAATTTAAGAATTTTCGTCATTTGCTAAAGGAGCCCCCATAGGGAAGTCCA
TAGTTTCTCTAATTTTCCGATGTAAAAAGACGTTGACCTCGACAGGTTTCATAGATACCT
TGCTAGAGGATATAGCTGTTTGTGATCAAGGAAATATCAGTTTCATCCAAATGAATCGAAAT
TAGCTGTCCCAATTTCTCGTTGCATTGATGTATCAGATGTACAATTTTCGTCCTAGTGCCA
CTCATAAATTTAGCACTGAAGGATTGTTTCTTTTATTGCGAATTTAATAAGAATCTATC
ATCATGTATTGAAAGTACCAGATACATGAATCAAAATATGAATTTGCATGTACAACTCAGA
TTTTCCAATATGAACGTAGACTATTTGATAATTTGCTATTCCTTTGATCTCTCTAGAG
GTATATTAAAGGTAAGTGCAGTCGCATCCTAAGCAAACTTATATGGAATTTTGTAGTAAA
ATATTCTAAAAATCATTTGAATTTGTCTACAAACTAGCACTAACCAATTTATACAAAGCAA
TGGTAAATGTAAATATTATTAGTGCAAGTCGAGGTCGTTAATATTATCACTAGTATAAATATTAA
ATATGGACAATTCCTCAGATCTGAAATCCTTGATAAGCGGTAGTTGGTGGAGAGATTTGTA
TTACAAGATTTATACGCTCTTTTGGAAAAAGGAAATTAAGAGTGGCGACGCTATATAATGAAA
ATGTGGATACACAACTCTCATATGTGCGAAGTACCATGACTTTTGGGTTAATCCGAA
ATATAGGTGATAATGAATTTGGGAGGATGATATCAAAGCTGATTATATCTAGCCGATTGC
AACGTGTGCCAAGGGTAAATTTCTAAAGAGGATATTTGGGATGGATAGCGCAAAATTTCACTG
CCCTCTATAATAGGTTTACAAGATGGAATAATGGCTTTTGAAGTTAAAGATGAAGTTTAA
ATATTTTGTAAATTTTATTAATGATCTATGGAGACGATGCGACCATAGTAAATGGAGAAA
TGCTCATTCACCTCTTAAATTTCTATCCAGGAGCAAGCGTTAATGTAGTAAAGAGTACG
TGGGACAAGACTCCCGAACTTGGACCTCAGATGCCATCTTATTGAACATACTTTTAAACCA
TAATATATAGGCTATTGGAAGACCAATTTCAAACAATTGCGTGAAGAACAATCAAGCAGG
TAGAAAGCCAAATTGATTATGTGCACTATGGAGGTTTCTCGTATGCCAAACCGAACTGTGA
CGCAACCAAGCAAGAGAAATGAGAGATCATCGACACCTTTGTAGATAGTTTGCATGATCTGA
CGATAAAGGATCAAGCTCTTATTACGAAGATGCTTTTGGAGATTTACCAGATATATCG
AAGAAGAAATTTGAAGATGCAATTTGAATAAAGAAAGCGGGAGAAATATGCAAGTAAAGTACG
ATGAGAAATTTCAAGAAATGGCAAGAACTATTCTTGAGTCAAAATCATTCGATCTAACCA
CACTAGAGGAGGCCGATTCTATATATCTCAATGGGACTGTAA

FIG. 1 - 25

YDR499W, 747 aa (SEQ ID NO 70)

MRRETQVGEFSSDDDDILLELGT RPRPRTQIPSSAALQTQIPTTLEVTITTLNNKQSKN
 DNQLVNLQKAQGEASMLRDKINFLNIEREKEKNIQAVKVNELQVKHLQELAKLQKSELQK
 LEDEKKFLQMEARGKSKREVITNVKFPSTTLSTNTITITPDSSSSVAIEAKPQSPQSKRKR
 ISDNLLKKMVLNPNRIIPDETSLFLESILLHQIIGADLSTIEILNRLKLDYITEFKFK
 NFVITAKGAPIGKSTIVSLLLRCKKTLTDLRFIDITLLEDIAVLKEISVHPNESKLAVPFVLV
 ALMYQIVQFRRPSATHNLALKDCFLFICDLIRIYHHVLKVPVIESNNMLHVEPQIFQVELI
 DYLIISYSPDLLLEGILRVLQSHPKQTYMEFFDENILKSFEEVYKALATI SVKPVNWNVIFS
 AVEVNNIITSIIILMNDNSDLKSLISGSWWRDCTIRLYALLEKEIKSDGVVNENVDITTL
 HMSKYHDFGLIRNIGDNELGGLISKLIIYTDRLQSVPRVISKEDIGMDSDFKTAPIIGYK
 MEKWLKLLKDEVNLIFENLLMIYGD DATIVNGEMLIHSSKFLSREQALMIERYVGQDSPN
 LDLRCHLIEHTLTIYRLWKDHFQKLRREEQIKQVESQLIMSLWRFLVCQTETVTANEREM
 RDHRHLVDSLHDLITKQDASYEDAFEDLPEYIEEELKMQLNKRTRGRIMQVKYDEKFOEM
 ARTLLESKSPDLTTLEEDSLIYSML

YDR507C, 3929 bp, CDS: 501-3929 (SEQ ID NO 71)

CTCTTTAAATATTCTATGTACTTTGTGCAAAACATCATTGTCATCACATAAATGCATCTCT
 ACTATTACTACTTTGAACCTTCACTTCACTGGAAGAACTGGGTATTCAAGAGTAAAGAAAT
 CATTTGTTTTCGCCCAAGTTTCGTCTGACAAGAAATTTTATTATTATTCCCATCTTTTC
 ATCGAAGAAACCGCTCAAAATCCATTTCGTACTACGCGCAATCTGCGTATTATTCTCTTTT
 CGGCATACCATCGCGAAATATCAACGGCCACACCATAGATTCTTTTGATGTAAATATAA
 AAGCGACTGAATGAAGTGCACACATTTTTATTCTCTTGATTCTTTCTTTCTTTTGT
 TTTGCTTTCTCTCTGTCGACACAGTCTCAACTGTA CTACCATTAGTATTCTCGAAGGC
 TTTAGCAGACTTGTGAATAATTAATTTGCCCACTTTGATCAAGAAAGATATTCGCGACACA
 ATACAATAATAACATTCAAAATGGCAATCAATGGTAACAGTATTCTCGCATATAAGGATA
 ATACCATCGGTCCATGGAACTAGGTGAAACTCTCGGTCTAGGAGCACTGGTAAAGTCC
 AGCTTGCTCGTAATGGATCCACAGGACAAGAGCGCGAGTTAAGGTAAATATTAAGAACG
 TATTCAATACCGGTAATGTCAGCGGTACTTCGATTGTTGGCTCCACCAACCCAGATGCTC
 TACCATATGATATAGAACGCGAAATATCATTTAGAAAGTGTATAAACCCACCAATGTGT
 TACGTTTATATGATGTCCTGGGAAACAAATACAGATTTATACCTTGTTTGAAGATACGCGG
 AGAAAGGTGAGTTGTTCAACTATTGGTTGAGAGAGGTCTCTGCCAGAGGATGAAGCTA
 TCAGGTTTTTTAGACAAATTAATTATTGGTGTGTCGTACTGTCTATGCGTTGGGTATTGTCC
 ATCGTGATCTAAAACCGGAAATCTATTATTAGATCATAAATATAACATCAAGATTGCG
 ATTTTGGTATGCGTGCTTTGGAACTGAAGGAAAGCTACTGGAGACGTCGTCGGATGAC
 CACATATTTCGTCCACACAGAAATGTATCTGGTATACCGTATCAAGGTTTCGCAAGTAGT
 TGTGGTCACTGCGGTGTGATCCTATTTCGCCCTTCTTACTGGTTCGGTTACCTCTTTGACGAG
 AAGATGGAAATATAAGAACACTATTACTTAAAGTTCAAAAGGTGAGTTGCAAAATGCGCT
 CTGATGATGAAATTTCCGCGTGAAGCTCAGGATTTGATTAGAAAAATCTTAAACCGTTGATC
 CTGAAGGAAGAATCAAGACCGAGATATATCTCAAAACATCCGCTATTACAAAAATATCCAA
 GTATAAGAGATTCTAAAAGTATTAGAGGCTTACCAAGAGAAGACACATATCTCACGCCAT
 TATCAGAAAGTAATCTTCTGATTGACGCTACGATTTTGCAAAATTTAGTAAATATTATGGC
 ATGGAAGAGATCTCTGAAGGAATTAAGGAAAACTAAGAGAACCTGGCGCTAATGCAGAAA
 AGACATTTATATGCACACTGTATAGATTTTAAGTGTGACATCAAAAAGAGCTTTATTAAGC
 AACAGCAAGTTAAGAAGAGCGAGTCAATAGTAGCGTTTCTGTTTCCCCATTAAGAAAG
 TATCGACAACCTCACAAACGAGAAAGAAATAGAGAATCTTTAATTAGTGTAAACATCTCTC
 GTAAAAGCCCAATATCCTTCAACAAATTCAGTGCCTCCAGTGCCCTCTCCAGCAATATCA
 CTACACCCGGTTCTTCAAAAACGCTTTCAAAAACCTCTCTPTCAAGAAAGAAATATPATCA
 CAATCGTTAAACCAATCTTCTCCAACACCGACTACGTAATAAAAGAGCTTCGGTTATATA
 ATTGGAAGAAAGAAATCAAAAAGAGCCTCTATCTTTTCTACTACCAAGAAAGAACAAAAGAT
 CTGTACAGCTATCAAGAGAAATGTCAATGTATCAAGCATGAAGCAAGTGAATTCGGTGACAA
 CAAAATTAATGTCAACATATGCGAAATTTGGCAGAGGATGACGATTTGGGAAATACATTTGAGA
 AGGAAACAAAAGAGAACGAGCTCAAAATTTGCAACTTTGATAGATGAAATTTTGTAGTACG
 AAAAGTACGAAACAAATAGGAAGAGAGGAAGAGCTAGAACGTAAAGTGAGAGAGAACAA
 AAGCAGCTGAAGAGCTGGAACGTGAAGACGTAAACAAAGAAAGAAAGCACTGCAAGAA
 AATTTACTAGAAAGGAAGATCTGAAAGAAAAACAGGAGGAACCTCAAGAACCAATTTGAA
 TTGATATAAGTGTATCTAGAGCAAGAGCTGTCCAAACCAAGAGGAAACCTGATGTGTA
 ATATTAGATCTATCTCTGCTCCTATGAAAAATGAAGAGAAAAATATCAATCATTTGGAGG
 TTGATATTGCAATATTTCTCCGTGCGCGCACTTTTCTTTCAAACTAGACCTGTGTCAA

FIG. 1 - 26

GGCTTGATCCGGGTATAATGTTCTCCAGTCCAACCTGAGGAAGTAAGTCCAGTGGAAACCA
 AGAGAAACAGAAAATGAAAGACTTCAACAGAAAAGAAAATTTTGAAGAACTATCAGAAAGAT
 CAAAATTTCTTGGGTTTCATCATTTAATATCGATAAAGAGTTGAAATTTGCTTAAATGGAAT
 ATCCAAGTATAATTTGCCACCAAAAGATTGTCAGAGGAGCGAGTGGTGTTCAGATTCTTAATG
 ATGGATATGAATCTTTGATCCTCCCGAAGGATGGGAATGGCGTATCTCAATTTAAAGGATA
 GTACCGCAACCAACTGCTCCCGTCTCTGATGGTAGTTGAGGAAGATCTCTGAAATTTAGAG
 TACCAGCAATTTTACTAGAAAATCAAGGCATTTTAGTGAGTCCAATAAAAGGCTATCTGTCC
 TGTGATGTACTCTACCAAGGAGTCGTTTACCACTTGGTTGATATTTTGAAAAACGGTA
 CCTTGTATGTCAATAACCAACAAAGCCAAAGAAATTTCCAAACCAAGAAAGTGCAGATGATT
 CAGAAATTTCTTTTGAACCTGTCAACGAGAAGAGCTGAATATACAGGAAAATAGTTTCCGAACG
 ATGAGAGATTGTACGATGTCGGTGATTCACCTATCAAAGACAAATCCGCGTTTAAAGCTGA
 ATGTTGTCAGATCGTTTAAATGGATCGAACGAAGAGCTGAATATACAGGAACTTACATCTTCT
 CGATCCTTTCTCCGCTTAATGGTGCAATGAATTGCGTAAACAGAAATAGCCCAAGAGGGGT
 ACCAGGCATCTCAAAGATTAATTCGATGATACCAAGATCAGGCTTCTTCTCAACATCTG
 AAAAGGAAGAGAAAATGAGGAAAAGGAAGAGAAAAGCCAGAACAACACAAACGAAGAG
 AGGATCAAGAAAAAGAGAGAAAAGTAGTAGATGATATGGAGCCACCATTGAAACAAATCTG
 TGCAAAAAATTTAGGAAAAAATGCTGGCTCGCAGGCCAAGGATCATTCAAAGAGTCACT
 TAAAGAGCATTAAGCAGGATAAAAAATCAGCAATTTGGAATTTGCTCTTCTTTAGAAAAT
 TCTCAAAATCTTCGGACAAAAACAATGGAATTTGATGGCAAGATTTCTGCAAAAAACAATTGT
 TTAATGGTTTAAAGAGCTGTTGCGTGGTTGGACTCAGTATGGTTTAAAAAATATAAAAT
 CGACCCGCAACAATCTGACCTTAACGGGTAACACTATCGAGTGAATAATATCTTCTACTAC
 GTTCAACACTCTTTTGAGGTTAATATTTATCCGAGAGGTAAGATGAGCGTTGTGCGAGTTCA
 AGAAAGTTTCTGGTTTCATTCAAAGCTGCAAAAAGTTGGTCAATGAAGTTGAGAACGCTCC
 TGAATAAGGAAGCGCTTCTACAAAAATAG

YDR507C, 1142 aa (SEQ ID NO 72)

MAINGNSIPAIDNTIGPWKLGETLGLSTGKVLARNGSTGQEAUVKVISKAVFNTGNV
 SGTISVSTTFDPALPYGIEREIIIMKLNHPNVLRLYDVWETNTDLYLVLEYAEKGELFN
 LLVERGLPPEHEARFRFQRIIIGVSYCHALGIVHRDLKPENLLLDHYKNIKIADFGMAAL
 ETEGKLLSETSCGSHYAAPEIVSGIPYQGFASDVWSCGVILFALLTGRPLFDEEDGNIRT
 LLLKVKQGEFEMPSDDEISREAOQLIRKILTVDPERRIKTRDILKHPLLQKYPISIRDSKS
 TRGLPREDTVLTPLSESNSSIDATILQNLVLVHWRDPGIEKELREFGANAARLTVALL
 YRFKCDTQKELIKQQQVKKRQSISSVSVPSSKKVSTTPORRRNRRESLISVTSSRKPISF
 NKFTASSASSNNLSTFGSSKRLSKNFSKKKLSTIVNQSSPTPASRNKRASVINVEKNQK
 RASIFSTTKNKRSSRSIKRMSLIFSMKRESVTTKLMSTYAKLAEDDDWEYIEKETKRTS
 SNFATLIDEIFEYKEYEQIRKEKEELERKVRREAKARELERRRRQKEEKERARKLLEKED
 LKRQOEELKKQIEIDI SDLEQELSKHKEEKLGNIRISAPMENEEKNINHLEVDIDNIL
 RRRNFSLQTRPVSRLDPGIMFSSPTEEVSPVEPKRTENERLTTEKKILETIRRSKFLGSS
 FNI DKELKLSKMEYPSIIAPQLRSEERVVSDSNDGYESLILPKDGNVGSQDKDSTATTAP
 VSDRLRKLISEIRVPQFTRKSRHFSSENKRLSVLSMYSTKESFTNLVDILKNGNLDVNNQ
 QSQRIPTPRSADDSFLEFETVNEEAETGNSSNDRERYDVGDSFTKDKSALKLNFADRPN
 GSNEAKQTDNLHLPIPLPLNGDNELRKQNSQEGDQAHPKIKSMIPESGSSSTHEKEENE
 EKEEKKPEQHKQEEDQEKREKVDDMEPLNKSQVKIREKNAGSQADKHSKDLHLEKHKQD
 KNTAIGNSFFRKFSSKSSDKTMELYAKISAKQLFNGLKLLRGWTTQVGLKNIKSHPNLIT
 LTGKSSDNIFSLRSTLFEVNIYPRGKMSVVQFKKVSFSKFAVKKLNEVENVLNKEGVL
 QK

YDR515W, 1844 bp, CDS: 501-1844 (SEQ ID NO 73)

GAGTTGAATCTATCGCTAACCAATTTTGACTACCGCTTCGTATGCTTTCTTGCACTTTTGTG
 GAGCTACTCATACAAAGCTTATAATCTGTGTAGTCAAACTATATACCTAGGCAAAATACT
 AGTAAATGCAGTATTATATGTCCTCAAACCGTTTGTGCAAGTATGTTATGATGCAATCG
 ATCAAAAATTTTTACCAGCCCAAGAGAACATACAAAGCCAGCTGAATCAAGAAAGAAATTTGGC
 TTAGTAAAGTAAAGCTTGAAGCACATACAAAGCCAGCTGAATCAAGAAAGAAATTTGGC
 ACATCCTTGGTTGACACTGTGCTATTATTATAAAAGGTTTAAAAAGTAGTGTTCAGAGCT
 TCTATCATATTTTATTATTAAAAAATACTGAGAGGAAGCGTATTGTTTAAAGACACAA
 TTTAGGCTGGCGTTAAATAAACGAGAGAGCCCAAAATATACCAAGATAAAGAAAAATCA
 ATCAATAAGTGAATTTCAAAAATGTTCATCGCAAAACCTCAATGATAATCCAAAAATACAT
 CCTCAGAGCTGAAGATAAGAAGAAACAACTTCATCTTAAAGTTGGCACCATAACCAA

FIG. 1 - 27

CCACATCGCCATGGAATCATCTTCGCCAGATAGCAATACAGTAATTCCTGTAGAGGAAC
 TAAGAGATATATCAAAGACTGCAAGGCCAAGTAAAAATGGTTCGGGGTCAATTAAATTTAA
 CAAGCAATACCCAAATGGACTCCAATTACGCCGTCTGTTATAATCTCAGGTTCAGAGGACA
 CAAATTCAAAGTCAGGAAAGAACTCTAAAAATTTCTAAGACTAATAAAAAAATGAAAAGAC
 GTGGCAAAATATAATAACGATATCAATAAAAAAGGACCTTAAACGGTCAAAACCAACAGTACAT
 CGGAAATTAAGTAACGTTTCCAATCTTGAATCCAAACCTTTAGATGCTAACGCTAAAGTAA
 ACATACATCTCAAGCTCAGGAGCAACTGCCAATGGGAATATAAAGAGGATAACAAACAACA
 ACAATTCACCAACAGCGGTAGACAATCAAGAAATTTATCAAAACAGGAATGGCAAAACAGAT
 ACAACAACAATTAGACACAGTCAGCGCGCTTAATAATGCCATCTCTCTTCCAAATAATT
 ATCAGGCTAGACCTGAATATATTTCCCAATGCCAGCCACTGGTTGAACAACAATTTCAAGAA
 ATAGCTATAAACAACCTGTCATACTTCCGTCAACAGCAGTATTTAATAACATCAACTATC
 AACAACAATTGCAACACCCATATTATTACTCAATGGAACCTATTTTTAAATCTATCGAAA
 GTATCAAAAACCCAAATTTGAATTTCTATTAGTGAAGAGAACTTGAAAACAGATGAATTTT
 TAAGATCTAAATTCAAAAAAGCCAATGACGGATTATGCCCATGAGTTTGATAGGGAAT
 TTTACCGTATGGTTAATTTATCTCTTGGTGGAGACCCAAATTTAATTTTGGCATCTATGA
 GAGAAGTTTACAAACATAAAGAAACAAACCATTTGGAAATTGCCCTTGGAAGCATAGAAG
 GTGCTCAGAAGAACATGGCAGATGATTTCAATCCATTGGAAAACTATTTTTATAGGCGCG
 AAAATTTGGGCTGAATACGCTATGGAAGTAATTTTGATGAAAATGATGACCAAACTGAAA
 AATACAACATTTAGAAACATTTGGGACCGAAGCATTTAGACAATTTATCTTTATATGGGCT
 ATCCAAACTCTCTTCCAGTAATGAAAAATGGGAAAAAGAGTCAGAGCTATGACCAAGGTG
 AAATTAGCAGGCAGTTTGAACAAAACCTTCAAAATAAATGATTAA

YDR515W, 447 aa (SEQ ID NO 74)

MSSQNLDNPNKNTSSAEDKKKQTSCLKLAPIPTTSPWKSSSPDSNTVLPVEELRDISKT
 AKPSKNGSGSIKLTSNTKWTFITPVSIIISGSKDTSKSGKNSKNSKINKMKKRGKYMND
 INKDKFNQCTNTSTSEISNVSNLESKFLDANAKVNIHSSSGATANGNIRKNTNNNSNMGSR
 QSRNYQNRNGKTRYNNSNRHSQAANNAISFPNNYQARPEYIPNASHWLNNNSRNSYKLS
 YFRQQQYYNNINQQQLQTPYYYSMEPIFKSIESIKQNIIEFYFSEENLKTDEFLRSKFKK
 ANDGFI PMSLIGKPYRMVNL SLGGDPNLILASMRVQLHKETNHLEIALGSIEGAQKNMA
 DNFNPLENYFIRRENWAEYAMESNLDENDDTEKYNIKLLGPNDLDNYSYMGYPNFPFS
 NENGGKQSVDQGEISRQFEQNLIND

YDR518W, 2054 bp, CDS: 501-2054 (SEQ ID NO 75)

GCAGCAGGGGCAAGATGACAACCCCTGTTCTCTGTTCTCTGTTCCAGTAGAATCTGAGACGGC
 TTTTGTGCCATCAGCATTCACAGCACCACCGGTGCCAACAAAGAAGAAATCAAAAAATAA
 AAAGGGTACCAGCCATTGGCAATGGATGACTATTTTAATGAAGCAGAGATAAGTCACT
 TACCCTGTCAGCTCAGCAGAACTCTGACATCTCGCCCCACCACCAAAAAACAGCTATC
 CTCTGATTAACCTTCCCTGGTTAGTCTTTTGGTTTGTGTTTATAGCAAAATTAATATATA
 TATATAAGCTTGTCTTCTCCCTTCAAAACACGTAAACGATAGTTGGCAATGTCGAAAAAGTA
 CCGAGACTTTTTCAAAGGCACGCGTGTCTTTTGTGTTAAGACAATAGATATTTTAGC
 ATTACAGAAAGTTTCAATTTCCAAGACTTGACGTTTCAATTATATGGCAATCTCCAACAA
 GCACCCGCTCATATAATACCATGCAAGTGACCACAAGATTTATGTCGATAGTCTCGT
 TTTGCTGTTTGTCTTCTTTCACGCTTGGCTGAAACACGCGCAAGAGTACGCCGGATCAG
 ATTACTCGTCTTAACAGAGAAGAAATTTAAATCATTCATCGAATCTCATCCGTTAGTCC
 TCGTCGAGTTTGTGCTCCATGGTGTTCGATCTTCAGACTTACGCCCTCAGTTAGAGAG
 AGGCCGCGCTCATTTTAAAGGAGCATAACGCTCCAGTTGTTCAAAATGATTGTTAGGCTA
 ACAGTATGGTTTGGCTGCAACAAACATATAAATACCTACCCAACTTGAAATCTTTAAAA
 ATGTCGTAATTTGATGGTCAAGTCTATCGCGGTGTCAAGATCCAGTACGAATGAAATCTC
 AGTACATGATTTAGCTATACGAGGCTTCTGTGCTATTATTTAAATTTCCGAAGATGAAATCT
 AACCATCAATTTGGAATAATGCAACTTTACCAAGTAGTAATAAACAGAGGCTTGACAGGCTGA
 ATGAAACGATATCAAGAAGTCGCACTGGACCTTGTGAGGATTACGTCTTTTATCCCTCT
 TAGATTAGAAAGATAAGTCAATTATCAATCCACTTGCCAAACACTACAGAAACCAATTTCTGT
 TTGATGAAATGTAGACTCTTTGGTGGGAAATTCGGTGTCTTAACCTCAGTGGTTAAAAG
 TGGTAATTTTACCTTACTTTACCAGACATCGAAGCTGATCTTCTCCCAAGTACATTTCTA
 GCAATTTGGCGTTTGGCTTACTTCTTTTACTCTGAGGAGAAGATTTGGAAGATTACACTG
 ATCTTTTCCAGCAGTTAGGTAAGGAAAACTGTGGCCAAATAAAATTTCAATGCAATTAACCT
 CTACAATGTTCCACACACGTTAGATTCTCTAAATATCAGAGAAGACAGTTCCCATTTATTTG
 CTATCCATAATATGATCAATAATCTGAAATATGGTTTACCACAACCTACAGAGAAGAGT

FIG. 1 - 28

ACGCGAAATTAGAAAAACCAACCACTAGACAGAGATATGATCGTTCAGTTGGTAAAAAG
ATTACCGTGAAGGTACTGCCAAGCCAAATTGTTAAGTCAGAAGAGATTCCAAAAAGACAAA
AGTCCAAATGTTTATAAAATAGTTGGGAAGACACATGACGACATTGTTCAITGATGATGACA
AGGATGTCCTTGTCAAAATATTACGCGACATGGTGTATTTCATAGTAAAGGTTTTCGCCCTA
TTTACGAAGAAATTGCAAAATGCTCTAGCATCTGATGAATCTGTTTCGCGATAAAATCTTTGA
TCGCGCAAGTAGATTTCAGGGGCAATGATATCTTAAGTTTTCCTGTGACAGGATATCCAA
CCATTGCTTTGTATCTTCGCCGAAATAACTCTAAGCCTATTATCTTCAATAAAAATTAGAA
ATTTCGAAGATGTTTTCGAATTATTCAAGGAATCAGGTACACATCAATSKRFAPITYEIAN
CAATTATGATAAATTGCACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTAC
ATGATGAATTATAA

YDR518W, 517 aa (SEQ ID NO 76)
MQVTRFISAIVSFCLFASFLLAENSARATPGSDLLVLTEKKFKSFIESHPLVLVEFFAP
WCLHSQILRPHLEEAASILKEHNVVPVQIDCEANSMVCLQQTINTYPTLFIKNGRIFFP
QVYRGVKITDEITQYMIQLYEASVIVLSEDEIQPYLENATLPVVINRGLTGLNETYQEV
ALDLAEDYVFLSLDSEDKSLSIHLNPTTEPIPLFDGNVDSLGVNSVALTQWLNVLLPYF
TDLEPDLFPKYIISNNLPLAYFFYTSEELEDYTDLFQGLKENRGQNFIALNSTMPFPHH
VRFLNMRQQLPFAIHNMNINNLKYGLPQLPEEYAKLEKPOPLDRDMLVQLVKDYREGTA
KPIVKSSEIPEKEQKSNVYKIVGKTHDDIVHDDKDLVLYKYATWCIHSKRFPAPITYEIAN
VLASDESVRDKILLAEVDSGANDILSFVPTGYPTIALYPAGNNSKPIIFNKIRNLVEDVFE
FIKESGTHHIDGQAIYDKLHQAKDSEVSTEDTVHDEL

YDR519W, 908 bp, CDS: 501-908 (SEQ ID NO 77)
GGGCGAAATGATATCTTAAGTTTTCCTGTGACAGGATATCCAACCAATGCTTTGTATCCT
GCCGGAATAAATCACTTAAGCCTATTATCTTCAATAAAATTGAAAATTGGGAAGATGTTTTTC
GAATTTATCAAGGAATCAGGTACACATCAATGACGCCACAGGCAATTTATGATAAATTG
CACCAGCCCAAGGATCTGAAGTGTCTACTGAAGATACCGTACATGATGAATATAATCA
ATAAATAAAGCATATATAATGCACATTTTAAACATCTGATTACTCGCATCGTTTCTCGAA
GAAAATAGCTTAATATTCTGTTATTATGGCATCACGATTATTCTCACAGTTACCCGTTAA
TGCTCTTGAAGAGATTAGCATTTACTGCCAGCGCATCTTCAAAATACAGGTTTATATGAGA
CCCATCTACTATAACCCTAAGAAGAGAAAAAGGAGTGCTTTTCGTTTCAATCAATCTAG
TTTACAGTAATTGAGTCTCGATGATGTTTAAATATTACCTTTTCCTCACTTTTTTTTCCA
CCATTCTTCGAGGTTTCCTGTGATTTGGAAATCGGTATTATCAAGAGATAACCGGTAG
AAGATTGCTTAATTAAAGCAATGCCAGGTGATAAAGTTAAGGTTCAATTATACAGGATCTT
TATAGAAATCGGGAACGTGATTGACTCAAGTTATTCAAGAGGCTCTCCTATCGCTTTTG
AACTTGGCGCTTGGCAGAGTAATTAAGGTTGGGATCAAGGTGTTGCGCGGATGTGCGGTG
CGGAAAAAGAAAGTGCAGAAATCCAAGTTCTTTGGCCTACGGAGAAAGAGGTGTGCCAG
CGCTCATCTCAAGTGCTGATTTGGTGTTTGATGTGCAATTGGTAGAGGTGAATACAG
CCGCCTAG

YDR519W, 136 aa (SEQ ID NO 78)
MMFNILFVFTFFSTILAGSLSDLEIGIIRKIPVEDCLIKAMPDGKVKVHYTGSLLSEGT
FDSYSRSGSPIAFELGVGRVIKQWDQGVAGMVGKRLQIPSSLAYGERGVPGVIPPSSA
DLVDFVELVDVKSAA

YER102W, 1103 bp, CDS: 501-1103 (SEQ ID NO 79)
CGAGCTTGGCAGCAATCCAATGCCATCGTATTGTACTCAATGGTGAACCTTACCACCAT
ATTGTTAAAAGCTATTATTATGATTTTACTTACCAAACTTGAAGGAGACGTGAACAC
ACCACGATAAAACGTATGTTCTGATACCCAGCAATGAGAAAGTAGAAGGAGAAACCTAA
AAACCTCTGGCGCATCAAGACTGCTAGCAAGATGGATATTAGATCAATAATTTCTAACGCA
TGACTCTGAGGCAATGAAATCAATGCAACCTAACATTTGAGGTTAATATATGAGAAATPAC
GGTCTAGGATGAATACGAGCAATTGAAATACATTTAGAAATACCTTGTGAATAATATCATAT
ACTTTCCGCTTCTATCTCGATGCGTTATTACAGAAAAATAGTTTACTACAAATTTAAACA
AAAAATAAAATAGTTGAAAAATGGGTATTCTCGTGATTCTCGTCACAAAAGATCGGCCA
CTGGTGTCAAACTGCTCAATTCAGAAAAAGAGAAAGTTCGAATTAGGTGCTCAACCCAG
CCAACACAAAAATTTGGTGCTAAGAGAACTCCACTCTGTCAGAACTAGAGGTGGTAAACAAGA
AATACAGAGCTCTAAGAAATGAAACCGGTAACCTTTCTTGGGCTTCTGAAGGTATCTCCCA

FIG. 1 - 29

AGAAAGACCAGAAATTGCTGGTGGTGGTTTACCATTCATTCACAAATGAATTGGTTAGAACTA
ACACTTTAGACCAAGGTCGCATTGGTCCAAATTGAGTGCTACTCCATTACAGACAATGGTTCG
AAGCTCTACCTACGCTCAAACTCTGGGTGAAGAAGAACGCTCAAGGAAGAAGAAACTCTGTG
CCAAAGGACGAAGACCTGTAAAGAAATGGGGTGCTATAGCTGCTCTTCGCAAGATCGAAT
CTTCGGTGTGAATCTCAATTCAAGCCGCGGTGATGTATACGCTGTGATCTCTCCAGACAG
GTCAATCCGGTAGCTGATGGTTATCATCTTGAAGGTTGAAGAATTGCTTCTTCTACCTAA
GAAGATTGACTGCTAGAAATAG

YER102W. 200 aa (SEQ ID NO 80)

MGISRDSRHKRSATGAKRAQFRKKRKFELGRQPANTKIGAKRIHSVTRGGNKKYRALRI
ETGNFWSASEGISKTRTAGVYVHPNNELVVRTNTLTKAAIVQIDATPFROWFEAHYQGT
LGKKKNVKEEETVAKSKNAERKWAARAASAKIESSVESQFSAGRLYACISSRPGQSGRCD
GYLGEELAFYLRITAKK

YER153C. 1265 bp. CDS: 501-1265 (SEQ ID NO 81)

ACCCTATATGGGAGGACACATCGCCCACTCTTTGGGTCGTGTTCAGCCATAAAGGTCGCCAAG
 TAGAGATAGAGAGAGAGAGAGGACTTGAAGAGGTTAAATCATCATGATGGAAGCAACATCGGTTT
 GGATTTCCCGAGACATCTGTGGCATTTTGGCCCGTCGAAATTAATATCTTTTGGCCCTGAAAG
 AGATTCATCATCGAGATGGGGCCGGGGCAATACTATGTTGCGACGGTGGCCCATCTCGAAG
 AGCCAGCAAAACCTTGAACGTGACGAGTGTGAGAGAGTGAGTTTGAACATCTGTCGGGAGGTTT
 TCTGTGGCTCCGCTTGTACTGACAGACAGATACGTATAGAGGGCGAGCCACTGGTTAAATTT
 TTTCATGCTCGGATTACTTTCGTACTGCTGGCTAAAATCGAAATCTCGGCCCTGCTGAGA
 GTGTGTTTGAACATAACAGGGAACTCTGAACGTGGAAGAGCAGACGAGGCATTAAGTCGA
 ACATAGAAGACGGAAACATCTGATCTGATCATGAGGAAATATGTCGTGACCCAGCGATGTGG
 GTGCGCAATATCTTTAAGCATCTTGAAGGTAATATGTCGTGATGCTGAGCCATGCGCTGCTGC
 TGCAGCAGCAGCAGACAGCAGGTGGATGTGGAGCTGCTGCACACAGTGTGAGCGCGAGCGC
 CTGCGCTTGCCCATGCGCACATATAGCATACATGTGGTATAGCATATGATGTGCCACGCC
 GTGTTGCCGATAGAGGGGCGCCCTGCTATGTGAAATGGCTGGCGTAGCATTTGTACGAGCA
 GGCCTCTTTCTTACCGGCGAGTTCTCTCAGCAGCATACCAGGCGATATACTGCGATCTGTCGCA
 CAGGCCCAAGAATGAATCTGATTTGAGTATGACTCTAGACGGATTAAGGTCTGAAGCGTTTG
 CGCGTGGCACAATGCACTCCAGCGCGCTCAGGGAAAGTGTGGAAGTATTTCTTGCAGGAGA
 TGTGATAGCTCTACAGGCGAGCGCCCATTAAGCTGCGCGCATTTCCCGCAAAATGACCAAGG
 CTATGGCATAGCATGTATGCACAGATGAGCAAGCAGCTGCCCTGGGGTTTGTGGAAC
 CAGACGCCCTTATGTTAAGAAGACGAATGTGTCACTACCGCTACTCTGGCTGGTGTCTCTTT
 GGCATTTTCCCGGCGCAGCGCGAGCGCGAGCTGTCTGCGCGAGTTTCCGTCAAAGTTATTC
 CGGGCTGCGGCTCTCTGGATGCCGAACATAGTGTATAAGAGAAGAGGATTTTGAATCAACA
 CATTA

YER153C, 254 aa (SEO ID NO 82)

MLTITKRLVTTDVRSKILLSSSLNGKMSDALALLRQQOQTSVDVELLHTMLARAAALAHAD
TIAWMYVHQMPRLRPEVGRLLCEMAGVALYQDRLLFPAQFLHQYQAMNRDRTTSPEDEL
IYEELRLTKVEAFARGMTMHSALTRKEKWKVFLQEMDITLPGQPLRLRDFPPQTKMAGIALM
QQDEQKAAALALFGRQPLVIKNEWSLPLLLAGVLVHWPVGPQAQRVLAEFRQSYRGLPLD
AETVTKRRGFENT

YFL014W, 830 bp, CDS: 501-830 (SEO ID NO 83)

[illegible]

FIG. 1 - 30

AAGGTGTCACGACTCTGCCGAAAAAGGCAAGGATAACGCTGAAGGTCAAGGTGAATCTT
TGGCAGACCAAGCTAGAGATTACATGGGAGCCGCCAAGTCCAAGTTGAACGATGCCGTCG
AATATGTTTCCGTCGTGTCCACGGTGAAGAAGACCAACCAAGAAGTAA

YFL014W, 109 aa (SEQ ID NO 84)

MSDAGRGFGKEASEALKPDSPKSYAEQKEYITDKADKVAGKVQPEDNKGVFQGVHDSA
EKGKDNABQGQESLADQARDYMGAASKLNDAVEYVSGRVHGEEDPTKK

YFL015C, 995 bp, CDS: 501-995 (SEQ ID NO 85)

GACCTTCAGCGTTATCCTTGCCTTTTTTCGGCAGAGCTCGTGGACACCTTGAAGACACCTT
TGTGTCTCTCGGTTGAACCTTACCAGCGACCTTGTGCGCCTTGTGACGTATGTATTCTCT
TACCTTGTTCAGCGTATGACTTTTGTAGAGTCTGGCTTCAAAGCTTCAGAAGCTTTTTAC
CGAATCCCTTTTCTACCTGCGTCAGACATGTGTATTAGTTTTTTTTGTGTTTGTGATTGT
TTGTTTGAGATTATCGAAATAACAGATGGTTTTTTTTCTATATATTAGAGAGAGATTAA
ATAAGATCAAACGCAATTGAGGAAGTAGAACGCAATTCACCGTCTTATTATACGTTTAA
ATATAGATTTAGAGAAAGACCTTTCAGATCAAGAGGGGGACGACCGCAACCTCAAAGTTG
ACCAACAGGATTTTCCAGGGGCTGTAGATCTAGTTACTCTCCGCTAGAGTGCTTCTGGTC
TGTGTTGTGGGTGTATTAATAGCTTGGGTATACCTTCTCTCTTCAATTTCTACGCTCA
ATGGGTTTTTTCTCTCTCTTTCTCTTTCTCTTTCTCTTTCTCTCTTCTACCTTTCT
ATGTTATTTTGTGCGCCCTTGCAGTGTGCAACATATCCCTTAAACAGATGCCAGCAAT
ATTCTAGTCTTGTCTATTTTACCGCCTCTGGCTTTGGCTTCTAGTCTTGTGCTTCAAGAG
CAAGGGCCCGGTCAACACGCTGTCTATTGCTACCGCCAGCTGGCACCCACATCACGACG
CCTTTTTTCTCTTTTCCGCTTGGGCTGTAGTGGGATCGCCCGCTCCCGGAGATTTTCA
CTTGGATTTGCGGCTCCCTTTTTTTCTTCACTTGTACTCCCTTCACTTCTCCCACT
TTTCTGTGTATCAAGAGGAAAAAGAGAGAAAGCAACTCCGAAAAATACCGAACAG
AGGGTAACAGATGTGCATTGGATGAGCGGTTAA

YFL015C, 164 aa (SEQ ID NO 86)

MLAYTFPSNFYVNGFFSFLFLFLFLLRPFVILCRPLQVATYPLNRCCQYSSLAIF
TASGFLLVLVPRAGKPSRRHCYQLAPTHHRPFSSIFGWAVSGIRLPLEIFTWICASP
FFLHSLTPPTFSHFSVYQEEKKERKRPKNTQEGBNRMCTWMSG

YFR022W, 2702 bp, CDS: 501-2702 (SEQ ID NO 87)

CTGCCCTCCGTACGTCACAACGCATACACAATATAGTTTATATAAACTCCTGCGTATAAT
CTATCCTTTTGCATAATATTTTCGTCACCATATCTTGTGTGCGGTGTTTTATTTAAAAAC
AATAGAACTCGCCTAAAGGGGAAATTTTCGATATAAAAAATTCAAAAAATGGCTTTCATG
GATCGAGTATTTGTTTGTGCAAAAAGGATCACTGGAGTGACGTTACTACGCTACGAAGCC
TCTTCCGGCTTAGCCCTGTTGATTACGAATTTGGATCAGTTGGTATTTGATTCCTCGGA
AGAGTTAACTTCACGCGGGTAAATCACTTGTGATGCGGTATATCTCTATACGGCTAATA
GATGAATCAGGGTGTTTTAAAGTGCGTATAAACCTTTTGTCTATTTTCGTTTATATAATT
GGCGTTGATAAAGAGCAATATCTATTTGTCTACATAGAGGCGAGCTCTCTTAGCAAAAT
AAAAATACAAAAGTTTCGACATGGGCTTCAGTAGCGGTAATCAACTAAGAAAAAGCCCTC
TGCTTTTCGATATCAGACTTAAAAATGTGTGACCAAGCATGTAATACCTCTCAAAGGTCTCT
CAACGAGGGCCCTCGGTGCTTTTATCTGGTTGCACTCGTTTATTCGATTAACGAACCCA
TCAGATACAAAAGCATATCATTTGAGACTTTATGGGAAGATACAAATAGACGTACCATTAG
AGAGGCCCCAGGACGCTAGTTCTTTCGTGTTGTCTTCTACGCGCCAAAGATCAGAAAGT
ACCAACAAAGTTTTTATAATTACGATGGGATAAGTTAACTCAAGGAGTATCTGAGTG
GTTTAAAGAGGCAATCTGGCTTTCGGGCGAGTAGCTCATCAAGTAATATCTTGGGCACTC
GCCAAAGAGCTCAGTCCACAAGTTCTCTGAAGTCTTTAAAGGGGTCTCTCTCACTCTT
CATGTACTTTAGATAAGGGCACTACGATTTTCCCTTAGTGCTATTTTGGCTGTTGCTGT
TACGAGAGCGGTAGAAATCTTTGCCAAATTTGCTTCGTGACATATAGCATGGAATCCGTTA
TTGAACCGCAGCAAAAATTATAGTGATTTGATCTGTAGGAAAAATATTAGAGTTCTGAGAA
CCATTTCACCGCAGCAGTGGAGTTATCAGAAACTGTTTGTGTAGATAACTCATGGCCCG
ACAAAGTGGATATTTCTATTTCAGTACCCACAACAGCCGTAGCTATTTGGTTTCAGCCACCT
CTATAAATATTTCCATGTGACTCTTTTCGAAAGTTTGAATTTGGGCTCAATCAAGTCG
TATTTATTTGAGAATTATCAATATTGTGACCCCTTCCCTCCAGTAATTTCTGAAAATAGCG
AAGTGACAGAACTAAATCTTGAAGATCCCTTGAACGAGTCATCTGGAGAAATTTAATGGTA
ATGTTTGCCTTGTAAATAACCCCTTTTTCTAGCCTGTATCATTCACGAACAAGTGGG

FIG. 1 - 31

AGATTGATACCATCTGCAAAATCCCGAACAGCTTATCAAACCTGTGTGCAAGATTGTGTAGT
TCCGCTCTAACATTAAAGGTTTCGCCATAAGCTCAAATTTTCATCATCTCAATTAAACCCAG
TCGGTCATAAATCTGAGTTAAGAGCGGTCCTTACGGATTCAAATTTTATTTACCAATTTG
TGGCACATTCAAATAAAACCATTTGTATCTCTCGAATTTGTATTCGCTTTTATAGCAACCTA
ACCGAAGAACGAAAACTCATCAAGAAGAGGAAGAGGAATATCTGTTTCTTAGATCAG
CATCAGTCAACGGGTTGGAATTATTAGCGGATATGCGTAGCGGTGGCTCTGTTCTCTACCA
TTTCAGACTTGTAGACGCCCCCAAAATTAAGAAATGCACGTATATGAATCTGCTTTATAGCG
GTTCTTTCACTCGCAGCGCTGTGGAACGCTCGGAACATGTACTCTTTGGGAAGCGAAT
GTTTCGACTGTGAGGATCAGCAACAGGATTAGAAAGATTACGTATACGGTTTGACAAAAA
TTAGAAATCAACGTGACAAATCTAGGGCTACCAACCGCTCTGCTCTGCTCTGCTCCGCTTCCA
GATCGCTTCTTCCATTACTATAACGTTCCAGCACCAGAGGATGCCAGGAGAGAATCTTAC
CTCAGAGTGCTCTTGTGTCCTCAATAGTGGCTCTGTGCCAGGAGTACATAGTAACGTATCAC
CTGTTTTCATTCTTCAAGATCCCGAGCCCCAAGCGTGTGAGCCCATGAGTGTATACAGTGC
CTCGGGCTTAAATTTATCCAGAGACTCAAAACCTGAACAAGGTTCGAATCGGTATGGCAAGG
CAATGAAATATGATATCATTTGGTGAGGACCTTCTCTCTTCTACCTTTGTGCGATACAAA
ATGTGCAACCAAGAAAACCCAGTAGGGTACATTCCAGGAACCTTTCGACAAACATTGTCTAT
CTTCTATACCAACTAGCTTTTCATTCTCTAGTTTATGAGTAGCACTGCTTCCCTTATTT
CCATAATTAATGCTCTAGAAGTAGTTCTAGTGGGGTATCTCTTAATACACTTAATGAGT
TAACCTCGAAAACTTCGAATAACCCATCCAGTAATAGTATGAAAGGTACCAACAAAGAC
GGAGGGCTACTTCTTAGCTGGGTTTATGGGAGGTTTCTATCAAAGGGTAACAAACGAT
AG

YFR022W, 733 aa (SEQ ID NO 88)

MFSSSGKSTKPKLLFDIRLKNVDNDVILLKGFPPNEAPSVLLSGCIVLSINEMQIKSIS
LRLYGKIQIDVPLERPDQSSSSLSLSSPKIRKYNKVFNVAWDMVNVLKEYLSGLRGQSG
LAGSSSSNLTGRQRAQSTSSLSKLGSSSPSSCTLDKNGYDFFFAILPNSLPESVES
LFNCFVITYSMESVIERSKNYSDLICRKNIRVLRITISPAAVELSETVCWSPWDKVDYSI
SVPNKAVAIGSATPINISIVPLSKGLKLSIKVLFENYQYCDPFPVPISENROVTELNK
EDPLNESSGEFNGNCFVNNPFFQPDHSPQDKWEIDTILQIPNSLSNVCQDQDVRSNIKV
RHKLFKFIILINPDGHKSELRASLPIQLFISPFVALSKPLSSNNLYSLFSTTMQKDENS
SQEEEELYLFRSASVTGLELLADMRSGGSVPTISDLMTTPPNYEMHYVDRLYSGSFTRTA
VETSGTCTPLGSECSTVEDQQQDLEDLIRLTKIRNQDNLGLPPSASSAAASRLSPLL
NVPAPEDGTERILFPQALGFNSGSVPGVHSNVPVLLSRSPAPSVSAHEVLPVPSGLNYP
ETQNLKNVPSYKAMKYDIIEGDLPPSYPCAIONVQPRKPSRVHSRNSSTLSSSIPTSF
HSSSPMSSTASPTSIINGSRSSSSGVSLNTLNELTSKTSNNPSNSMKRSEPTRRRATSLA
GFMGGFLSKGNKR

YGL011C, 1259 bp, CDS: 501-1259 (SEQ ID NO 89)

AGACAATAAAATATGGAAATAAAACGCTTAGCACAGCAGTCAATGAAATACTCTGATAT
ATTTTGACTCTGTGGAGCATACAGCTACCACATAATAGGATTGTGGGGACAAATATGGAA
TGGATCAAAACGTTCTTAGGATTGTGGTGGTAAACCTGTAAAATCCAAGCTGAGATCTT
AAATCCAGCAAACTTCGCCCATATTTATTTCTTTTATAACAGAAGAAGACATATATCTT
CAAAACCTCGTATATTTATATACATATCTCTCAAAACAACTCCAAGTTTCACTTTCTCTG
GATTACCTTGGCATTCCTTTTCCCACATCTCTTATAATGGTAAATCGCGATCCTTAAATTA
TGATATCAAAATAGACGAAGGGCACACACCAATTTGCCACCGTAAGGATAGAGTAGTTA
AATGGCTAACTCATTATAATCTTTCATGCTAAATCATATAAGGGCAGAGACGAAGCAAGC
GAAAAAACAATATTAACAATCATGTGGGTGCTGCTGCTGCATCTGCTGCTGCTGTTATGACA
GGCACAATCACTATCTTTTCCCCGAGGGTCGTTTATATCAAGTAGAATATGCTTCTTAAAG
CGACTAATCAAACTAACATAAATCACTAGCGGTGAGAGGTAAGAGATTGTACAGTGGTGA
TAAGTCAAGCCAAAGGTCCTGATAAACTGTGTGGATCCAACTACTGTTTCTGTTCTGTTT
GTATTTCAAGAACAAATTGGTATGGTAGTGAACGCCAATACCGGATGCAAGAAATGCGG
CCCTAAGAGCCAAAGGCTGAGGCTGCAGAAATCCGTTATAAATATGGTTATGATATGCCAT
GCGATGATTGGCTAAGAGAAATGGCTAACCTTTCCCAAAATCTATCTCAAGAGCATATA
TGAGACCAATTAGGTGTTATACTACATATTGTTTGGGTAGATGAAGAATTGGGTCCTCCA
TTTACAAAACCTGACCTGCGAGTTATTACGTTGGCTACAAAGCTACTGCGACAGGACCAA
AACACAGGAGATCAACAACAACTTAGAAAACCATTTCAAAAAGAGTAAATCGACCATA

FIG. 1 - 32

TTAATGAAGAATCAATGGGAGAAGGTGGTAGAATTGCTATTACTCATATGATTGACGCAC
TGGGTACCGAATTTTCAAAGAATGACTTGGAAAGTCGGTTCGCTACAAAGGACAAATTCG
TTACCTTGAGTGCTGAGAACATCGAAGAAAGGCTAGTAGCAATTGCTGAACAAGATTAA

YGL011c, 252 aa (SEQ ID NO 90)

MSGAAAAAAGYDRHITIFSPEGRLYQVEYAFKATNQTNINSLAVRGKDCSTVVISQKKVP
DKLLDPTTVSYIIFCI SRTIGMVVNGPI PDARNAALRAKAEAEFRKYGYDMPDCDVLAKR
MANLSQIYITQRAYMRPLGVILTFVSVDEELGPSTYKTDPAQYVYGKATATGPKQOEIT
NLENHFKKSKIDHINEESWEKVVFAITHMIDALGTEFSKNDLEVGVA TKDKFFTL SAEN
IERLVAIAEQD

YGL031c, 968 bp, CDS: 501-968 (SEQ ID NO 91)

CCAAGTTAAGCAAGACACCAAGCAATAACCTTGAGAGGTATGTCCTATATGATGATGAT
TCATAATTAATGGCGACCGGAGGCGAGCGTTGTGCTAGAAAGCAATGTATTAATATATGAG
AGAGCTTCAGATGACCAATACACCGGAATTTAGACTTTGACAGGATTTGGCTTGTTCCTCA
GTATAACTTTATAATATATGTCACACCTTTGACGAGGAAACCAATGAAATGCTTCATTAAC
ATATATACGATATGGAGAAGCATGAAAAATAACACCGTGAGATGTTATCATGTTGCAAG
AACCTAGTAAAAATGAATTCGAATTTGCAAAAAGTCCATATTTCCACGTTCTCCCTCTTCC
TACAATTTTTCGCAAGCGCTGAACAACCATGCGGATTACCATTTATATATTGACAAGATG
GCTACCTATGAAAAGCATAGACTTTACTTAACATTTTTCATTAATATGTTTGAAAAAGC
TGGATTTAATATAGTGATAAAATGAAGGTTGAAATCGATTCTTTTCAGGTGCCAAAAATCT
ACCCAGGAGAGGTACCTTGTGTGTCGGTGTGACTCCAAAATCTTCAGATTCCAAAATCT
CCAAATCTTGCCCTCTTTGTTCAGGCAAGAAAGAACCCAGAAAGAAATCGCTTGGAGCTGTCT
TATTCAGAAAGCATCAACAAGAGGATATCACCGAAGAGGTTGCTAAGAAGAGATCTAGAA
AAACCGTTAAGGCCCAAGACCAATTTACCGGTGCTTCTTTGAGACTTGATCAAGGAAAGAA
GATCTTTTGAAGCCAGAGTTAGAAAGGCTAACACAGAGAAGAAAAATGGAAGGCCCAACAAAG
AAAAGAAAGAGGCTGAAAAGGCTGCTAGAAAGGCTGAAAAGGCTAAGTCTGCTGGTACTC
AAAGTTCTAAGTTCTCCAAGCAACAGCTAAGGGTGCTTTCCAAAAGGTTGCTGCTACTT
CTCGTTAA

YGL031c, 155 aa (SEQ ID NO 92)

MKVEIDSFSGAKIYPGRGTLFVRGDSKIFRFQNSKSASLFQKRNPRRIAWTLVFRKHKK
KGITEEVAKKRSRKTVKAQRPTGASLDLIKERRSLKPEVRKANREEKLANKEKKKAEK
AARKAEKAKSAGTQSSKFSKQQAAGAFQKVAATSR

YGL032c, 764 bp, CDS: 501-764 (SEQ ID NO 93)

CTCCCTCATATTTTATTTCACAGGCTAGACAATGGTAATGGTGCTTTAGATGATTTTCAGT
GGATTACATTCGCAATAGAATAAATGACTAATTTTCAAGAAATTTGTTTCAACCTGCCG
GCTATTCAGTTAATTAAGTTATTTGTTGATGGTAAAACCTTCGCCATCACCGGTTGCTGCG
TTTATTGCAAAATTAAGTAACTGTAATTTCCGAATACGGTAATTAACCGGATTTTGA
AATTTGACATCAAGTTTAACAAAAAACTTCTGTCGCCATCTAAAGCTTAATTAAGGGA
CTGTTTCTACACTTCAGATCCAATATAGTGAATATCAGGCAATTTGATTTCCCTTTGTAAT
ATACAATATAATAGTTGTAAGAAGAGGTGATATGTTAAGTTTCCATTTTGACGTAATCC
TCATTTCTAGAATGATTTAGCTCTCAACAGTCACTTTGTGTGCCAAAATATATACCTAC
TTCATACATTTTCAATTAAGATGCACTTACTTCGCTGTTTTTCAATATTTTCTGTTATTG
CTTCAGTTTTCAGCAGGAAGTACCACTATATGCGAGCAAAATCCCTCACCACCTTTAG
AATCGAGCCGCTACTCTTTGTCAACGACTACTATTTTGGCCACCGGGAAGGCAATGCAAG
GAGTTTGTGAATATTACAATCAGTAACGTTTGTGAGTAATTCGGGTTCTCACCCCTCAA
CAACTAGCAAGGAGCGCCCAATAACACACAGTATGTTTTCGTA

YGL032c, 87 aa (SEQ ID NO 94)

MQLLRCSFISFVIAVSLAQELTICEIQPSPTLESTFYSLSSTTILANGKAMQGVFEYYK
SVTFVSNCGSPSTTSKGSFINTQYVF

YGL043W, 1430 bp, CDS: 501-1430 (SEQ ID NO 95)

TCCGGATGGTGGGTGTTCTGTACCCCGCATTACACACCGCTCTGCCTATTCATTTTATC
GTTTTCGCTTTTCTTCAATGTATGTATAATTAACGTGCTATGTGATGCTATTTGGTAT
ATAGCCTTTCTTGTATATCCCTCTAACAAATTAATACAAGTGTTTCTGTTTAAAGCAAGTG

FIG. 1 - 33

CTAGAAGTGACTCGGTTCTCTTAGGAAATCTAAACGCAAGATTCTCTTATGGTGATTG
 TAACAATTATGAGTACTTCACTAGCCCACTTAACTTTACGGAGCTTCTTTTGAACGA
 TGCTTCGAATGACACGCCCTTTTGTATATATAATATCCAATTTCAATATAGGGAATTTT
 CAACTCTTACCCGCCCACTGTGCTGATATGACCAAGTGATCACTCGATGATGGGACATC
 GTATTGAAAAATATTGAATGAAAAATTACTCAAGCAGCAGAACATTACAGTGTAGTCTAG
 TCCGATATAAGAGCATTCATCATGGATAGTAAGGAAGTACTGGTACATGTTAAGAATCTFAG
 AAAAGAACAAAAGTAATGATCTCTGCAGTTCTAGAAATCTTACATGCTCTGGATATAAGAAT
 TCGTCCCCACTGAAAAGTTACTGAGAGAAAACAAAAGTTGGTGTGGAAGTCAACAAGTTTA
 AAAAACTCCACTAAATGTAGAGATCAGCAAACTCGTGAAGAAAATGATTAGCTCTTGGAAAG
 ACGCAATTAATAAAAAATAAGCGTTTCCAGGCAAGCAGCAGCATCATCAAGATCATGCGC
 CAGGCAATGCCAGAGGACAAGCAACTGTAGGTGAGTCCGTGAATGGTGTCTCAACAGCCGG
 CCTCTCCAGTCTAGATGCCATGAAAACAAGACAAGTACGTACGACATAAACCAAGAAATA
 GTAAGAACGATGGTGTGGATACAGCTATATACCACCACAAAATTACGTGATCAGGTACTAA
 AAGCACTTACGACGCTTTTGGCCAAGGAAAAGTGAGCATCCACCTCAATCTATTTTGCATA
 CTGCAAAAGCCATAGAAGTGAAATGAATAAAGTTTAAACACTGTGACACCAACGAAGCCG
 CTTACAAAGCCAGGTATCGTATAAATTTATTCAAACGCTCATATCAAAGAATAACCCAGATC
 TCAAACATAAAATTGCCCAACGGTGATATAACACCTGAAATCTTGTAGCTACATCGGATGCCA
 AGGATCTGGCCACCGCCCTTAAAGCAAAAGTAGAAGAAATTGCCAAGCAAAACTTAT
 ACAACGCACAGGGTGCCACCATAGAAAGGTCAGTCACCGATAGATTTACATGTGGTAAAT
 GTAAAGAGAAGAAGGTATCTTACTATCAATTGCAACAGATCTGCGGATGAACCAATTGA
 CCATCTTCTGACATGTGAAGCATGTGGTAACAGATGGAATTTCTTATG

YGL043W, 309 aa (SEQ ID NO 96)

MDSKEVLVHVKNLEKNKSNDAAVLEILHLVDKEFVPTKLLRETKVGVVFNKFKSTNVE
 ISKLVKMISSWKDAINKNKRSRQAQHHQDHAPGNAEDKTTVGESVNGVQPASSQSDA
 MKQDKYVSTPRKNSKNDGVDTAIYHHKLRDQVLKALYDVLAKESHEPPQSILHTAKLATES
 EMNKVNNCDTNEAAYKARYRIIYSNVI SKNPNDLKHKLANGDITFEPLATCDKLALAPF
 LKQKIEELAKQNLVNAQGATIERSVTDRFTCGKCKEKKVSYQLQTRSADLEPLTFCTCE
 ACGNRWKF

YGL102C, 929 bp, CDS: 501-929 (SEQ ID NO 97)

TGTTACGATCAACATCTTCTGTCGGTAAATCAGCATGGTAGTTAAACCCATCTGTACATAT
 GGTGAGATATACCTTTCGCATGGGTCAATACCATGGTCAACCAACCACTCTCTTTTTCG
 TTTTCAAAGATTGTATAATATTCAAACGCTAATGATAATTTGGGTGAGGTTTCGAA
 GAATTTGCCAAATCTCCCTAGGTATATTATCTTCTGCGCTCCAGATGTAACTGCGAGTCA
 TTTTGTCTTTTCTCGGTCTTACCTCGCAATAGGTTTCTTGTCTTCTTATTTCTTTTCTTT
 TTGGACCTATGTTTATATATGGAATTTTGAAATCTTTTAAAAAGCGATAAAAGCGTTG
 GGATCTGCCACTGGTAACTTCAAATAGACAAGACGAAAAAACGTTGAAATGGGTGATA
 GAAATAATACAGAAATAGATGTTGAATTAAGTTAACTGAAGATATATAATTTATTTGGAA
 AATACATAGATTTTGTGTGATGCGCTTAAGCGATCAATTCAACAACACCAACCGAGCT
 CTGATTTTCTTCTCAGCAACTTGGAGACGAATCTAGCTTTGACGATCAACTGGAACATTT
 GGAATTTCTACCTTACCACAAGATCTTACCGTAACCGGCTGCCAAGGTCTCAATAACTGGA
 CGAGTTTCTTGAAGCAGATTTCAAGTATTGGTCTCTCTTGTCTTCTGCGGATCAATGTC
 CACAATTTGTTCAAGTTCAAGACTGGCTTCCAGAAATGAGCTTGTGGCTTGTGGAAAGTAT
 CTCATACCAACTTTACGAAATTAACCTGGATGGTATTATCCATGTTAATTTCTGTGGTGA
 TGTTGACCACCGGCCATACCTCTACCACCGGGTGCTTCTGTGCTTACCGATACGACCT
 TTACCGGCTGTACAAAAAAATATTGTAA

YGL102C, 142 aa (SEQ ID NO 98)

MRLSDFNNNTSSDFFFSQLGDESSFDNWNINWSTLTQDLTVTGQCSVNNWSSFLRSR
 FQVLVSLVFWDDCPQFVQVQDWLPEMSLLLEVSHNTLTEITWMVFIHNVSVVMLTTGHT
 STTGVLVSLDTTFTGCTKKIL

YGL103W, 1461 bp, exon1: 501-549, intron1: 550-1060, exon2:
 1061-1461 (SEQ ID NO 99)

AACAAGCTATAATATTGTTAAATATAGTTGATCAACAGCATTGTAATGAGTTACAAGAGC
 GAGGTGGAATGAACCTTATGAAATGCGTATTATATATAAAGCTGTAATAAGAGCTAAGTTG
 AATTGAAATCTACGATACTTGATGTTGACATTATAGCACTAGTTCCAGGAACCCCTTC

FIG. 1 - 34

GAAAAACACAGCAAAAAACAAGAGTACTGTAACCAATGTAACATCTGTACACCAGGAGCCC
 ACACATTACCAAAATCAAAATATTTTCTAATGCCGTGTTATTTTCCCTATTTTCCCTCT
 GCGCGGTGAATAGCCCGCAGAGACGCAACAATTTTCTCGCAGTTTTCGCGTGTGTTAA
 TCGGTATTTTCCAGATAGGTTCAAACTTTTCATCTGTATCCCGTATATTTAAGATGGCG
 TTTGCTTTCTCCGTGATTTTTCCTTCTTAGTGATTTTGTGCATTAAATCCCGAAGAC
 AATCATCCAAGCTAATCAAGAATGCCCTCCAGATTCACTAAGACTAGAAAGCACAGAGGTC
 ACGCTCTCAGGTATAGTATCCATTTGGAAGAGGGAATGAAGAACCAGAGCGGTGACTTT
 TTTTGTAGTGTGTCACCAATATGTCGTGTATATCATGGTACAGGAGAATGTCAT
 CAGCTTAAGTGATCTCAACATATTTCTTTGTGTTTGTATGCGAACTTTGTATTTACCATCT
 CACTGTGAGACGGCTTATTTGAGGTAATAGCTCGAGTAATGTACTCTTCCATCGCAAA
 CTGAGCAAAAAGAAAGTGTGCATAGCCCTTTGTCTATCTTCCCTTTATTTATACCATGTATA
 TTCAGAACAGTCACTAGTCTACTCATTTTACGGCTATAAAGGTAACTTTCATTTAGAT
 TATGGAAAGCACTAATTTATCGCTGTATCAAAATGGTGTAGAGAGCGCAATTTATGAAAAG
 AGTTACACCGTTCTCTTTGTTTCGATAAAATGTCCAGTTGAAAAACCTGTTTACTAACGGA
 TTTAAAAATTTGATTTTCATTACAATATTTTGTACAGCCGGTAAAGGTCGTATCGGT
 AAGCAAGCAAAAGCACCCCGGTGTAGAGGTATGGCCGGTGGTCAACATCACCACAAGAT
 AACATGGATAAATACCATCCAGGTATTTTCGGTAAGGTGGTATGAGATACTTCCCAAA
 CAACAAGCTCATTTCTGGAAGCCAGTCTTGAACCTTGGACAATTTGGGAGATTTGATCCCA
 AAGACAGAGACCAATACTTGAATCTGCTCTAAGAGAACTGCTCCAGTTATGAGT
 ACTTTGGCAGCCGGTACCGTAAGATCTTGGTAAGGGTAGAATCCAAATGTTCCAGTT
 ATCGTCAAGCTAGATTCGTCTCCAGTTGGCTGAAGAAAAATCAGAGCTGCTGGTGGT
 GTTGTGAATTGATCGCTTAA

YGL103W, 149 aa (SEQ ID NO 100)

MFSRPTTKRKHRRHVSAGKGRIGKHKRHFGGRMGAGQHHRINMDKYHPGYFGKVGMR
 YFHKQAHFWKVLMLDKLWTLIPEDKRDQYLKSAKETAPVIDTLAAGYKILGKGRIPN
 VPIVVKARFVSKLAEKIRAAGGVVELIA

YGL130W, 1880 bp, CDS: 501-1880 (SEQ ID NO 101)

TTTTGGTACTGAAATTTCTCGTTTCTACTAGCTGGATTGCTGTGCTTTTACAATTCCTG
 GGAGTTTGGTATTGCTACCTTGGTCTTAGCACCACCTTTTCCGCTATTTGTATTGTT
 TGAACTAATTTAGTATCTATTTCCATTTCATTTAATTTACGTTTTTAGCAGCCCTCTCT
 CTCTTAGTGAATGGAAATCTCTCTCTTTAGGCATAGCGTGACAGCTGAAAGGCAGATG
 ATCTCAATATGTCGCGATAGGCCAATTTGGCACCAGATAGTTCGATGGCATTTTATTT
 TAGTCTTTTGAAGCAATATCATAAAAATATATATAGTTCTCCATGATGTTCTGGGTCAGT
 CGCTCCGAAGCGTAACCTAGTATAATAAATAGTTCAITGCAGAAAAATACGAAAGAAATG
 GTGGAATACGATCTGTTATATCTAAACTAAAGCTTAACTAACGGAATAAGCAAAATACGAAT
 CGACCGCTAATTTAACAAATATGGTTTTAGCAATGGAAAGTAGAGTGGACCAAGGAAATTC
 CTGGGCTCATTTCAACCTGGGAATGTCAAGCAAGACTTGAAGATGATGGTCTGTAATAT
 TGAATTTCCCAAAACCTACGAAACATTCCTGGTTCCAGCTGTGCTCTTCAGACTT
 CTGATGTGGAAGAGAAGCTGCTTGGCGATGATTACTACGTTTGTGAGAAAAAGATGGTC
 TGCGGGTGTGTATGTTTATAGTGATAAAATCCTGTGACGGGTGAGCAAGGATGCTTTATGA
 TGTAGGAGAAATAACTATTTATCTGGTTAATGGATTAGGTTTCCAGATTACCCCAAA
 AGAAGAAAGAGAGCTGCTAGAGACTCTTCAAGATGGCACTTATTAGATGGTGAACCTG
 TCATACAACTTAACCAATGACAAAATACAAGAGTTGCGTTATTTAATGTTTCGATTTGTC
 TTGCTCTCAATGGTAGATGTCTCACAAATCACCACAAAGTTCTAGACTAGCCACCTTG
 GAAAAAGATTTTAAACATACTCTGATTTAAGAGCAGGTACCCTAATCGTTGTACTA
 CTTTTCCGTTCAAAATTTCCATGAAACATATGGATTTCAGTTACCAATTAGTAAAGTTG
 CTAAAGAGTTAGATAAACTACCACATCTTTCTGATGGTCTGATATTTACTCTGTGAGG
 CACCTTACACTGCGCGGAAAGATTCATTTGTTATTAATGGAAGCCAGAACAGAA
 ACACCGTGGATCTCAATTTGATTTTATGATATCCCAATGGTGGAGGATCTCTTTTCGCTA
 AAGATGATCGGAACAGGTGTTATTAACAATATGACGTTAAGCCAGTTTTCAGCTATATG
 TCTGGCAGGCGGAGCTGATGTCAATTCAGTTTAAACATTTTCGACCGACCTTTTCGATA
 GGAAGGAATTTGAAATATTAGAAAGAACATACAGAAATTTGACAGATTGAGCGTTTCAG
 ATGAGGAATGGCAAAATTTGAAGAACCTTAGAACCCATTAATGTTAGAAATAGTAGAGT
 CGCGCAAAAAACCAAGAGACTGGGGCGTGGGAAATGTTAAGATTACAGGATGATAAGTTAA
 ATGGTAAATCATACATCGGTGGTCCAGAAAGTTTGGAGAGTATCAACGATTAAGTTTCAAT
 TGGAGGACCTCGAGGAAATTTGTTGGTGATATTTAAAGGTGCTGGGACGAGAGAAGACCA

FIG. 1 - 35

ATATGGCTGGTGGTAGTGGGAGACCACTACCGTCTCAAAGTCAAATGCGACATTATCTA
CCTCTAAGCCAGTCCATTACAGCCCCAAGTAATGATAAGGAGCCAAATATGTAGACG
AGGATGATTGGTCGGATTAG

YGL130W, 459 aa (SEQ ID NO 102)
MVLAMESRVAPEIPGLIQPGNVTDLKMVCKLLNSPKPTKTFPGSQPVFSQHSVDVEKL
LAHDYVVCCKTDGLRVLMFIVINPVTEGQCFMIDRENNYLVNGFRFRLPQKKKEELL
ETLDQGTLLDGLVLIQTNPMTKLQELRYLMFDCLAINGRCLTQSPSSRLAHLGKEFFPK
YFDLRAAYPNRCITTFPKISMKHMDFSYQLVKVAKSLDKLPHLSDLGLIFTVPVKAPYTAGG
KDSLLLLWKPEQENTVDFKLILDI PMVEDPSLEPKDDRNRYNYVDVKEVFLYVWQGGAD
VNSRLKHFDPFPRKEFEILLERTYRKFELSVSDEEWQNLKLEPPLNGRIVECAKNQET
GAWEMLFRDDKLNGNHTSVVQKVLSEINDSVSLEDLEIVGDIKRCWDERRANMAGGSG
RPLPSQSQNATLSTSKFVHSQPPSNKEPKYVDEDDWSD

YGL147C, 1076 bp, CDS: 501-1076 (SEQ ID NO 103)
CAATATTATAGTTACTACCTATTGTATTATTAAGATCAAAGTAACTCTTCACTCATAT
CAAAAAGAAAGGTTTGTAAAGAGCATTGGCGAGAGAGTATTGTCTGCGGTATAGAGGA
GAAAAAATTGTACTGATGCTAAATTTTGGTGTCTGTTCTCTTTTATTTTGTAAAGACTGT
TTTTCCAGAAATGTTTGGGTTTATTTTTTAATTTTGTAAACATTTTTCATCGCTTTCTC
ATTTTGTCAATTTCATTTTCTGTGGAAAAATTTCACTGACGCGAAGAAGCGATGAAATTT
CAACATCGCTCCCATCATCCCAATATTGGCATACACACATGACGACACAGCGGAAGTCGG
GAGGTGACAGGCAATGTGGCAGAGACGCTGGCGCGCTGTATTGTATTAATAGTATATTTT
ACACTCAATTCATTTTGTGATATTAATTTAGTGTGTAAAAAGCTTCTGAAATCAAGAAG
CCCGTCACAGAAGTTCAATCATGAAATACATCAAACCTGAACAACAAATCGAAGTCCGAC
AAGGTGCTCACTGTCAGCATCAAGTCCAGAATCGTCAAGGTTGTGGTCCAAGAGGTACTT
TGACCAAGAAGTGTGAAGCACATTGATGTTACCTTCAACCAAGGTCAACCAACCAATTGATCA
AGGTTGCTGTTTCAACAAGGTGGCAGAAAGCAGCTGTGCTTTGAGAACCGTCAAGCTT
TGGTTGACAACATGATCACTGGTGTCAACCAAGGTTTCAAGTACAAGATGAGATACGCTT
ACGCGCATTTTCCCAATCAACGTCACCAATTTGTGAAAAGGATGGTGGCCAAATTCATGAAG
TCAGAAATTTTGGGTGACAAGAAGATCAGAAACGTTTCAAGTATAGATGAGTGGTGTACTA
TCGAATTTTCCCAACGTTAAGGACGAAATTTGCTTGTCAAGTAACTTCTCGAAGACG
TTTCCCAAAACGCTGCTGACTTGCAACAAATCTGTCGTGTCAGAAACAGGATATCCGTA
AATTTTGGACGGTATCTACGTTTTCACAAAGGTTTATTACTGAAGATTTATAA

YGL147C, 191 aa (SEQ ID NO 104)
MKYIQTEQQIEVPEGVTIVSKSRIVKVVGPRGTLTKNLKHIDVTFTKVNNQLIKVAVHNG
GRKHVAALRIVTKSLVDNMITGVTKGYKYMRYVYAHFPINVINVEKDGAKIEVRNGLDY
KRIKRNVEVRDGVLTIEFSTNVKDEIVLSGNSVEDVSQNAADLQCIKRVKDKIRFLDGIY
VSHKGFITDEL

YGL213C, 1694 bp, CDS: 501-1694 (SEQ ID NO 105)
AATCAAAACGATCGTTATACAATTCAATTGAGGAACCTCTCTAGTCCGATCCGCTTTTCAT
CGATCATTTCCGGATCATCATATCTTCTTTGCCACCTCCTGTCCAATACACCGGGCTTTT
CAGGGAAGTCATATGGGATGGTGTCTTCTTACATCTCTCTCCAATCGTGTCTTCAGTTTCC
AAAACCTCGGAATACCTTTTGTAAAGGCGCTGTGTTGGTGTACTAACACCGGTATAAAACAT
ACTTGGGGTTGATTTTAACATCGTCCACCTTGATTCTTAACTTTTCACTCATTTTCCCTA
CAGAAATAGCTGCCATCAATATCAATATCAACCCCTATATGACTTTATTGTTTGTGTT
TTGTTGGCTAAATTTGATACAAATCTTTAGGCGAAAAATAAAAAATATAAAGTAAA
GAAGGAAAAATAGGCGATATTAACAAATCTAAATATAAGACAGAAGAACGAAAAAGAC
GTTAATCAAGTATTTGAAAAATGTCCAAAGTGTATTGCGCACAGCAATCGAGTAAAG
CTCATGACGCTGATATTTTCTCGGTTTCTGCTTGCAATTCATTTACGGTAAGTTGTTTCA
GTACCGGTTACTTAAAGGTGCGGATAATAAGCTGTTAGATAATGAAATCCAAAGATA
AGTCATATTTCTCACTTTGTCCATAAGTCCGGATTGCACCATGTGATGTCTTGCAAGCTA
TTGAGAGAGATGCAATTTGAATTTATGCCTTGTGCTTACCACCTTCATTTTCTGGCGATTTAC
TCTTCTATCGTATCACTAGAGAAGATGAGACTAAAAAAGTTATATTTCGAGAAATTTGAGAT
TCTTAGACTCAGACATGAAAAAGCATTCTCTTTGGGCATTAATTTGGGGTCCCTCAAAT
ACAGACTACTTTTCCCATAGGCTGGTTGCTACAGACGTCAAAGGGACCACTTACATTTGGA
AGTTTCAACCGTTTGAGATGAGTCAAAATCTTTTAACTATAATTTGAGAGCCCCACGTTAG

FIG. 1 - 36

AATTACAAGGCACTGTGCAATCGCCTATGACTCCAAGTCAATTTGCCACTTCTGTGGATA
 TCCTCGAACGAGGACTAATGGCCACAGGTTTAAATAATGGAAACAGTACAAATTTGAGAAC
 TATCTACATTAGCCCGGTTGTACAAATTTGAATCTCAGCATTCTATGATTAAATAATCGA
 ATTCCATCAGATCGGTGAAATTTTCTCCTCAAGGATCCTTATGACCATTTGCTCAGGATT
 CAAATTTGATTTGGTTGCACTCACTCTATATGAACCTGAATTTGGTGAAGAAATAGGCTCTCT
 TATCCGTACCAACCCATAGCTCGCAGCCAGCTGGGTGAATTTGCACATTCTAGCTGG
 TCATGAGTCTATCGTTTAAATGATTCTGGTGAACATTATGACAGTCCGGATGGGATGGTA
 AATTGAGATTTTGGGATGTAAAAACAAGGAAAGAACTCACTACATTGAATATGCAATTGTG
 ATGATATTGAATTTGAAGAGGATCTTAGCTGTGTGATGAACATGGAGATCTTTAGCTG
 AACCTGGTGTCTTTGACGTGAAGTTTGTGAAAAAGGTTGGAGATCTGGTATGGGAGCTG
 ATTTAAATGAAAGTTTATGCTGTGTTTGTGTAGATAGAAGCATCAGGTGGTTTAGAGAAG
 CTGGCGGTAATAA

YGL213C, 397 aa (SEQ ID NO 106)

MSKVFIATANAGKAHDADIFSVSACNSFTVSCSDGYLKVWDNKLNDNENPKDKSYSHFV
 HKSGLHHVDVLQAIERDAFELCLVATTSFGDLLFYRITREDETKKVFIEKLDDLLSDMK
 HKSFALKWGAENDRLLSHRLVATDVKGTTYIWKFPFADESNSLTINWSPTELOQTVTE
 SPMTSPQFATSVDIISERGLIATGFNNGTVQIISLSTRLPLYNFESQHSMMNSNSIRSVK
 FSPQGSLLAIAHDNSFCITLYETEFGERIGSLSVPHSSQASLGEFASHSSWVMSLSPN
 DSGETLCSAGWDGKLRFDWVKTKERTITLNMHCDIDIEEDILAVDEHSDSLAEPGVDFV
 KFLKKGWRSGMGADLNESLCCVCLDRIRWFREAGGK

YGL235W, 1037 bp, CDS: 501-1037 (SEQ ID NO 107)

CTGGTTCACCATATCTTATGGAAGATCTATCAGGAAACCTTAGAATCTTAGCTTCGA
 TGGAGGGACAATACCGGGGGCCTTTGATGGTCTGTCTCTGAATAGAAATGGATGATGCA
 AGTTATTTCCGCAAAAAGTCTGTCATTGAGGTGGTATGTGTGCCAAAACATCTCAGTT
 GCTTCGTGGGTTCGACTGACACGGTTTCATTGAGAAAACCTATAGGGACAGGCAACGAT
 CTCCTCTTTCGACCTCCAGAGCGCTGAAATCAATGGATTCTTTGGCCAGCTAGCCGGAG
 TGCTGTCTTCAACACGCCCTTAACGAAAGCCACCTCATTTGTAGAGATTGCTGATCC
 CATATGTTGGCTGCTCGCCAAATCTTCTGCTGCAATACGCTTGTGCGCGATGTGAATTT
 CTGCACTGAGAAACGTACCTGTAGTGATTTATGACCTGATCTGCCCAACCTGGGTACCGT
 CATCCAGAACCCACCTTTGATGACCTTGTGGCCACATCCGGGGTACATACAAGATCAAGT
 CAGCAACTTTGTTCTGCGAGCAGAGACAAGTTGGGGTGTGCTTTCTTGTGCGAAAGTTCCC
 TTTGCAATGATTTCTTTATATACTCTCTGTCTATCTGGGCTCTGGGCCCCCAACAGCAG
 GACCTTCTGCTCTGTTTCAGCATTTTGAATTCACCTCCAGCGAGATCAGTTACTTTGGCCA
 TCAGCCCATCGAGAGCGTCGATTCTCTTTACAAGGATGCCCTTACCCTTCCACCAATAG
 AGGGGTTCACGAAACACTTACCAATATCTGTTAACGATGGTGTAAATGAGAGTAGTATGCG
 CACGAGTCTTAGATGACGCGAGCTGCACTTCGCGAGCTGCAATGTCAGGACCGATGACCA
 CGACCTGTGCTCTGGTTGTGGGTGGAAGCTTGTCAAAGAGATATGGTCAACCGCCTCC
 TGAGGACCTGTAAGGGAATAAGTACACGAAGACCGCAAGGTTGTTACGCGAGCATCG
 TTCTTTGGGGCGTTTAG

YGL235W, 178 aa (SEQ ID NO 108)

MTLWHPGYSYKIKSATLFCRDLKGLCAFLSESSLCMYFLYNSLSIWLGPHTAGPLLLFS
 ILNCTPARSVTLFIPSPRASISFTRMPLTPPIEGLHEHLFISVNDGVMRVVCAFLVDDA
 AASQSPACFAPMTTTCVLVVGWLKVKEDMNVNRLRCKGNEVHEDAKVTVRSIVLWGV

YGL260W, 731 bp, CDS: 501-731 (SEQ ID NO 109)

TACCATTGGAACACCGGTGATCATTCTGGTCACTTGGTCTGGGGCAATACCAGTCAACATG
 GTGGTGAAGTCACCGCTAGTTGAAAAACGGCTCAGCAACTCAACTGGGTAGGTTTCCGTT
 GGGTGGGCGGCTTGAACATGTGATTTGAGCCAAAGTGAGCTCTGATATCAGAGAGCTAG
 ACACCTAATTCAACCAAATTCAGCTCTTTCGTGACAGTGAAGCTAGAGTGGTGGTGGCGAA
 CAGATGAGCAGGATGGCAGCGACACACGCGCGATTGAAGTTAAATTTGACCATTTGATTT
 GTTTTGTGTTTATGTGCTGATATAGCTTAAACGAGAAAGAAAGAAATAAGATATATCT
 CAAAAGCATATTCAGTTGAAGCAGCTCTATTTATACCGCTTCTCTATGACGTACATCACT
 TAAACGATTCGTAAACAGATGCTCATTTAGCACCTCACATATCTCCATATCTCATCTTT
 CACACAATCTCATTTATCACTATGGAGATGCTCTGTGTTCTGAACGAATCATACATCTTCT
 ATAGACTTCGTATGTGGAGTATGTATTATGGCACTCATGTGATTCTGATTCGCGAGAAAT

FIG. 1 - 37

GTGGGAATGCCAATTATAGGGTGCCGAGGTGCCTTATAAAACCCCTTTTCTGTGCCTGTGA
CATTTCCCTTTTTCGGTCAAAAAGAAATATCCGAATTTTAGATTGGACCCCTCGTACAGAAG
CTTATTGTATA

YGL260W, 76 aa (SEQ ID NO 110)
MEMLLFLNLSYIFHRLRMWSIVLWHSVFCVCAECGNANYRVPRCLIKPFSVPVTFPFSVK
KNIRILDLDPREAYC

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 111)
TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCCTAAATATGTACTCTTTTATTT
TTTTTAATTGGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAACATTATTTTCCT
GTGTAGCCCTAATGTTTAAATGCCCTAATTTTTCCTAAATGCAGCAACATACATATGTTGA
GTGCTATAGACATCTATATATAACAAGCAGAACCCGTCTAATTTGGTATTTTTCAGGACA
TTTTAAACATCCGTACAAACGAGAACCCATACATTACTTTTATAATCTCTTTTGTGTTT
CACCCTCTCTTTTATTTTATCCGAAGATCTTTTGGAAACCCGCTCTGCGAATAGCGAA
GCTAGGATACCAAAATTGAAACTTGGACATACTCATCTTAAAGAAGTATACTGTTAAGA
GAGGCATTCATTTTCGTGTATTATAACGTTTAGCATCAGTTACCCCTGAAAGCCCAACATA
TACAAAATACGCGTCCAAAGATGTCTACTAAAGCCCAAAACCCATGCGTGAATTTGAAGA
TCGAGAAATTTGGTCTGAACATCTCGTGTGGTGAATCTGGTGACAGATTAACCCAGAGCCT
CCAAGGTTTGAACAATTTATCTGGTCAAACTCCAGTTCAATCCAAGGCCAGATGACTGT
TCAGAACTTTTCGGTATCAGAAGAAACGAAAAAATTGCTGTTCACGTTACCGCTCAGAGGTC
CAAAGGCTGAAGAATTTTGGAAAGAGGTTTGAAGTCAAGGAATACCAATTGAGAGACA
GAACTCTCTGCTACCGGTAACTTCGGTTTCGGTATTGACGAACACATGACTTGGGT
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTCTATGTCGTGATGAACAGAG
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACTGTTGGTGAATCCCAACAAGA
CAACTAAGGAAGACACCGTCTCTGGTTCAAGCAAAAGTACGACGCTGATGTGCTCGATA
AATAA

YGR085C, 174 aa (SEQ ID NO 112)
MSTKAQNPMRDLKIEKLVNLISVGESGDRLTRASKVLEQLSGQTFVQSKARYTVRTFGIR
RNEKIAVHVTVRGFKAEELLERGLKVKEYQLRDRNFSATGNFGFIDHIDLKGYDPSI
GIFGMDFFVVMNRFARVTRRRKCKGTGVNSHKTTKETVSWFKQKYDADVLDK

YGR118W, 1258 bp, exon1: 501-565, intron1: 566-885, exon2:
886-1258 (SEQ ID NO 113)
AGCCATGTCGGTGCCTAGACTTTTCTTCTCACTGTCACTTACCTGTTTGAAATCATGT
CCTTTTCTTTTATTTGGCCATTCTTATACATTTTCTTTCTTCTGAAATTAACGTACACCCA
TACCTATATACACCCATACCTTATTTTAAATATAAAAGTAAACTTCAATTTTGAAAGA
CCACTCTGATCATCAGACGCGGGCTTGGAAAGGAAGAAATGACGTTTCGGCGGAATACCTT
TTCAGAAGGTCTGCTCTTTGGGCTGCTCATGGGAGACACCCAGCGGAGCTCCTCCCGAG
AAAGGCCCTTCACTCTGCGGATTGCTGACGGAAGCAGTAGCGAGGTTTGAGTTCTC
TACGCCGAGAGTACACTGCCGTAATATCAATGTTTCGACTAACGGTTACAGTACGTTA
AATTAGATCTGCTTATGAATTGACATATTAGATAATGTCAAAATTTTACAAAAACCTTAAG
ACAAAGGAAATATAACAAAGATGGGTAAAGGTAAGCCAAAGAGGTTTGAACCTCTGCTAGAA
AGCTACGCTGTCCACAGAAAGAAACAGTATGTTGACTATTTCAAATTAATAAAACACTATC
AACCCTCTATTGGATATCGTTTATGTTGAAGGAAATGTTGTGAGCTCTGGAGTGATATAA
TTTATCAAGTAACATATCTTGGCGCAAACTCAGTTTGGAGAGGCTTAAATATGACACGTCAC
AGTGATAAAAAGTAATGAATAGTGAACGCTCAGCTCTCGGCCATTCTTCCCAATCTATAGT
GTGGAAAAATAAACCTTTTCTTCCCAAAATAACTCAGAAAGTCACAGGAGGCGGTTTATTA
CAACGGAATCATTTTCTTACTAACAGTTTCTTTTATTTATATAGCCGTTGGGCCGAAAAA
CAACTACAAGAAAGAGATTTTGGGTACTGCCTTCAAGTCTTCTCCATTTCGGTGGTCTCTC
TCATGCCCAAGGTTCTGCTCTTGGAAAAATTTGGGTATCGAATCCAAGCAACACTTACTGCTG
TATCAGAAAGTGTGTTAGAGTTCAATTAATCAAGAAACGGTAAGAAAGTCTACTGCTTTTCGT
TCCAAGCATGTGTTGTTGAACCTTTGTCGACGAAATGATGAAGTCTTGTGACAGGTTT
CGGTAGAAAGGGTAAAGCTAAGGGTGATATCCAGGTGTTAGATTCAAGGTCTGTTAAGGT
CTCTGGTGTCTCTTGTGCTTTGTGGAAGAAAGAAAGGAAAGCAAGATCATAA

FIG. 1 - 38

YGR118W, 145 aa (SEQ ID NO 114)
 MGKGKPRGLNSARKLRVHRRNNRWAENNYKKRLLGTAFTKSSPFGSSSHAKGIVLEKLGIE
 SKQPNISAIRKCVRVQLIKNGKKVTAFTVPNDGCLNFVDENDEVLLAGFGRGKAKGIDIPGV
 RPKVVKVSGVSLALLALWKEKKEKPRS

YGR142W, 1733 bp, CDS: 501-1733 (SEQ ID NO 115)
 GGATCTACTTTACAGGGTAATGAATATTTGGGCGTTTTTCGCTATTTTAGCATGCTGTAGT
 GGTACTGTCTGTCATCGTCATGTAGCACTATTTCAGCCGTATTTTCTTTTCTTTCTTTTCG
 CACCGTCTGTGGTTGTAAAGTTACTGACACTTTTTTTCTAGAAAGTTCGGGAAAATTCG
 GACACTCCGGTGGAGCTCGAGAGTTGTATCCAGTTTCTTGTTCGGCGGATATTCGGAACCA
 GGTCGGGTTGGCGTAAACAGCCGCCAGGATGGAAGAATTAAAGAAATTCATAGAAGCCCTC
 AGTTCTTTGGCGAAGTAAAGTGGCAAAACAATAAGAGATCTATTGCATTCATATATAA
 AGCATTAGAACAATCTTTTCTCATTGACAGGATCTCATTGTCTCTATATATATTTTCTT
 CTCTCTGAAAGAAATATCAGTATTACAATCATAACAACCAACCAAGAAAATAACCTAATA
 GACCCCATTCACAATATAGAAATGTTTCCATATTCATTCCACCATGTGTTTTGAAACGC
 TGCCATCTTTTAGTCAGCCCTACATTCGCGTTATTTTGATGTCAGTCTCCAGTGAGCT
 ATTATCCGAAGTGTAAAGGAGGAAAGCAATAAAGCTAACCTTAAGAGCTCCAAAAA
 CGGATGCAAAATGTTTCAGAACCTTTGAGGTATGCACTTGCTGAAACACCAAAATGGTTATA
 CATTAAAGCTTGCTTAAGCGGATCCCATATGAACTTTTTTCAAAGTACGTTAATGAGAAAT
 TAGGTTGAGCTAAAGGAGAACCATTCACAGCAACCTTACCATTGTTGTCCAAGATTTTTTTG
 GAAACCAAGTATTATGTTGAAGATGAAGCGGATGAAGATGCTCTATTGAGATCTGCATGAT
 AAGATCTCGAATTTTAGAGCCATAGGAAAGAAAATTGCTAAGGATCTTTTCCRAAGCATCG
 AAATAGAATTGAAATCATAGAGGTGATGAATTGAGCATATTGAGTAAGAAGGATAAAATCT
 TTAAGGAATCTCTCTAGACCAAGTGTTGAAGATGTTTGTATTGCTGTGGAGTTG
 AAAACATAGATGATGGCTCGAGAGAAAAATATGCACTTTTAAAGATTGTTTGTATTGAAGC
 ATGAGGAGAAGAAATTTCCGAAGGTGGCATCAACGAACCAAGATGCCAAATTAATGAAATCCA
 AAAAGTAGCAGGTCTCAGATGATGTTAACATGTCTGAATCTTTGAAGGAGGAAGAACCGG
 AGAAAGCGAAAGAACCTTAACCAAAGAGACCAATAAAAAAATGGATAGAGGAAGAAA
 GTTATGTCAGGAGGAAAGCAGAAATCAGAACGAGAAAGCTGCCAAGGAAGATGAAG
 AAAGCGAAAGAAAGAGAAGGAAGCCAGATTGAAGGCAAGGAAAGAAATCTTTGATATAATA
 AGCAAAAAACCAAGAGGTCCAGCAAAAAAATTCGCAAAATTCGAATCTATGCTTATCT
 CTGAGATTGAGGCCAGCAATAAAAAATAATAGCAATTTCTGTTTCCAGCAGAAAGTGATA
 ATGAAAGTATAAAACAGTGATTCTGATACGACTTTGGATTCTCTGTCTGGTATATACAC
 TAAAAAAACAGCGTTTCCCTTATTAGAAGACGTTGAGGATGAGGAAGTTGACAGATACA
 ACAGATCCCTAAGCAGATCTCCAAGGGAACCTCTATTATTGAGGAGATATAA

YGR142W, 410 aa (SEQ ID NO 116)
 MFSIFNSPCVFEQLPSFSQPLHSRYFDCSSPVSYYPECKRRRKAIKANRAPKSDANCSE
 PLRYALAEATPNGYTLSLSKRIPELYFSKYVNEKLGELKENHYRPTYHVVDQDFGNQYYVE
 DEADEDALLNSALKDLDFRAIGKKIAKDLFQDYIELNHRGDELSILSKDKIKFKEFLSD
 QVFEDVFIIGCGVENIDDSREKYALLKIGLVKHEEIESEGGINEPKMPIIESKIDESH
 DVNMSESLEKEEEAEKAKEPLTKEDQIKWIEERLMQEEESRKSEQEKAKEDEERQKKEK
 EARLKARKESLINKQKTKRSQQKILQNSKSLPISEIEASNNKNNNSNGSAEDNESINSND
 SDTLLDFVSQNTLKKHASPLLEDVEDEEDRYNESLSRSPKGNSTIEET

YGR236C, 890 bp, CDS: 501-890 (SEQ ID NO 117)
 CAAAAAAGTTTTCGGATGAACCGGATTAATACAAGTAAATCAGCAAGATATAGAAGAC
 AAAATAAGCGGTGAAAAACAATCATAAACCTCACAACGGGGGTTTTCAGCTGTATTCTCTC
 CCATACATACATTTTGTATAAGATATAATGTTATATTCTTTTCGTAATTTTGTGTTTACT
 TCGGTTTGTCTTATAGATTTTATCAGCCGCACCGGAAAGGAGATCAATAAGGTACCTTCT
 TAAAGAGGATAGAAGCCTACATCACCCTCAATAATGGAGTAATGCCAGCATTTGGATGA
 AGAGAAGAAATTCAGGATACCTGGGATAACACTGTTAAAAAATGCTTCGCGACGTGAGGT
 CTCTTTCATATAAATGGAATGCCAAATCTCTTTCATATTCAGGATAGTTTGAATG
 TTTGTTTACTGAAGATCAGAATCAATAATACAATCAATCAAAATTTTAGCGCATAAAA
 TTCAAAAAAGTTTACTGAAATGAAGTTAGATTGAGGAAATATATCTCAGAGGCAACAAAG
 TTGTGCAAGACTCCAAGTTTAGATATATATTGTTAGGGCTGGTGGGCGCTGCTGTGGTACG
 CGACCGCATACATGAGGAGAGGCTATACGGTTTCTGCACATAGCTTAGACACATCAACG
 CGGTAGACACAACCTAAGGCGTCTGTTATGGGTACAGAACAGAGAGAGCTATGACGGAAG

FIG. 1 - 39

GTAAGAGTTTACAAGAGATGATGGATGATGATGAAGTAACGTATTGTAGTGTCTCTTCA
 ATCATGTGAAGGAATTTGTACTTGGTTCCTGCATTATGTCTTTGCATTTTGTTCG
 CATTTAATCATAGTACGACAAACGGGGAAGGGATGTGATTTTACATAA

YGR236C, 129 aa (SEQ ID NO 118)

MKLDGSIYSEARQVRVTFKFRYIMLGLVGAUVPTAYMRRGYTVPAHSLDNINGVDITKA
 SVMGTEQRAAMTKGKSLQEMDDDEVITYLMFLFNHVREFVLGSLHCLSLHFVAFNHSTT
 NGECDPDT

YGR277C, 1418 bp, CDS: 501-1418 (SEQ ID NO 119)

AATCTTTGCGATTGAATTCGTGCACGAACATTAACTATTAGTTCTTTTGCTAAAGTTTCTC
 CAATATCTGGGAATATCAGAATTTAGCAAGGCAATCAAAGCGGATAAAGCAGGGATTAGCC
 TGCCATTCTGTTTGTTCAGAGTAAAAATCCACAACTTTTACAAATTAATGTTGCGGCCAA
 TAAGTATATTGACTTTGAAATAAGTCTCTGTGCGGATTCCTGTAAGTTGTCATTGTTAAAT
 TGGATATTATGGGTGAACCGTGTGACCTTATCATTTCCAGTTTCTCTCTGAAATTTAA
 TGCTCTTCATCTGCTATGGTAGCGGTAGACATGCTGGTTGTAGCCTTTTATTCCTTTT
 AGGTTCTTTACTCAATGCCAAAATAAATATCAGTGTAAATAATTTTTTCAAGAGTACG
 TAATGGAAAAAGATAAAAAATAAGGACCGTCTATAAAAGAGACGTGATTAAACCTAAAAAT
 CTTAAAGTAAAGAGTCTAAGATGGTTCAGGAAAAATCCAGAGTTTGTATGTTCTCTCCTT
 ATACACCGCCTAGTGCTACTTTGCGAGGATTATAGGSCAACTATTCGTTCTTTAAGAG
 AATGTCAAAGTCAACTAGACATCGTGATTGTACCTGAAATCAAACCTCATTCAGTTGG
 ATTCTGCGCTAGGGAAGATGTACAGTATTACCAAGGAGTCTCTTTTGGGCTATGGAATGA
 TCAACAGCGGAATCAACATCATATTCAACAATATTCATTGCTCGAGAGTAATTTGCAAT
 GGAAAGTGGTTTATTTGCCACAGGAATCCACTTTTGAACTTTGGAAGCTAGAGTTGGGAC
 GAAAGCAATACCATAGTATAGAACATTATGCATTACAGATAATAATAATGGAAGAGATAG
 AAGGTCCTCAAGATGTCTAACTTTTATGTCACCGCATTTGGCGGAAAGCTTCGACCCACA
 TTCACGATGGACATAAAATATTGTTGAGCGTCTCTACATTTCATCAGTCAACAAGGTTAA
 TTTTGGAATACGTGCGATGAGCTCTTGCAAAACAAAGAAATACAAAGAGTTTGTGAAC
 CTTATGATACAGATGCAAGGCACGTACATCAATTCATCAAGTTGTTTAAACCCGGATCTCT
 CCGTAGAACTAGTTCCCTTAAGGGACGTGTGCGGCCACAGGGGAAAGTACCCGAGATAG
 AATGTTTAGTTGTGAGTAGAGAAACCGTCAAGTGGGCGAGAGACTGTGTAATAGACATAGGA
 TTGAAAAAGGCATGAGCCCATTTGGCAGTACATGTGTTTAAATGACTTGGAGGAAGGGAGG
 AAGACCGCTGGAGCGAGAAATTAAAGCAGCACGGAAATCAGACGCTACTTTAAGTCTCTGT
 CTTGCCAACCGTGCACTCCACAAAACCCCTGCGTATAA

YGR277C, 305 aa (SEQ ID NO 120)

MYEENSRLVILPYPPTPSATLQRIIGQTIPLFRECSQLDIVIVPEFKTSFQDLSALGKM
 YSITRDVLLVGMINSINILFNHIEFVESNLQWKVVLLPQESTFETWKLELGGQYQYHSI
 EHYALHDNIMEIEGPKDANKFHVLTALGGTFDHIHDGKILSVSTFITSORLICIGITCD
 ELLQNKYKELIEPYDTRCRHVHQFIKLLKPDLSVELVPLRDVCGPTGKVPETECLVVSR
 ETVSGAETVNTKRIEKGMSPLAVHVNVNLGGREEDGWSKLSSTIIRLLKSSASPTCTP
 QNPV

YGR284C, 1433 bp, CDS: 501-1433 (SEQ ID NO 121)

AGAGAGCCATCCGTAACCTGTCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGGCCA
 CCACGATTGACGAACAAGTTGGTTGTATCGTTGACAGTTTGAATGACGAAGAAGTTAGTGT
 CCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAAGGAAGTTTGAAGGAATCTG
 CAAAGACATATTGTGATTCTGGCAAACTACCAATCCAGCTTGTGTGCTACTTCGTGTGAA
 TACCGTAAGAAATGGAATAGAAATATACAGAAATGTATACGAATATATTAGAGAAGCTGTCT
 CTTTATTCTTATATAATGAATAGGTTGCGGTAAACGGTTCCCTTTTGGTATTCTTGAAG
 ATGAGAGAAGAGGGAATAATGAGAAAGGCCGAAAAATAAGGACACCTTTTACGAAAGATC
 AAAGGTGCTCTTATTCTTACATAGCTGCAATTTAGTACGATCAAAAAAAGTAAAAAC
 AAAATGAAAGATAGATCAATGTCTTACAGAGGACCTATTGGAATTTTGGCGGTATGC
 CAATGTCAATCCGCAAGGACCATACTTGGCGGTGCAAAATTCAGATTTAAACCAAGAAC
 AATCCACTTCTGGCATCTTAAAGCAATGGAAGCATCTTTTGAAGGTTTGGCTCCAGAA
 TTGAGGGGCTCAGTGACAAATGCAAGTTGTTTATAAATGAAGCCCTTACATTCGAAGTTGT
 CAAGATTTTTCATGTGGCCACCTTTTATGAAGATTGTTTGAAGTCTTATCAAGATTTGT
 CAGATCAAAATTTTATCTGAATAAGTGAAGCATTACCCATACTTCTTTGTCGTGTGT

FIG. 1 - 40

TTCTAGTGGTTGTTACCGTTTCCATGTTGATTGGCGCCAGTTTGTGTAGTTTAAAGAAAGC
 AAACCAATTATGCCACCGGTGTGTTATGTGCTTGCCTTATTTCTCAAGCATTAGTTTATG
 GGTGTGTTTACGGGTTCATCATTTGTCCTAAGAAACTTTAGTGTATTTGGTGGGTTGTTAA
 TTGCATTACGCGATTCAATTGTTCAAAACAAGACAACATTCGGTATGCTTCCGTTGAATTA
 ACAGCAAAAACGCAGAACGGAAGGGTTACCTGTTGTTTGTCTGGTAGAATTTTAAATTGTTT
 TAATGTTTATCGCTTTCACCTTTCAGTAAATCATGGTTTACTGTTGTTTGTGACCATTAATCG
 GCACAATATGTTTCGCCATTGGTTACAAGACAAAATTCGCATCCATTATGTTGGGTTTGA
 TACTAACTTTTACAATATCACGCTAAACAACACTACTGGTTTATAACAATACAGAGATGAG
 ATTCTTGAAGTATAGTGTTTTACCAGAATTTAAGCATCATTTGGTGGGCTTCTATTAGTTA
 CTAATACCTGCGCTGGTGAATTTATCCGTTGATGAAAAGAAGATTACTAG

YGR284C, 310 aa (SEQ ID NO 122)

MSYRGPIGNFGGMPSSSQPYSGGAQFRSNQONQSTSGILKWKHKSFEKFSASRIEGLTDN
 AVVYKLPYIPSLSRFFIVATFYEDSFRLSQWSDQIFLYLNKWKHYPFVVVVLVVVTV
 SMLIGASLLVLRKQTNATGVLCAVCISQALVYGLFTGSSFVLRNPFVIGGLLIAFSDSI
 VQNKTFPGMLFPELNSKNDKAKGYLLFAGRLILVLMPIAFTFSKSWFTVLLTIIGTICFAI
 GYKTKFASIMLGLILTFYNIITLNNYWFYNNKRDFLKYEFYQNLISIIGLLLVITMTGAGE
 LSVDEKKKIY

YGR285C, 1802 bp, CDS: 501-1802 (SEQ ID NO 123)

CATTTAGTCTGATTACAGCAGAAATCGTAGCGCGATGAGACATTTCAATCAAAATGGCCTT
 TTTTTTTGGGCAATTTTATATCTTGAAATGATAGTTGCCTTGTACTTTCACCGGTT
 CATTTCATTAGAAGCTTGACTAAATATGAACATTTCTTAAAAAAAAGGTTGACATATAAA
 AATAATCGAATATAAACGATGGAATTTTATAAAATTAACACATATATATATATATATAT
 AACTATAAATATATGTCAAAGAAACCATACAATCATAGATTATAACTATCTTTTGGATGAC
 ATTAATGAACATACAGCTCCCTAATACAAATGTCCTCAAAAATATTACCGCAAGATCAAGT
 CTTTTTTTTTTCTCGATGAAATTTTGCAAGAGTTTGAATTTTATTTCAAAGCTGGT
 AGAGAAAATTTCAAGGTTTTCCTACCGATGCTTTTATAAAATCTTCGTTTGTCTCAC
 ATATACCAACAAGAGTAACGATGTTTCTTCTACCTCAACCTCAGACATCACTGTTG
 AAGTCAACAGTTCCCGTACCAAAACCCCATTCGTCGCTCGTCCGGTCGAACCGGTTGGTA
 AGTCTCTTTTTCGAACATGCTCAAGAACTTTGAGAAACACACCTCGTCTGAATTTGAAA
 GAATTTGAAGCTGAAAAGAACGTCAAAACCGTTGATGAATCCAATGTCGACCCAGATGAGT
 TGTATTTCGACACTGAATTTGGCCGATGAAGATTTACTGACTCATGATGCTAGAGACTGGA
 AAATCGCCGATTGTATGCTGCTATGGGTTTGTCAAGTTGCGTTTCAGAGCTACTGAAA
 GTCAAAATCATCAAGGCTCACAGAAAAAAGTTGTCAGTACCATCCAGACAAGCAATCTG
 CTGCTGGTGGTAGTTTGACCAAGATGGCTTTTCAAGATTATTCAAAAAGGCTTTGAAA
 CTTTGACTGATTCCAACAAGAGAGCTCAGTACGACTCATGTGATTTTGTTCGGATGTTTC
 CTCTCCCAAAGAGGATACCGATTATGACTTTTATGAAGCTTGGGGCCCGTTTTCGAAG
 CTGAAGCTCGTTTTCCTAAGAAGACTCCTATTCCTTCTCTAGGTAAACAAAGATTCTCCA
 AGAAGGAAGTTGAACAATTCATGCTTTCTGGCACAGATTGACTCTCGGAGAACCTTTG
 AGTCTCTTGGACGAAGATGTCCTCAGATGACTCTTCTAACAGAGACCACAAGCGTTACATTG
 AAAGAAAGAACCAAGGCCGCAAGAGACAAGAAAGAGACTGCTGATAACGCTAGATTGGTCA
 AACTTGTGAAAGAGCTGTCAAGTGAAGATCCCCGTATCAAAATGTTCAAAGAAAGAGAGA
 AGAAGGAAAGAGAAAGAAATGGGAAAGAGAGCGGTGCCAGAGCTGAAGCTGAAG
 CTAAGGCCAAGGCCGAAGCTGAAGCGAAGGCTAAAGCTGAACTCTGAAGCCGAAGGCTAACG
 CCTCCGCAAAAGCTGACAAAAGAGGCTAAGGAAGCTGCTAAGGCCGCAAGAAAGAGA
 ACAAGAGAGCCATCGTAACCTCTGCTAAGGAAGCTGACTACTTTGGTATGCTGACAAAG
 CCACCGAGATTGACGAACAAGTTGGTTTGAAGCTGTGACAGTTTGAATGACGAAGAGTTAG
 TGTCCACCGCGGATAAGATCAAGGCCAATGCTGCTGGTGCCAAAGGAAGTTTGAAGGAAT
 CTCGAAAGACTATTGTCGATCTCGGCAACTACCATCCAGCTTGTGTCTTACTTCTGTGT
 GA

YGR285C, 433 aa (SEQ ID NO 124)

MFLSPLTSDIIVENVSSAKTTPFVRFPVEPVKGFLLQHAQRTLNRHTWSEFERIEAEKN
 VKTVDESNDPDELLFDELADELLTHDARDWKATADLYAAMGLSKLFRFATESQIIKAH
 RKQVQVYHPDKQSAAGGSLDQDGFKKI IQKAFETLTDNSKRAQYDSCDFVADVPFPKKGT
 DYDFYEAQWVPVEAEARF SKKTP I PSLGNKDSKKEVEQFYAFWHRFDSWRFTFEFLDEDV
 PDDSSNRDHKRY I ERKNKAARDKKKTADNARLVKLVVERAVSDPRIKMFKEEKKERKERR

FIG. 1 - 41

KWEREAGARAEAEAKAEAEAKAESEAKANASAKADKKAKEAAKAKKKNKRAIRN
SAKEADYFGDADKATTIDEQVGLIVDSLNDEELVSTADKIKANAAGAKEVLKESAKTIVD
SGKLPSLLSYFV

YHR010W, 1472 bp, exon1: 501-531, intron1: 532-1092, exon2:
1093-1472 (SEQ ID NO 125)

GACTCGGACGGAAACCGTCTCATATTATACGTTTCAGTGAATATTTTTCACGGAAGAATGGA
AAGGGCTCGAAGACGTTAAATGCATCCGTACACCTACATCTTTACATTTTGTGCTGTG
CACCTACACTGTTTTTTTCACCTTATGAGTCTGTATTTCTTGAAGAGCGGAT
AACAAATATCCAGGTGGAGTCCCGAGGCGAATCAAGGCTCGCGAGAGAGTTCCTCTCA
AATAATGGAGTGTATCCGCTCAGTCTCTCCATCAGCAGAACTGTCTGAGACAAAGTC
TTTCCAGCAGAGTCCGCTACGCTCTGTCTGCAGAGATTCCGCCAAGGCGAGTTTCCGT
AAATTTCTTTTTCAGTAGTAAAGTGTTCGTTTCATGTAACAACTATCGCCGTAGTTTTCAGCT
AAAATTAAGATATATTAGATTTCCTAGATAGTCTCAACGTTGTAACAA
AAGCATACCAAGAAAAAATGGCTTAAGTTCCTGAAAGCTGGTAAAGTTGGTACGTATC
ATTTTCAGTTTTCGACATCAACAAAAACCGTGCACCTGTGGTATTGAGAAATCCAAAGTT
ATTAGCAGTTGATGTTGATAATTGAGTTTGAATTCGAGTATTTGATATCTTCATATGGGA
GTAGGGAGGAAAAAGCGTGGAGATGTTAGATCTGGGAAAAAACCTTTAAATTTGAATGAT
AGCTTATTAATAGAAATATTGGACAAAAGATGAATGATTTAGGAGCGAACTAACGATT
ATTCATATTCATTGAGCTATACGAGGCGAGTGAAGGGTTATCAAAAAGTTGTAATTTAAA
AGAAAAGAGCATCAATAGCCACCAATAGATGGTGAAGTTCCCGCATATATTTCCTAA
GACCATAGGCACATGTACGACGGCGACGAGGCTTTTATTACTGTAGTTCTTTCCATG
CCCTATTAAAAATTCGTGGCCCTATGATAATTTTCTCTCCCTAGTATTGAAGAACAAAA
TTGAAATTCGCCAAACTTAAAGAGGGTTCACATTTACTAACTATTTCCTTTCCCTCTCT
TTTTTTACACAGCTGTCTGTGTCGCTGGTGGTGTACGCGCGTAAGAAGGTTGTTATCGTTA
AACACATAGTAGAAGGTTTCAAGTCTCACCCATTTCGTCACGCTTTGGTTGCGGGTATGT
AAGATACCCATTGAAAGTGCACCAAGAAGCAGCGTGCCCAAGAGGTTGCTAAGGACAA
AGATCAAGCTTTTCATCAAGGTGCTCACTACAACCATTTATTGCCAACCAGATACACTT
TAGATGTTTGAAGCTTTCAAAATCCGTGTGTTCTACTGAAACTTCGCAACCACTTTCCCAAC
GTGAAGAAGCTAAGAAGTTCGTAAGAAGGCTTTGCAAGAAAGACCAAGCTGGTAAAG
ACCAATGGTTCTTCTCAAGTTGAGATTTTAA

YHR010W, 136 aa (SEQ ID NO 126)

MAKFLKAGKVAVVVRGRYAGKKVVIVKPHDEGSKSHPFGHALVAGIERYPLKVTKKHGAK
KVAKRRTKIKFFIKVVNHLPLTRYTLDEAFKSVSTETFEQPSQREAKVKVWKAFEE
RHQAGKNQWFFSKLRF

YHR021C, 1299 bp, exon1: 501-503, intron1: 504-1053, exon2:
1054-1299 (SEQ ID NO 127)

TTACTTACGTCTATTATAACCTTCCGCGTAAAAAGAAATATTGACATCCCTTTCTGTAT
TTAGCCCATACATTTTACCCATGCACCATTGGATTATAAAGAAAAAATTTAATAAAAA
TCTGCCGGGGAAATTTCAAGAAAAAAGGAAGGTGTGTTCCGATTTAAACACGGGCCACC
ATAAACTTTTGTTCACCCATCTAGACGGATCCGCCCCCGCAAGGCTCTCTTCTCT
TAGCTAGGCAATGTGGCTCTCGGAAAGGAAACTCCCAACGAGGAGTGGTGGGAAATGCAG
CAATTCCTCTCTGCTTCCCGCTGACCTTTCTTGGGCCAGTTTAGTAAATATGCTCTCAT
CTTTCATGTGCTGTAACTTGAAGTCAATTAACACTATCTATAATTGATATTAGCGGTT
AAAAGTTCTATATAGCATTTGCTTTTATTAGAGAATACGAAAAACACACAGATAATTAG
TGATATATATTAGATCAATATGGTATGTGAAAGAGATATTAAACATTAAGATGTGAAGGA
AACAGAAGAGAACCAATTTAGGGAATGAATTCGGATGAAATTCATGATAGAAGAAAAAG
CCTTAAATAAAAAAGAAAGAAAGAAAAAAGCAAGTAAATCAACCTCTGACATTTGATAGG
AGTATGCGTTTCCGCAAAATCAACAAATCATGCAATTAACCTGGTAAACGAGACTTTAAAG
ACGTGCAAGAAAGCAATTAATTTTATAGTAGGGAATTGAAAGGCTCTGTATAGCAGAAA
ATTTGAGATCTACTGTGGAGATAAGCATATGGTGTGTAGTTATGGGTAATCAACAATAA
TAGAACTTATAGCAGTTGAAGATGCGGAGATGATGATGCGGAGTACTGCTGGGTAAGAT
TTATCTCTCTTTTTCGAGACAAATGCTCACTTTTCTGTCTCTCACTAACTTTTCTG
ATGTATCTTACCACCCCTACAGTTTTCAAATTAACATCAATTTTTCGTGAACGAC
CTTTCGTTTTCGTTTCTATTTATTTCATACAGGTTTTCAGTCAAGATTTGTTGACCCCA
ACTGCTGCTTCTGAAGCCAGAAAGCACAAGTTTAAAGACTTTGGTTCAAGGCCCAAGATCC

FIG. 1 - 42

TACTTCTTGGATGTCAAATGCCCAGGTTGTTGAACATCACCAGTGTTTTTTCTCATGCT
CAAACCTGCTGTCACTGTGGAATCATGCTCTACTGTCTTATGTACTCCAACCGGTGGTAAAG
GCCAAATTAATCTGAAGGTACTTCTTTCAAGAAAGTAA

YHR021C, 82 aa (SEQ ID NO 128)

MVLVQDLLHPTAAASEARKHKLKLTVQGRSFLDKVCPGLNITTVFSHAQTAVTCESCS
TVLCTPTGPKAKLSEGSTFRRK

YHR141C, 1262 bp, exon1: 501-504, intron1: 505-945, exon2:
946-1262 (SEQ ID NO 129)

TAAACATGGCATTTTAAATAGTACTGCCAAAATTTAATGCAATGGCAATTAGTTGGCTA
TGTGTGCTACATATTTATTTCCATAGCATTCTCTGTGCACAACTTCAAAATAAAAGACAGT
GACATCCGAACATCCGATACACCCATACATCATGAAAAATAATCCTGACATTGGAAAGAG
TCTTGTATACAAAAAAGATCGCTGTCAAAAATGCGGCCAGACTGCCCGTGCATCGTACCA
ACAGTGCCTATGTTTCAGACGGAGAGACGACCTCTAGAGAGACGTCCTCGGTGCGGCAAC
GCTCAGCGTTTAGTTGTTTCGACGGGATGATGGGTTCCGCCAGGGGGAGGGAAGGCTTTCC
ACCAAGAGAGGTAATAATTTATTCGTGAAATGAACTCAGAGATACATCCATATTTGTTGACA
ATGTATATCTTAATTTGATGTGGTATTTTCACTGTTTAAACGTAATTAAGAGAGATTAAAG
CAAAAACCAATCAGTAATAATGGGTATGTGGACGATTAGGAATAGACAAAACCATGTTAT
TTATCTCCATTAGGGCGTGAGAGTGTAAATAGTACACAGGTAAGTACTAGAAATGCTAAAGA
ACTTTTAAAAATATCCTGAATCGTAGGCCAAATCCATGTCAAGCAAGAAACATATAGTTA
TTAAACTTCAATTTACTTTTGAGCTAGTTAAATATTTTCACTCAATTTCCAAAAGTACTGAAC
ACCTGAATGATCACTTTTATGGCCCTTTTAAATAGAACTCTGGTTAGAAAATATATTTGAG
GATATCATTAGTAATACTCATTTAGATATTTGTGAATTTAGCCGTTTCCCATTTACAGAAA
AAAGATACAATAATACATGTCCAGTCAAATTTACTTTTTTTTAAAGATCAATTTACTTAAC
AATCAACTATCATGCTAAATTTGCTGTGATATCATTTTGAACCAAGTTAAGTCCCAAAGA
CCAGAAAGACCTACTGTAAAGGTAAGACCTGTGTGAAGCACACTCAACACAAAGGTTACTC
AATACAAAGCTGTGAAGGCTTCCTTGTCTCGTCAAGGTAAGAGACGTTATGACCGTAAAC
AATCTGGTTTCGGTGGTCAAACCAAGCCTGTTTCCACAAGAAAGCTAAGACTACCAAGA
AGGTTGTTTGTAGATTTGGAATGTGTCAAATGTGAAGACTAGAGCCCAATTAACCTTTGAAGA
GATGAAGCACTTCGAATTTGGTGGTGAAGAAGCAAGGAGGTTCAAGCTTTGCAATTTCT
GA

YHR141C, 106 aa (SEQ ID NO 130)

MVNVPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGFGGQTKPVFHK
KAKTTKKVVLRLCEVKCKTRAQLTLKRCKHFLGGEKKQKGQALQF

YHR217C, 962 bp, CDS: 501-962 (SEQ ID NO 131)

CATCGCTTGATTTCGGCCTGCAAAAATAAGTAGTCGGTACGTACTTTTCGTTTTCATTT
TCCATGGTGCACAGTATCTTAACTATCTGCTTAGTCGAGGAGAACCAAGGATTCGTGTCGT
TGCTCAGCCGCTTCGTGGATATCTCTTGGATACTTTAAACATGGACCTACGTTCCGCTC
TCGAAAAGACAAATATAATAAAAAGTTATAAATTACATTTCTTATTAGGTATACGACCT
CGCGCTTCGGAAGTAGAGGAGCCCTTTTGGCGTACCTACATATGGCGCGTCAGACAGACA
AAGCTTCCCCCAAATGTATTACCCCGCCGAATAAGAAAAACAGACCCATTACCCACGAC
GTATCAAGTTACTTCTTGGTGAATGTCCCACTATAAAAAAATTCCTTGACGCTAGATC
GTGGACTAAATCTGCGTGCACAACTGCCTAAACAGGAATATTGCCTATTTTGTACAA
GGTTACTTCTAGATGCTATATGTCCCTACGGCCTTGCTTAACACCATTCAGCATGCAAT
ACAGTGACATATATATACACACACCAACCCACACCCACACCCACACCAACACCAACCA
CACACACACCCACACACACCCACACCCACACCCACACCCACACACACCAACCCATCTA
ACCTGTCTCTTAAACCTACCCCTACCATTAACCTTACCTCCCACTCGTTACCCCTGACCT
CAACCATACCACTCCCAACCACTCCATCTCTACTTACTTACTTACCATTCCACCGGCCCA
CTATAACCGTTACCTTCCAATTAACCATATCCCACTCCACTACCATTAACCTGCTATTAC
CCTACCATCCCACTGTCTACTCACTGTACTGTGTTCTACCCCTCCATATTGAAACGTT
AA

FIG. 1 - 43

YHR217C, 153 aa (SEQ ID NO 132)
 MSLRPCLTPSSMQYSDIYIHTPHPHPHPHPTHTHTPHPTPTPTPHPHPHPTPHPTPTPT
 TPHHTHTPHLTSLNLSLNLPSHYTSPVLTPHSTIPLPTTIHLSTYYHHPPPIITVTLQ
 LPINSTTITILLPYHPPCTHCTVVLPSILKR

YIL112W, 3752 bp, CDS: 501-3752 (SEQ ID NO 133)
 TTCCATAGGGCTTATTTTCCAGTTGATGGAATGGGAGGTTCGCTCTTAACCGCAAGACTAA
 CGTGCAAGCCAACAGTTATAGAAAAAGTACCGTGAGAGAGAAAAAAGAGATATAGCA
 TCTAATAGGCTTTATTGAGGGGCACGATGCTCTTTTTCCTCTGACTTTATAAATAA
 TTCGTATTTCTTCGCTTTGTTTTCATGCTCTGTTCTGAGCTTTTAGTTCCTTTATTGAG
 AGCCTTTTCCAAATCAAGGCTCAGGAAGTGACTCGCTTTAGAAGAACAAGGTTTGGATT
 TGGTAGGGTTCTTGTACGAAGTTCTCAATATAAATTTGCGCATTTTACTGTCGGTTTCATAC
 TAGTTTATTTCCGGGTAACAAGTTTCTCTGTGATGCTAAATCAATGTGTATATTGAGAAAA
 CATATGTAGAAGTTACACAAAGCAACAAGGATATATTATATGTGACAGAGAAAGATTG
 CTGTAGAGATTTCATGACAAATACAAATGAGACTACTACAAAAACAGCCGCTAAAGAAAAGGT
 CCCTGAGCAGCTATCTTTTCAACCGTGAGCACGAGACGGGAGGAGCTGGAAAAAGATTCTTA
 AACAAAGAACATCCGAAGAGGAAGATACTGCCGGCAAGCATGAACAAAGGGAAGAACATGT
 CGGAAGAAGTAAAGTAAAGTTTCCAGAAAAATGTTGCATCGTTTTCGCTCACAGACTCAAA
 GCGTTTCATCAAGCCACCCAAAAATAAAGTGAATGCAAGGAATCCGAAGACCTGGCCATA
 AGAATAGTGCGAGTTTACACGAAGGAGAGGTTAAATGGGGACAGCCGTCGGGACCATGTTT
 CTGAAACGAATGAAAAAATAAGCCAAGCAATACGAGCGAAAAATTTTCGTATCATCATCAT
 CACCAATGTACGTTAATGTTGATATCCAAACCATCAACCTTTTTCAGAGAACCAACTTC
 GAGCGATGTTGAAAGAACCAAAAGGAAAACTGTTGATGATTTCATAGAAGAAGAGGGTT
 TGGGAGCTGTTGAAGAAGAGGATTTAAGTGATGAGGTACTTGAAAAAATACACAGAAC
 CAGAAAAATGTGAAAAAGATATAGAGTATAGCGACTCAGATAAGGACAACAGCATGTGG
 GAAGCGATGATCCCAAGCCGCACTCACTCAACATAAAACTTGGTCGTGCGAACTGGTTA
 GAGGTGACCAATCTGATGACCAACAAAGTTCCATGTTTAATAACGAATCAGATTCTGAAT
 TATCAGATATCGATGATAGCAAGAAATATGCTTTTATCCAGTAGCCTATTTAGAGGCGGTT
 CTTCCAGCTGTGAAAGAGACAAAAACAACCTTTCAAATAAGAAATTTTCCACGACGCAAAA
 ATCCAAAAAGGGGGTTCTGCTCCAGGAGTAATGATAGTAACAAGAGTTCTCATATAGCTG
 TTTCCAAAGCGCCCAACAGAGAAAGGGCATATATAGGGATTCTCGGTGGTAGAACAAGAC
 TACAGATTGCTGTGACAAAGGGCAATATGATGTAGTCAAAAAGATGATTGAAGAAGGAG
 GTTACGATATTAATGACCAAGACAAATGCTGGTAAATACAGCATTTGCATGAAGCGCGTTGC
 AAGGTCATATTTAGATTGTGGAACTGTTGATAGAAAAATGGTGCAGATGTAATATCAAGT
 CTATTTGAAATGTTCCGGGATACCTCCCTTGATCGATGCTTCCGCCAATGGACACTTTGGATG
 TTGTCAAGTATCTTCTTAAAAACCGTGCAGGCCCACTATACGTAAACGCTAAAGGGTTAA
 CTGCGTTTGAATCTGTGATGATGAATCTGAATTTGATGATGAAGAAGACCAAAAGATT
 TGCCTGAAATAAAAAAGGTTGAGTATAGCCGCTTAAAAATGGACTAACAGAGCAGGAA
 TTCTAATAGTACAAATCTAAAAATGGCAATAATGCTCACACAAATAGATGATGACCGACTTTG
 ATAATACCACAAAAGCCAAAAACGAAAGGCGCTGACTCACTTCAATGGCTTCCAAATA
 TTGATGAAGAGCTCCGGAAGAGGAATCTAATGGACAGATGTTACTTCTAGAGCGGAA
 AAGAAAAACTGTTTAAAGCTTCAAGGAGGGACATTTACCATACGTTGGTACGTATGTAG
 AAATGCTGTGTAAGATAGACTTAAGTCAATTTTCGAAAGCGTTAAGTGTGGCCATGAAG
 ATATTACAAGTATCTTTTGGCAATTCGGATTTCCTGTAATCAAACTTCAAGGGATATA
 AAACACTCCGCTTTAATGTGAGTGTAGGTCGTGGCCATCTTGAAGCTTTAAACTGCTAT
 TAGAGGCAAGTGCAGATCCAAACCAAGAGATAAAAAGGGTCGTACCGCTTTGTACTATG
 CCAAAAAACGATTAATGGGAATAACAAACAGTGAAGAATAATCAATTGATTGAAATGCTA
 TAAATACTATTGAAGAAGCACTCTGAAGATAAATATGATGATGATGATGATGATGATGAT
 ATAAATATGAAACATATAACATGAAAAAAGAGAGAGAAAAACGCAATCAGCCCATATTAC
 CAAGCCGAAGAGATTGCCACTCTTGAAGATGAAGACGAAGAGGACGATACGAGGATGCTCA
 ATCTGGCAGACGATGACTTTAATAACGATCGTGATGTCAAGGAATCTACAACCTTCGGATT
 CGGCCAAGAGATTGGATGACAAATGAAAAATGTTGGTACTCAATACTCATTTGGACTGGAAAA
 AACGTAACCAAAATGCTTGCAGATGAAGAAAAATTAAGTAATCTCACCACCTCTCTTA
 TGGAACTCATTTCTTCAAAGAGGCAAAATCTGTAGAGATAAGTAATAATACATGAAGAAA
 CGGCTGCTGAAAGAGAGCAAGACTCAAGGAAGGAGGAAGATACAGAAAGAAAGATTAG
 AAAAGAAAAGAAAAAGAACAGGAACACTACAAAAAGCTGGCCGAAGTACAGAAAAAAA
 GGAATCGAAGAACAGGAGAGCAGAAAGTCTTGAAGATGGAAGATTTGAAAAAGCTACTT
 TAGAGAAGCAAGAAAAATGAAAGGGAAAAAGAAATGGAAGAAATCTCTTATAGAAGG

FIG. 1 - 44

CAGTAAGGGACTTATATCCGTTAGGACTGAAGATTATTAACCTCAACGATAAACTTGATT
 ACAAAGAGTTTTTGC CGCTATATTTATTTGTAGACGAAAAAACGATAAAATTTGTGCTCG
 ACTTGCAGAGTAATGATATTGTTGAAGGATATCGACTTGCTCTCAAAGGACAACCAACCAA
 CTTCTGAGAAAGATTCCCGTCGATCCCTCGCACCTGACTCCATTGTGGAAATATGTTGAAAT
 TCATTTTCTCTGATATGGAGGTAGTTATGATGATAAAAGAACAACATGGAAAAATAAAGAT
 ATGTTGTAAACTTTGTATGGGGTTGATTTGGACACAAAGATTGGGTATGGACTTTTGGAGT
 ACAAATAATTTGTTAGTTTGCCCATGGCTGGGATTAATGGGATAACGTTGTTATTTGAAA
 ACCACGCAAAAAGAAAAATGAAGGAAATATGATTCAAATATCAATAAACGAATTTG
 CACGATGGAGAAACGATAAGCTGAACAAAGCCGACGAGCCGACGCGCAACACGCGTTCTC
 TAAATAACCTCGAGAGTTTACCGTTAAATTTCAACACCGTATGAGCATATCTCCGTC
 TCCAGCAGACATCCAAAGAACCATTTTGGTAA

YIL112W, 1083 aa (SEQ ID NO 134)

MNETTTKQPLKKRSLSSYLSNVSTRREELEKISKQETSEEDTAGKHEQRETLSEEVSDK
 FPENVASFRSTTSVHQATQNNLNAKESIEDLAHNDASSHGEVNGDSRPDDVPETNEKI
 SQAIRAKISSSSSPNVRNVDIQNHQPF SRDQLRAMLKEPKRKTVDDFIEEEGLGAVEEE
 DLSDEVLEKNTPEPENVEKDIEYSDSKDITDDVGSDDPTAPNSPIKLGRKRVLRGDQLDA
 TTSMMFNNESSSELSDDIDSKNIALSSSLFRGGSSPVKCTNNNLSNMNSSPAQNPKRGVS
 SRSDNSKSSHIAVSKRPQKKGIYRDSGGRTLRQLIADCKGKYDVVKMIIEEGVDINDQ
 DNAGNTALHEAALGHIEIVELLIENGADVNKISIMFGDTPILIDASANGHLVDVVKYLLK
 NGADPTIRNAGLTFAFESVDDESEFDDDEEDQKILREIKKRLSIAAKKWTNRAGIHNDKSK
 NGNNNAHTIDQPPFNTTKAKNEKAADSPSMASNIDEKAPEEFYWTDVTSRAGKEKLFKA
 SKEGHLPYVGTIVVENGKKIDLRSFESVKCGHEDITSIFLAGFVFNQTSRDNKNTSALMV
 AVGRGHGLTGVKLLLEAGADPTKRDKKGRATLYYAKNSIMGTINSEETOLLIENAINNYLK
 HSEDNDDDDDDNNNETTYKHEKKREKTSPIILASRRSATPRIEDEEDTRLMLNLAADDFF
 NNDRDVKESITSDSRKRLDDNENVGTQYSLDWKKRKTNALQDEEKLKSI SFLSMEPHSPK
 KAKSVESIKTHEFTAAEREARLKEEEYVRKRLKEKKRKEQELLQKLADEKTRGRIIEQEK
 QKVLIMERLEKATLEKARKMEREKEMEEISYRRAVRDLYPLGLKINFNNDKLYKRFPL
 YFVDEKNDKFDVLQVMILLKIDILLKSDNQPTSEKIPVDPSHLTPLWAMLKPIFLYGL
 SYDDKKNMNMENKRYVNVNFDGVDLDTKIGYELLEYKFKVSLPMAWIKWDNVVNIENHAKRKE
 IEGNMIIQISINEFARWRNDLKNKAQOPTRKQRLSKI PRELPVKFQHRMSISSVYLQTSKE
 PFW

YIL115C, 4883 bp, CDS: 501-4883 (SEQ ID NO 135)

TTTCAATGCGCTACAACCTGACTGAACCAAGTCCACAAATTTGGCTGGTCTCTATCGTTCTC
 GCCCTGAGAGATTTTATTTTCTTATAAATTTTACTAAATAAGGATTGTGACTTTTGTATAG
 AGTTTATTTTCTTCTGACGTTTGTATTAGTTAAATATATATAATAGTATTTAGGAAACTA
 GGTGGGAGGGGACATCGCAACTTTTATCGTGACCTACGACCAAGTGTTTTTCATTTGTTT
 GATCAAAAGAGAAAAAAGACAAAGGACCGAAGGATAGTTGACGCGATAAACTGGAGAAA
 AAATGTGTTTGTACATCGCGCTTTAGGCTTGTTTGTTCTGTACACATACGCTGCTTCAC
 ACCAATTCATATTCTCAGGTTAAATTTGTCTCTCTCCCACTTCAATAACGATTTTGGCT
 GAAGGTTTAAATTCATATTGTCAATTTTAGCAGAGAAACGCACATAAATATATATATATT
 GATTACAGAACCATATTAACATGTCTCTTTGAAGGATGAAGTACCACCTGAGACTTCCG
 AAGACTTCGGTTTAAAGTTTATAGGTCAAACAAACAAATTTCTACCTTCCCTCAATGAAAAAC
 TGCCATTGTGATCTCTACAAATCTCGATATTTCAAACAGTAAGTCTTTATTCGTTGCTG
 CCTCTGTTAGTAAGGCGGTGGTCGGCGAATTACAATTACAGTACGATCATACCACTCCG
 ACTCTACTCGGTTAAAGTTCAAGTGGGAGAAAGAAATCCCAAGATGTAATATTTGTGTGCT
 TTCATGGTGATCAGGTTTGGTTTCAAACAGAAATGCAATTATTCGTTAGACTGGAGG
 AATTGAGTGAATTTGCAACGGTCACTCTTTGAGAAGCCAGTTTCCCAATTGAAGAACG
 TTAATAACACTTTGTAATTTTAAATTCAGTCAATGATTATCAGCACTGGATTTAAGA
 CAAATCGCATAGCAACTGGCACAAAACGTTACTCTTTTGTATGTCACAAATTCGAGT
 TAGCAGTTCTACTAAAAGATAGAAGTTTCAAAGTTTTCATGGCGAAATGGCGAAATGG
 AAAAACAATTTGAGTTCTCTCTACCGTCAGAAATTAGAAGAGCTTCCAGTAGAAGATATT
 CCCCTTTGAGTGTATACCATTCTCTCTCCACAGGATTTTGTGGCGGTTTTCGAGTAATGTTA
 TATCAGAGACCGATGACGAAAGTTTATACGATCAAAAAATGTACATTATAAGCAATAG
 ACGGCAGCGCCCTCAATTCAAGAAATTTTGATATTACACCTCCATTGGGCGAAATGATAA
 GGTTCCTCATATATGTACAAAGTTACTTGTCTGGTTTAAATGAACCTGATGCAACGATAA
 ATGTGCTAGCATCATCATGTTCAAGTGAAGTAAGTATATGGGACTCGAAACAGTATTG

FIG. 1 - 45

AACCTTCCCAGGATTCTGAACGAGCAGTATTGCCCATCAGTGAGGAAACAGATAAGGACA
 CAAATCCAAATAGGTGTGGCAGTTGACGTCGTACTTTCAGGCACTATTCTAGAACCCTTGTT
 CCGGTGTTGATACGATAGAGCGATTGCCCTCGTTTACATATTGAATAACCAAGGTAGCT
 TACAGATAGTCGGGTGTTTTCATGTGGCAGCAATCAAAGCGGCCATTATACGATAAATC
 TGGAAATCTTTGAACATGAGAAATCTCTCTCTCTACATCAGAAAAAATTCCTATTGCTG
 GACAGGAGCAGGAAGAAAAAAGAAAAAATAATGAATCAAGTAAGGCTTTATTCAGAGAATC
 CTTTTCACATCAGCAAAATACATCAGGCTTCACTTTTCTTAAACACAAACCCGCTGCCA
 ATAGCCTGCGAGTCTCAAAGTTCCTTCAACCTTTGGTGCTCCCTCATTTGGATCATCCGCAT
 TTAATAATTGACTTGGCCATCAGTCTCATCTACCAGTACTGGTGTAGCGTCCAGTGAACAG
 ACGCAACAGATCTCTGCTTCTGCTAAGCCAGTATTTCGGCAAAACCCGCTTCGGAGCTATTG
 CCAAGAACCGTCAACATCAGAATATGCTTTTGGCAAGCCATCTTTTGGTGCTCCCTCCCT
 TTGGCTTCGAAAGTCATCTGTTGAATCGCCTGCGCTCCGGATCTGCCCTTTGGTAAGCCCT
 CTTTGTGATCTCTCTCTCTTGGCTCTGGAATTCATCTGTTGAGCCGCTGCCCTCCGGAT
 CTGCATTTGGTAAGCCCTCTTTTGGTACTCTCTCTTGGCTCTGGAATTCATCTGCTG
 AGCCGCTGCTTCCGGATCTGCTCTTGGTAAGCCCTCTTTTGGTACATCTGCATTCGGAA
 CTGCATCAAGTAACGAACTAACTCTGGATCCATATTGGAAAGGCTGCATTTGGTTTCT
 CATCTTTTGCACCCGCCCAACAATGAACCTTTTCGGATCAAACTTTTACTATTTCAAAACCTA
 CAGTTTGACCCCAAAGAGGTAGATTCAACGTACCTTTCCCATCTTCTGGCGCAATAA
 GTGAAGATGAGTCTAAGAGTGTGTAGACTCTTCTTCGACACCTTTTGGTACGAAACCTA
 ACACCTCTACGAAACCAAAGACCAATCCCTTTGATTTTGGGAGTCTCTCTTTTGGATCTG
 GATTTTCAAAGGCTCTGGAATCTGTTGGTTCCGATACAACTTTTAAATTCGGTACTCAGG
 CTCTCACCTTTCTCTTCCAGTGTAGGAAACAAATCACCATTCAGTTCTCTTACAAAAGAG
 ATACTGAAATGGATCTTTAAGTAAGGGCTCTACCAGTGAATCAATGACGATAATGAAG
 AACACGAAAGCAATGGTCCCAACGTAAGCGGTAAATGATTGACAGATTCTACGGTTGAGC
 AAACATCTTCTCATAGATTACCGGAACTCCCTCGGATGAAGATGGTGAAGTTGTGAGG
 AGGAAGCGCAAAATCCCCCATAGGCAAGCTAACTGAAACTATAAAAAAAGGTGCCAATA
 TTGACATGGCTTGTTTAAAAAATCCCTGTATTTTGGAATTCATGTCAAAGCAAAATCCGAAT
 CGCGTTTTCAGCATTTGCAACAAATATTACCAAAACCAAGCTCTACAAACCTGCTTTTT
 CGTTTGGTAACTCCCAATGAATAAAGTAATACATCTACGGTTTTCACCAATGGAAGAAAG
 CTGATACATAAGAAATAGTGAATAAGGGCCCCATAACCTTGAAGAGTGTGAGAAATCCGT
 TTCTACCAGCGAAAGAAAGAACTGGAGAAAGTTCTAAAAAGGATCATACAGTAGCC
 CAAAGATGGTTATGTATCAGGAAGTGAATATCTGTGAAGACTTCTGAAAGTCTTTTGT
 ATACACAGCAACGAAAGAAATTCCAAAGTACAGGACGTGAACATCATGAAAAAGCG
 AAACAGACGCCAAAATATAGTCAACATGCTGTGGTTGATCAGATTAACAGTCTAAAGAAA
 TGAATGAACTTCGAAGAAATAATGAAGGAGCGGTCAACCAATCATGGTTCTCAAGGAG
 ATGGAATAGCATTTGAAAAAAGCAATGAAAAAGAGAAATTTGATTCAAATATGCGCAATA
 AGCAATTCGAAGACCAACCAATCTTCAGAAGAGGACGCGAGCCAAAAAGACAGTAGACAAA
 CGAGTGAAGTTAAAGATCAGATGATAACATGTCACTCAACAGTGACCGGGATGAAAGTA
 TATCTAGTCTTACGATAAACTGGAAGATAATTAATCTGATGAGCTACCTCATGGTGGAG
 AAGCTTTTAAAGACGTTGAAGTGAGCGCTTCGCTGATTTTGTATGACAACTCATTTAG
 AAGCAATATTGCTGAATCTGGCATACAGACAGACCTTTCAGAAAGTTCAAGGAAAGT
 AAGCTTCAAACGGATGCCATACCCTGAAACACAACAGTACACAACTGTTTAAAGAGGAAG
 CAGTCGACAAATGCTGCAAACTGAGCCTGTTGAAACATGTAATTTTCTGTTCAAACAT
 TTGAAGGTCAAGGAAATTTATTAGCAGAGCAATCAACCAAGCAATTTGAAAGCAATTT
 ACACAAGTCAAAAGTATCAAAATTTCTCTGTTTCACAAAATCTACGTTTGAAGTTGA
 TTGAGATGCAATTTTCAGACGGTCAAGCTGAGTTTACTGTTGATGGAAGAACTCCGGA
 ATATGGATACCTTTTACTGATCAATCGAGCATCCCTTTGGTGAAGGCTACAGTCCGGT
 CTATCAATAATCTGTATACTTTGGAGAATCCAGAGCGTGAATTTCTATTAAATTTGAGA
 ATAATATCAAGTGTGAACAAATGCAAAATACCAATGCTTAACATTCAAGCATCGAGGAAA
 AAGTTACAGATTATGTCAGGAAGAATATGCACAAAATCACTGAAGATGTAGCCCAATGCA
 AAGAGGAGTATCTGTTTAAATGCATTTTGTATGATGCTTTCAGTGGATACGTTTAAAGT
 TCAGACCGCATCTGTTTGAATGCAAAAGACATTACGTCAAAAGCTATTCGATGTGCTC
 CCAAAATTAATCATATGAAAGTGTGCTGAACATTTTAAATTTGTCTACTGTAAAGATA
 AGAATTTGGACGATAATCCATTTAGTGGCAAACTAGCTTAAAGAACTCTTGCACGTGACG
 GTTTACTTAAAGAAATCAAAATTTATTCGTTGAGCAAGTGAAGTAGGTTCAAAATTTGGAGAGA
 AAGTAAAAAGGCTTCGCTGTCGATGATCTCTTCAATTAACAAAGGACATGAAAGGAT
 TTAAGTAGTGAAGTTGGGTTGGCCATGAATACGAAAAAGCAATTTGGTGAATTTCTTCA
 AAAATTTGAACATGGCAAAATAG

FIG. 1 - 46

YIL115C, 1460 aa (SEQ ID NO 136)
 MSSSLKDEVPTETSEDGFKFLGQKQILPSFNEKLFPASLQNLNLDISNSKSLFVAASGSKAV
 VGLQLLRHHITSDSTPLTFKWEKEIPDVIVFVCHGDQVVLSTRNALYSLDLEELSEFPT
 VTSEFEKVPQLKNVNTLVILNSVNDLSALDLRTKSTKQLAQNVTSFDVTNSQLAVLLKD
 RSFQSAFWNRNGEMEQFEFSLPSELEELPVEEYSLSVTILSPQDFLAVFGNVISETDDE
 VSYDQKMYIIKKHIDGSAFQETFDITPPFGQIVRFPYMYKVTLISGLIEPDANVNVLSSC
 SSEVSIWDSQVIEPSQDSERAVLPISEETDKDTNFIGVAVDVVTSFDITLEPCSGVDITIE
 RLPLVYIILNNEGSLQIVGLFHVAIAIKSGHYSINLESLEHEKSLSPSTSEKIPITAGQEQEEK
 KKNNESSKALSENPTTSANTSGFTFLKTPAAAANSIQSQSSSTFGAPSPFGSSSAFKLDLPS
 VSSTSTGVASSQDQATDPASAKPVFGKPAFGAIAKEPSTSEYAFGKPSFGAPSPFGSGKSS
 VESPAAGSAGFKPSFGTSPFGSGNSSVEPPASGSAGFKPSFGTSPFGSGNSSAEPASGS
 AFGKPSFGTSAGTASSNETNNGSIFGKAAGSSSFAFANNELPGSNFTISKPTVDSPE
 VDSSTSPFSSSGDQSEDESKSDVDSSTPFGTKPNTSTKPKTNAFDGSSSFGSGFSKALE
 SVGSDITFFKFTQASPFSSQLGNKSPFSSFTKDDTENGSLSKGSTSEINDNDNEEHSNGP
 NVSGNDLTDSTVEQTSSTRLPETPSDEDEGEVVEEAAQKSPIGKLTETIKKSANIDMAGLK
 NPVFGNHVKAKESEPFSAFATNITKPSSTTPAFSFGNSTMNKSNSTSTVSPMEEDTKETS
 EKGPIILKSVENPFLPAKEERTGESSKKDHNDPKDGYVSGSEISVRTSESADFDTALEK
 IPKSQDVNNHSEKSETDPKYSQHAVVDHDKSKEMNETSKNNERSGQPNHGVQGDGIALNK
 DNEKENFDNMAIKQFEDHQSEEDASEKDSRQSEVKESDNNMSLNSDSEISSESYQK
 LEDINTDELPHGGEAFKAREVSASADFDVQTSLEDNYAESGIQTDLSESEYENVTDAI
 PVKHNSTQTVKKEAVDNGLQTEPVETCNFVSQTFEGDENYLAEOCKPKQKLEYITSKAVS
 NIPFVQNSLTLRIESTFTQVEAEFTVLMENTIRNMDTFTDQSSIPLVKRTVRSINNLMT
 WRIPAEAILLNQNNIKCEQMQITNANIQDLKEKVTDYVRKDIQITEDVANAKEEYLF
 MHFDDASSGYVDLSTHQFRMQLRLQKLFVDSAKINHTHEELNLILKLFVTKNRLLDDNP
 LVAKLAKESLARDGLLEIKLLREQVSRQLQLEKGGKASSFDASSSTTKDMKGFKVVEVG
 LAMNTKKQIGDFFFNKLNMAK

YIL148W, 1321 bp, exon1: 501-508, intron1: 509-942, exon2:
 943-1321 (SEQ ID NO 137)
 TCGATCAACTCTATCCAACAATTCTATAATATCCACTGTTTCATTAAACGAATATTTGGTCTT
 TTTCCCTTATGTGTGAAGTAAATTTTCCATGCAATATCCGGGTAAGCTATCGACAAGTTTA
 TTGACTGCAATTGTAGTTTATTACATCCGTACATTACTAAGATGTATGGTPTTTCTATT
 TTGTGCTCCGTGCGATATTTTCGTGGAGCAAAACGAGAAAGATGCGGAACCTCTTAGCAC
 TCCCGCTGGACATAGGCGGAGCATATTCTCCTATGGGATGGGTTTGTGTGTACTCTTTT
 CTCCTAGACAGGACCTCCGATGCGCTCCCTGAGGGTGAGATGGTTTCCGCGCTCAGGAC
 GGCCTTCTCCAGTTTCTAGCGAGGCATACATTCCAACCAAGGTGATCAAGAATATCTG
 AAATTAAGGTAAGTTGAATCTCTATTGTGTGTGTATTACCGCTTATTAATCCCAATAGTT
 GAGACAGCAAGATTCAAAACATGCAAAATGTATGCACCATATCCATTCTAAACATAGTTT
 TCGAACCTGTACAGAGCTTAAAGGGCAAAATTTTATAGAAACTGAATTTTACCCAGTGGAA
 TAACATCGTATCTGTAAGTCTACAAAATTTTATCCATCAAAAATTAAGAAACAAAGAAA
 ACTGCGCAAATGAATATGAGGAACCTTCTCTAGGAATGACTTAGTGAATGTACAGTG
 ACTTTGTGGAATAATGATGATAGATTGTGAGCGGGTGATGCGACTTAACAGCTCATTGCGCT
 AAGAAATATCCAAATTTGTGGTTCATGCTCTCCCCAAGATATGACGATGAGAGCTCGTT
 TAAAATTTTGTCTTCCGAAACAGTTATGAAAACATTTACGTGTTTTATGATATCTC
 TTACTAACTTGTCATTTTATATAAAATATTTTAAACAGTTTGTGCAAGACTTTGACAT
 TGCTTAAGACATTCACCTTTGGAAGTTGAATCTCTGACACTATTGACAAATGTCAAGTCAAA
 GATTCAAGACAAGGAAGGTATCCACCTGACCAACAAGATTGATCTTTCTCTGGTAAAGCA
 ATTGGAGAGCGGTAGAACCTTGTCTGACTACACATTTCAAAAAGAAATCCCTTTGCACTT
 AGCTCTTGAGATTGAGAGGTGTATCATTTGAACATCTTTGAAAAGCTTTGGCTTCCAGTA
 CAACTGTGACAAATCTGTTTGGCCTAAGTGTATGCTAGATTGCCACCAAGAGCTACCAA
 CTGTAGAAAGAGAAAGTGTGGTACACCAACCAATTCGCTCAAGAAAGAAATTTAAAATG
 A

YIL148W, 128 aa (SEQ ID NO 138)
 MQTFVKTLTGKTIITLEVSSDITDNVSKIQDKGIPDPQQRILIFAGKQLEDGRTLSYDN
 IQKESTLHLVLRLLGGIIEPSLKLAKASKYCNCKSVCRKYARLPFRATNCRKRRKCGHTNQ
 LRPKKLLK

FIG. 1 - 47

YIL150C, 2216 bp, CDS: 501-2216 (SEQ ID NO 139)
 AATATTCAACCTGAAAGTTGCAGTCAAAGCGCGGATTAACTTTTCCAAACGTAACCGATCTA
 ATTAACAATAGCACCGGTGGAGCAAAAATTAACAGAAATTTGGAAGTACATCTTAAACGGCCA
 ATTGAGAGCGGTACATCTTCTGATCCAGACACCAGAAAGGTTAAAGAGAGTCCAGCAAAAT
 GATCAAGCTTCCAACGAGTGATGTAAATATTAACAATGTAAATATATATAAATATGAACAT
 CTACATATTTTAAATGTCATTAATGTCTATTACAGAGGACATAAAGTGATTTATGACACAT
 CCGTACTAGTGTAAAGTATGAACAAATTTTGGGTTTATTTGCCATTTTPTTTCACGGCGG
 GTTCTTGGATGGCAGCAACCCACCTTTCTTAACACCACATAAGAAATATCAACTTTTATAGG
 CCATCAAGATAAAGGAACGTAAAGTTTGTCAATTTCAACCTCACATTTTCAACGCAACATTA
 AGCCTTGGTTCGTGGAGAAATGAATGATCCTCGTGAATTTTAGCGGTGTGATCCGTACA
 ATAATATTACTTCTGATGAAGAGGATGAGCAAGCCATCGCGAGAGAACTTGAATTTATGCG
 AACGAAGAGCGAGGCCCTTAGTGGAAACGATTAAGAAAGAAAGCAAGAAATTAAGAAACCCC
 AGGATCTCAATTTTGAAGCCATCGAGGTACCTCAATCTCTTACCAAAAACCGGTGTGAAGAG
 TGGGTCTCATAATGCTACACAACAAGGCAACAAAATTCGAAGGTTTCCGAATATTAATGAAG
 TAAGGTTATCTCAATTACAGCAGCAACCAAAACCACAGCTAGTACAACACATACTTTTA
 TGGAGAAATTTCAAAACGCAAAAGAAAGAAAGATAAACAATTTGCCAAGTTTGAAGACGA
 TGATGAATGCAAGAGTACATACGTTTCAAGTACCGATGAGAAGAAATATGTGCCGATAAATCA
 CAACGAAATTAGAAAGCTTTTCAAATCTTTGGTTTAAAGAGGTTACATACCTGAAGATG
 ACTTAAACCGGGCTTTGATGAGATCAAAATCCTTCGGTTGGGCAAACTTTTGTCTAAAA
 TTGCCCACTTAAATTTCAAGAGCTTGAATACGCCACCTTGGGCAACCGGTAGGCAATTA
 GCCACAAATCGGACATCAAAATTTACATCATCTGAAAGCCAGCTCAAATTTCTCATGTGTCA
 CCATAAGCGGACTTTACGATACACTAGATGTTTATATCTTCGGGAAAGAGGTTGAGAA
 GATATTATACTTCTCGCTGGGTGATGTGATAGCAATATTAACCCAGAAAGTACTACCAT
 GGAGACCTTCAGGCGGAGGAAATTTTATCAAACTCTCAACCTTCGAATTTAGTACTGACT
 TCAAATGTATCTCTGGAGATAGGTTCAAGTAGAGATTTAGGTTGGGTGCTCCCATAGTGAATA
 AAAGACTTCACAAAATATGTGGCTCTCCCATTAACATATCTCTTCAATAGTGTTCGCGATT
 ACCATAGAGAAGTGCAATTTTCGTGGAAAGTGTCTAAAGAAATTTGAATTTAAATGGTGGGT
 ACGGCTTTGGCGCGGCTTACGAAAGTGAGCTCTCAACCAAGCCTATATTAAGGCCAAAGGGG
 AAACCGGTTTAAATATAATCAAAAGGTACTCGTAAGCGCTGTGAGAAGGAGGAAAGAC
 TTAAGAAAGGCTCTCAAAATTTACGAAATAGTAATTTTCGCCAAGCAATTTTTCAGCGAGA
 AATTTTCAGAAATCCAGATATGCTCGGCAAACTTAGACAATAAAGAGGAGGAAATATAGTAA
 CTAAGAAATCGACAGCACTGAGCCGCGAAGTACGCAAAATTTAGAGAAGGAGGGAATCCA
 GCGGATTAGAGATAAGAGCGCTCGGAGAGCGACAGAAATGAAACGAACACAGAAAAGTG
 CCCTCCAGACAGGGCTTTATCAACGCGCTAGGATTCGATCCCACTCATGGAAAAATTTCCC
 AAGTACTCAAGTCTTCTGTATCAGGGAGCGAACCTAAGAACAACTTACTCGGTAAAAAA
 AAACCTGTTATAAACGATCTCTTCGATTACAAGAGGAAAAAGTCATCTCGCACCTTCAA
 AGAACCAATGTTTCAAGAAAAAGAACCATCGCGAAGAAAGTTTGGCAAAAAATTTCCGAT
 CCAAGGAACTAAAGAACTTCTGACGGTAGTGCCAGCGATCTTGAGATAATATATA

YIL150C, 571 aa (SEQ ID NO 140)
 MNDPREILAVDPYNNITSDDEDEQAIARELEFMERKQALVERLKRKQEFKKPQDPNFEA
 IEVQSPPTKNRVKGSHNATQQCTKFEFSNINEVRLSQLQQPKPPASTTTTFMEKFNQA
 KKNEDKQIAKFESMMNARVHTFSTDEKKYVPIITNELESFNLWKKRYIPEDDLKRALH
 EIKILRLGLFKAIRPPKFKQPEYANWATVGLISHKSDIKFTSSEKPKVFMFTITDPQH
 TLDVIFYGKQVRYNNRLGSDVIALNLNPEVLFPWRPSGRGNFIKSNLRLISHDFPKILIEI
 GSSRDLGCPWPNKTHKKCGSPINISLHKCCDYHREVQFRGTSAKRIELNGGYALGAPT
 KVDSQPSLYKAKGFGNIIKGRRLSEEEERLKKSHSNFTNSNSAKFAFDEKFNQDGLI
 LANLDNKKRRIETKKSTALSRELGLKIMRRRESSLEDKSVGERQKMKRTTESALQPTDI
 QRLGPDFTHGKIQLVLSKSVSGSEPKNNLLGKKKTIVINDLLHYKKEKVLAPSKNEWFKK
 RSHREVWQKHFSGSKETKETS DGSASDL EII

YIL167W, 1133 bp, CDS: 501-1133 (SEQ ID NO 141)
 GACATTTTGAAAAAATACATTATATAGAGTTTATTATATAACGTAACAGTTTAAACAACAAAG
 GCTCATAGTCCGAGATCAATATAATAATTTATCAAGGTTTAAAGGAAGAAGTTTACCATGG
 AAATGCTTACTATGAAAAGACACCTTTGATTCGTCAATTTTGAACAACTGGTGAAGACAA
 ATTCTGGTGTTTACGTTAAGCATGAGATGTTTAAACCAAGTGGGAAGTTTCAAGTTCGAGAG
 GAATCGGGCATTTGATAAGGAAGAGTAAATGAAGAAGCGCTAAGCGAGGTTCTGGGAAGC
 TTGCTGTATTTTCTAGCTCTGGGGAAATGCTGGTTTACGACGACGAACTGCCTCGAGAT

FIG. 1 - 48

CGATGGCACTTAATTGCAGTGTAGTGGTTCCCTAAAACACAAAACCTAGATAAGTAAAGA
 AAATTCAAAGTGCAGGAGCCAAAGTCATTATCCATGGTGATCATTGGGGGGAAGCAGATG
 AATACTTGAGGCACGAATGAATGGCGCAAGAAAGCCAACTGGTTCGGAAGCACTATATG
 TGCACCCGTTTGATAACGAGACAATTTGGGAAGGTCATTCTACGATTCTGGTCAAACTCA
 TAGAACAAATGAAGGAAATGATATATCCTTACCTAGGGTGAAAGCTTTGGTTGTAGTG
 TTGGTGGTGGTGGGCTATTAGTGGCATAATTAAGGCCCTAGATAGGAATCAGCTTGCTG
 AAAAAATTCGGGTTCGTTGCTGTGAGAACTCCGGGTTGTGACGTATTGAAATAAGTCTCA
 AAAAAGGTATGTCAGTTACTCTTGAAAAATTGACAAGTGTGCAACTTCTTTGGCCCTCCC
 CATACATAGCATATTTCGCGTTTGAGAGTTTAAACAAGTATGGATGTAAGTCTGTAGTTT
 TATCAGATCAAGACGTTCTGGCAACATGCTTGAGATATGCCAGTACACTAAATTTTATAG
 TGGAACAGCGCTGTGGAGCATCCTTACATTTATGTTATCATCCAGAGATCTTGAAGACA
 TTTCTGGAACAAAAATATATGAGGATGATATCGCTTATTATAATCGCATCGGGTGGATCAT
 GTATGACGTATGAAGACTTGGTGAAAGCGCTCGAGCACATTAACCGTATCATAA

YIL167W, 210 aa (SEQ ID NO 142)

MAQESQHGSKTLYVHPFDNETIWEGHSTIVDEIIIEQLKENDISLPRVKALVCSVGGGGLF
 SGIKGLDRNLQAEKIPVVAVETAGCDVLNLSLKGSPVTLKLTLSVATSLASPYIASFA
 FESFNKYGCKSVVLSDQDVLATCLRYADDYNFIVEPACGASLHLCYHPEILEDILEQKIY
 EDDIVIIACGSGCMTYEDLVKASSTLNVS

YJL034W, 2549 bp, CDS: 501-2549 (SEQ ID NO 143)

CCATGAACCTCAGCATGTGCTACTCCAGTTAATGACTTGTTCGTATCGTTCATGCCATAAG
 CCATCAGCTGGCCAGTTGGCGTATGTACAAAGATGCAAGCTACCGGTTGCTCATCGTGGT
 CAAGAGCCGTATCTAGCCAAACGGACAGCTGTCTCATATGTTTAAATGTCTGCATAGTGT
 GAGTCCCTCTAGTTTTCACCGCAGCCACCGCCGCTTCTCGAGCAAAGGTAGATGCCATT
 AGGACTCATCATCTCTAAATTTTGCTATGTTAGCTGCAACTTCTATTTTAATAGAACC
 TTCCTGGAATTTTCACCCGCGCGGCACCCGAGGAAGCTGGACAGCGTGTGAAAAAAGTTCG
 TTTTATATAAAGGACACGAAAAGGGTTCTCTGGAAGATATAAATATGGCTATGTAATT
 CTAAGGATTAAAGCTGTACTGTTTACTTTTTTAAAGTCCCCAAGAGTAGTCTCAAGGGA
 AAAAGCGTATCAAAACATACCATGTTTTTCAACAGACTAAGCGCTGGCAAGCTGCTGGTAC
 CACTCTCCGTGGTCCGTGACGCCCTTTTCGTGGTAATATTACCTTTACAGAATTCTTTTCC
 ACTCTCCCAATGTTTTAGTTAGAGGTGCCGATGATGTAGAAAACACGGAACCTGTTATCG
 GTATTGACTTAGGTACTACTTATTCCTGTGTGCTGTGATGAAAAATGGTAAGACTGAAA
 TTCTTGTCTAATGAGCAAGGTAAACAGAATCACCCCATCTTACGTGGCATTCACCGATGATG
 AAAGATTGATTGGTGATGCTCAGAAAGAACCAAGTTGCTGCCAATCCTCAAACACCATCT
 TCGCAATTAAAGAGATTGATCGGTTTGAAATATAACGACAGATCTGTTCAGAAGGATATCA
 AGCACTTGCCATTGTAATGTGGTTAATAAAGATGGGAAGCCCGCTGTAGAAGTAAGTGTC
 AAGGAGAAAAGAGGTTTCTACTCCAGAAGAAATTTCTGGTATGATCTTGGGTAAAGATGA
 ACAAATTTGCCGAAGATTATTATGGCACTAAGGTTACCCATGCTGTCGTTACTGTTCTCTG
 CTATTTCATAGACCGCAAGACAAGCAAGCCACCAAGGATGCTGGTACCATCGCTGGTTTGA
 ACGTTTGTAGAATTGTTAATGAACCAACCCGAGCCGCCATTGCCACGGTTTGGATAAAT
 CTGATAAGGAACATCAAAATTTATGTTTATGATTGGGTGGTGGTACTTTTCGATCTCTCTC
 TATTGCTCATTTGAAAACGGTGTTTTCCGAAGTCCAAGCCACTTCTGGTGATACCTATTAG
 GTGGTGAAGATTTTGACTATAAGATGCTTTCGTCAAATTGATAAAAGCTTTTCAAGAAGAACG
 ATGGTATTGATGTGCTGCACAAACACAGGCCCTGACTGCTAAATTTGAAGAGAGAAGCTGAAA
 AGGCTAAACGTTGCCCTTGTCAGCCAAATGTCCACCCGATTGGAATTGACCTCTCTCGTGT
 ATGGTATCAAGTTAAGTGAAACCTTGACAGAGCTAGTTTGAGGAATTTAAACCTGAGCT
 TATTCAGAAGACCTTGAAAGCCTGTCGAGAAGGTTTTCGAAGATTCTGGTTTGGAAAAAGA
 AGGATGTTGACTGATATCGTTTGGTTGGTGGTTCTACTAGAAATCCAAAGGTCACCAACT
 TGTPTAGAACTACACTTTGATGGTAAGAAGGCCCTCAAGGGTATTAAACAGATGAAGCTG
 TTGCAATACGGTGACGCCCTTCAAGCTGGTGTCTTATCCCGTGGAAGAAGGTTGCAAGATA
 TTGTTTATTGATGTCACACGCTTTGACTCTTGGTATTGAAACCACTGGTGGTGCTATGA
 CTCCTAATAATTGAAGAAATACCTGCTATTCTCTACAAAGAAATCCCAATTTTCTCTACTG
 CCGTTGACAAACCAACACCGTTTATGATCAAGGTAATACGAGGGTGAAGAGCCATGTCTTA
 AGGACAACATCTATTAGGTAAAGTTTGAATTAACCGGCATTCCACAGCAACCAAGAGGTG
 TACCTCAAATTGAACTGTCATTTGCACTTGACGCTAATGGTATTCTGAAGGTGTCGTCCA
 CAGATAAGGGAAGCTGGTAAATCCGAATCTATCAAGCTACTAACGATGAAGGTAGATTAA
 CCCAAGAAGAGATTGATAGAATGGTTGAAGAGGCTGAAAAATTCGCTTCTGAAGACGCTT

FIG. 1 - 49

CTATCAAGGCCAAGGTTGAATCTAGAAACAAATTAGAAAACACTGCTCCTCTTTGAAAA
 ACCAAGCTTAATGGTGACCTAGGTGAAAAAATTGGAAGAAGAAGACAAGGAAACCTTATTAG
 ATGCTGCTAACGATGTTTGTAGAATGGTTAGATGATACTTTGAACCCGCAATTGCTGGAAG
 ACTTTTGATGAAAAGTTGCAATCTTTGTCCAAGGTGCGTTATCCAATTACTTCTAAGTTGT
 ACGGAGGTGCTGATGGTTCTGGTCCGCTGATTATTGACGACGAAGATGAAGATGACGATG
 GTGATTATTTCGAACACGACGAATTGTAG

YJL034W, 682 aa (SEQ ID NO 144)

MFNRLSAGKLLVPLSVVLYALFVILPLQNSFHSSNVLRGADDVENVYGTIVIGDLGTT
 YSCVAVMKNKGTETILANEQGNRITPSYVAFPTDDERLIGDAAKNQVAANPQNTIFDIKRLI
 GLKYNDRSVQKDIKHLFPNVVNKDGKPAVEVSVKGEKKVFTPEEISGMILGKMKQIAEDY
 LGTKVTHAVVTVPAYFNDAQRAQTKDAGTLAGLNVLRIVNEPTAAAIAYGLDKSDKEHQI
 IYVDLGGGTFDVSLLSIENGVEFVQATSGDTHLGGEDFDYKIVRQLIKAFKKKHGIDVSD
 NNKALAKLKREAEKAKRALSSQMSSTRIEIDSFVDGIDLSETLTRAKEELNLDLFKTKLK
 PVEKVLQDSGLEKKVDVDDIVLVGGSTRIPKVQOLLESYFDGKKASKGNINDEAVAYGAAV
 QAGVLSGEGVEDIVLLDVNALTGIETTTGGVMTPLIKRNTAIPTKKSQIFSTAVDNQPT
 VMIKVYVEGERAMSKNNLLGKFELTGIPAPRGVPOIEVTFALDANGILKVSATDKGTGK
 SESITITNDKGRLTQEEIDRMVEAEKFASEDASIKAKVESRNKLEYNLKNQVNGDL
 GEKLEEDKETLLDAANDVLEWLDNFETAIAEDPDEKPELSKVAYPITSKLYGGADGS
 GAADYDDEDEDDGDYFEHDEL

YJL035C, 1253 bp, CDS: 501-1253 (SEQ ID NO 145)

TACCTAAGTCAATACCGATAACAGTTCCGTAGTTTTCTACATCATCGGCACCTCTAACTA
 AAACATTGGAGGAGTGGAAAGAATTCTGTAAAGGTAATATTACCACGAAAAGGGCGTACA
 GGACACCGGAGAGTGGTACCAGCAGCTTGCACCGCTTAGTCTGTTGAAAACATCGGTAT
 GTTTGATACGCTTTTCCCTTGAGACTACTCTTTGGGGACTTTAAAAAAGTAAAAACAGTA
 CACGTTAATCTTTGAATTAACATAGCCATTTATATCTTCCAGAGAACCCTTTTCGTGT
 CCTTTATATAAAAAAGCAACTTTTTCGACACGCTGTCCAGTTCTCCGGGTGCCGCCGCG
 GTGAAATTTCCAGAAGGTTCTATTAATAAGTATGAGTTCGAGTAACTAGCAAAATGAGA
 TGAATGATGAGTCCTAATGGGATCTACACTTTGCTCGAGAAGCGGCTGGTGGCTGCCGTA
 AAAACTAGAGGACTCACACTATGCAGCATATTAACATATGAGGACAGCTTCCTGTTTGG
 CTAGATACGCTCTTGACCACGATGAGACACCGGTAGCTTGCATCTTTGTACATACGCCAA
 CTGGCCAGGTGATGGCTTATGGCATGAACGATACGAACAAGTCATTAACTGGAGTAGCAC
 ATGCTGAGTTGATGGGGATCGATCAGATCAAGCGCATGTTGGGCTCCCGAGGAGTTGTGT
 ACGTGTTCAAAGACATTACTCTATATGTTACTGTAGAACCCTGTATAATGTGTGCACTGT
 CTTCTCAAGCAATTAGACATTGGAAGGTGGTGTTCGGTTGTGGCAACGAGAGATTTGGAG
 GCAACCTGACTGCTTGTGAGTAATCATGATACGTGTACATTAGTGCCCAAGAACATA
 GTGCGCGCAGGTACGAGAGTATACCGGGATCTTGAGGAAAGAAGCAATAATGCTGTCTGA
 GATACTTTTATGATAAGACAAAATGAAAGGCCGCCAAGCCACGGTCCAAGATGTACAGAG
 TGTGGATAAAAACAGCTTTCCGCCATGGAATGGTCAAAAGTATCTTAATGAAGAAGCAT
 TCATTGAGACTTTTGGTGATGATTACAGGACTGTGTTTTCGGAATAAAGTTGACTGTGCTCA
 GTAATTAGCTCGATTGGGATTGTGATTGACTTCCACCAAGATATATAATCCAAGAAGTGG
 AAGAACAATGCAAAATGTTTAAAGTTAATGTACATAAGAAATCTAAGGTTTGA

YJL035C, 250 aa (SEQ ID NO 146)

MQHIKHMRTAVRLARYALDHDDETPVACIFVHTPTGQVMAYGMNDTNKSLTGVAHEFMGI
 DQIKAMLSRGVVDVFKDITLYVTVEPCIMCASALKQLDIGKVVFGCGNERFPGGNGTVLS
 VNHDTCTLVPKNNSAAGYESIPGLRKEAIMLRIFYVVRQNERAPKPKRSKSDRVLDKMT
 PPMESWXYLNEEAFLETFGDDYRTCFANKVDLSSNSVDWDLDSHQDNI IQELEEQCKMF
 KPNVHKKSIV

YJL070C, 3167 bp, CDS: 501-3167 (SEQ ID NO 147)

TCCCTGATGGTCAAACTACTGTGCATGGCATCCCGTGCAGTCAAGGATGCTTTGAGACTA
 GTTCATCTGCCCTCTTTGAGCGTGTTCAGCAACTGGCCCTACCAGCGGAGCGCCTTTGGGT
 AAAGTTACCAGTGTGCGATTTCGCCATCTGTTGGGCTACTGGCCGTGGGTGAGCAAGCAA
 GGTAAAGTGAGGCTCTGGAATTAACCACTACTAAATTTCCATTATAGACAACTTAG
 ATATTAAAAGCAATGTACAAATACATACACAAATATCACTGTAAAAAAATTTGCGAAGAA
 ACTTGAAATTGAATATGATTCTGCCCACTTTTTCTTGCTGTCAATTATAGTCAGAAATG

FIG. 1 - 50

AAAAATGTCCTCCGAGAAATTAATATTAATATATGGAAAAAAGGGGACATTGAGTTTAAAG
AATTGTGATTAATAATGCCTCTCAATATCCCTCTGAAGAGTTATCTAAATCTCACTTTACT
TATTCATCTCGCTGGGAAATATGACAGGCGGTAGAGAGAAGGCCCTCGTTACTCTTTGAAG
AATATCAAAATCTCTGTTACTAAGCCTAATGAGACGAAGAATAAAGAAAGCCAGGGTCTTGT
CAGAGAATGACCGTGATGTCTCCCATCTGTTTTGAAACAGAAGGAAATATCAGTCGATG
ATATGGATATGATTTCTTTGCCACGGAATTTGACAGGCAAAATGGTTTTAGGTTTCACTTA
TGTTTTTGCATCTTTGAAGACGAAGAAAAACAAATTTGATCCACTTCCTTCAAGTTTCCCAT
ATTTATGGAATGAGAAAGTGACAGCTTTGTCTCATCGTACAGCCGCTCAAAATTCGAAAA
CGGGTGAAGAACTTAAAGATCTTTTCATTAAATCCGTTTGAATTTGGTTTCTCAAATGAGAA
AAAGATACATTCCTGCTCTTCCAACAAAGATGGCAATTTCAACATATAAAATGACTCGAAA
AGTGGTTTTTATACCCAAAAACACTGCCAAAGTTTTGAGAGATTGAAGACCATTAACGAT
TCCAAGATCCCTCTGACTCTGACTTAAATGACGATGGAGACAGTACTGGGACCGGAGCG
CTACACCGCACCGCCATGGCTACTATTACCAAGTTACTTTACCGATCACTACTACTACT
ACACAAATCTGGTTTGAAGAGGAAAGGAAATATAAAGTACCATACACCGGTGAATATT
TCGATTTAGAGGATTACAAAAACAAATACATTTTACCATTAAAGTATCAGGAAATACCG
AAAACCCACTTCACTTATTCTAGTAAGGAGGAGTCACTAGAGGAAAGATTTTTAACAG
ATGTGCTACGTTTCAAGAATTAGGAGTATTTTGCATACATAATGAGTTAAATCGGAA
CTCATAAATCAACGAGGTTTCAAGAAAGCGATTATCTTATTATTAGATATAAATTCGAAT
TGTTTTAGTAATCTTAACTCTAAGAAGAAATTTTAGCTAATAAAATGTTCCTTACGAG
ATTTTATGATTTCTCGTAAGGTAGATCGAGACTTGTCTTTAAGTGGTTGGTATTCTCAAC
GCTAATTTAGTGTGAATATATATGGGAGAAAAATAAATTTAGAACCCTGAAGAAAGTATTATC
AAGAACCGGAAACGCTCAAGGAAACTCAGTTTGAGAGACATTTTTCAGTTTGGTTGTTCTT
CTAATGACCAACCCATTGCGATTGGGTTGAAATTTGATTGATGATGAATTTCTGGATTGGT
ATAGAATATTTTACCTAATAGATTACCTCTAACTCCTAACAAAGTAGCAAGTTGGTCTG
GCAAGAAATAGAGGTTTACCTATTAGCCAAAGTGTTTCTGGAGTTTGTATGATTTTCAATG
AAGGTGAGTACCTAGCAGAAATTTTCATAAAATACGTTATTTCATATCTCGTGAAGAACTCA
AGTACCAATTTGGCCCAAGTATCAGTTAATTTTCAATTTTATCCAGTGGTGAACAGTGT
ACAAGAATTTTCTCAATGGTTGCTACGATGGAAGCTAGTATCGTATAATATCTCGCTGGA
ATGATCAAAATGGCCAGGATTTTTCCTCAAACTATTCAAGGAAATGTCTGTGTCAAATTTCC
AGGAGTTTTGGATCTTATCTTCAATCTCTTATTCACCTCTGGAAGAGGACAGTTACCA
TAGATTTCATCTGTAAATACTGATATCATGTGCTCTGAGTTTTTTTTTCAATGTGATGTGTT
CTATGGATCTGGTCAATTAAAGAGTCGGATGAATATTACTGGAAGAAATTTACTGATATGA
ATTGTAAGCCAAAAATTTTGGACAGCACAGGCTGACAACTGTTGCGCATATACATGT
ATTATATTTATATAAAGTTTGAAGAAAGTTAATTTTCTGCGGTCACAAAATCTTCAAAATA
CAATCAACCTTAAGAAATTAATGTTCTCCACTATCCAGCAGAACTTCCAATTTGGAGTGG
ATTTATATTTTACAGATCAAGTTGAATCGTTAGTGTGCAACTTACTGCTTGTATGTGTG
GTCTGCTACAGGTAGAACCCTTTGGGATCTGCAACAATGATTCAATATTTATTTTATCT
TCTTTCAAAATACCACTTTTAGCTGCGCCATTATCATCTGTTTCAATFACTGAATTCGCAAA
AATCGACCTTTTGAAGAATAAAAACGTGCTTCTAGAACATGATTATTTGAAGACCCAGG
AAACAGCCAAAAATCAATCCTTCTAGAGATATCACTGTGGCGGAACAAAGATCATATGAGA
CAAACTCCTTTCATGAAAAATGTTTAAAGTGGGACTAAAAATTTCTTTATCATCAAAATCGA
TCTTTTCAATAGTTCATACACGCTAGAACCTCTCATTGAAGAATACAGTGTAGCAGCAA
GTAATTTACTTGCTGAACCCCAACAGATTTGTGCGAGTTGTGAGAACAGGTGTGCTATCTA
GTGCTATGAAGGTTGGTACAAGGCTCATTGGATTGGCGTTGGAGTTAAAAAGGCGCCTT
ACTTTGAGGAGAAGCTGGGTGGGATAGATAATTTGGTACGATACAGCGAAAGATACCTCGA
TAAAGCAACAGCTTCCGATGATTAGAAGAAGATATAGAAGGAGACATTGGATCAAGAGT
GGAACCTCGTTCCGGATCACTTTGGAGTAATTAACCTCCATTTGGTAG

YJL070C, 888 aa (SEQ ID NO 148)

MQAVERRPSLLFDEYQNSVTKPNETKNKEARVLSENDGVSPVLKQKEISVDDMDMISL
LPEFDROMVLGSPMFFDLEDEENKIDPLPSVSHHYNGESDSFVSSYTPSNLKTGEETKD
LFINPFELVSQMKRYIAASKQDGISNKNKNDKFWLPKPLKFWRFEDDKRFQDPDS
DLNDDGGTCTGTAATPHRHGYYPYSYFTDHYYYTSGSLKGKGNKIVPPTYGEYFLEDDYK
KQYLYHLSNQENQNLSPYSKKEESLEEPLTDVPTFQEFRDDFYAIIELIQSHKNEY
SRKRLSYLLDKFELFQYLSNKKKEILANKNVPRDYFNSRKVDRLSLSGCI SQRLSEYI
WEKNLNEPERIVQDPETSRKLSLRDIFQFGSSNDQPIAIGLKLIDDEFLLDWYRNIYLI
DYHLTPNKVAKLVGKEMRFYLLAKVLEFDNFIEGYLAEIFIKYVHIHLEKSKYQLAQV
SVNQPFYSSGEDWYKKFSQWLLRWKLVSYNIRWMIQIARIFPKLFKENVVSNFQEFLLDI

FIG. 1 - 51

FNPLFTLEKEQLPIDSSVNTDIIGLQFFLSNVCSMDLVIKESDEYYWKEFTDMNCKPKFW
TAQGDNPTVAHYMYIYKSLAKVNLRSQNLQNTITLRYNCSPSSSRTSQFQVDLYFTDQ
VESLVCNLLLCNGGLLQVEFLWDATMIQYLFYLFQIPIAALPSSSVLNSQKSTFLKN
KNVLLLEHDYLDQETAKINFSRDI TVGEQSRYSYENPFMKFMKGLKLSLSSKSILYNSSY
TLEFLIEEYVSAASYLLNPTDLCELSRTSLSSSYEGWYKAHWIGVGVKKAPYFEENVG
GIDNWYDTAKDTSIKHNVPMI RRRYRKETLDQEWNFVRDHFVINSIW

YJL078C, 3146 bp, CDS: 501-3146 (SEQ ID NO 149)

TTTTTCTTCGCACATGGCTGGTTCGTCTGGAGGCGGCTGGGTGTTTATAGTTACCGCAAT
GCAGGTCGCTTCGTTTACTTTTCTCTGCGTGCCTCGAGAACTGATAAAATCTCGGTTTAGGA
AAACCGTCCTACTTATGGAATTTAACAAAGGAGGTGAAAGGTAGGTACCATGCAATATAGCT
AGCAACGACTACGCACCTAGCTGTGTGTGCTTGCTCTCTGTGTTCGTCTTTCGTATATATGC
GGTTCCTCCGCGTTAATTCAACAACAAATATGGTATCTAGGCAGGACCCGACGCAACGGAA
GGATGTAAATTCGTATATAGGGCCGATGAAACAGTTTCTCATGTTTCACTCGCTCGAAGAA
TTCTCTAAAAACATATTTCTATACTTCAAAGTTTTCAGCTTCTTGCTTTCGGTAGTTGCCA
AACCATAATCGGCATAAAAATTATAATTGCTGCACCCCTGCAACTCCAAACCACTTAAAC
AACTTAAAAACGAAACCGCTTATGCTGGAGTTTCCAATATCAGTTTCTGCTAGGATGCGCTAG
TAGCCGTCAAGGCACAAACACAGTTTCCAACTTCGAGAGCGATGCTGCTGAACGAGCATATA
CAAGTTTCAGAGCGCTACATGTTGACACAGCGCGCTCACCTGGTCGCACCTTCGCGCA
CCTATGCGCAGAACTACGCCGACCAATATGATTGTTGGGTGCTCTTAACGCACTTCGATG
GCCATATGTTGAGAACCTTGCCCTTGCGTTACACAGACACGGGAGCGGTGGACCGCCTGGT
ACGGGAGATAAGCAAGTATAATTATTCAAATCCCGGATTTTCTGAAATCCACCGGTCACCT
TCACACAGGTGGTTTGGAAAGTCAACCGCGAGATTTGGATTTGAAATATTTGTGGTA
GCACATGCCAAATATATTTGTGTGCTCTCAACAACTCTCGAACTCTCTGGAAGCTTGGAGT
TTGCAAGGAAAGTGGAAACCACTTATAAGCACTGTTTCTCGTCTCATCTCGTCTCTCTCT
CTACCTCAACTACATCAGACACAGTCTCCACCATCTCATCAGTATATTCGCGCGCTGTAG
CGCAAGGGTATACAAACAGGTTATCGTCTGCGCGCTAGCAGCAGTTCTTTAAAAATCGACGA
CCATAAACCTCGCAAGACCGCTACCTCCCTAGCTGCTCTTCTACCGTAATTAATCTAGTA
GCACAGAAATCAGTTGGATCTCTCCACTGTCTCATCAGCTCAAGCTCTCTCTGTCTACTACT
CCTATGCTACCTCTCGAGTACCGTCTGCTCTCTAGTGTGCTACTTTCATCCACTACCACTTA
CCTCATCGGTTGCTACATCGTCCAGTACCACCTTCTTCGAGCCCTACCTCGAGCAGCTGCTG
CTGCTCTCTCTCTGATCTGCTCAAGTTCGCGTGGCGCTTCTCTCAGCGCGAGTACC
AGAACCGCGCTCTCTTAGCAGCGCCATCTCGAGCTCTTCATCAATGTTTCTGCTCCTT
TGAGTAGTACTTTACTACTTCCACCGCAAGCTCCAGAAGTGAATTTCCAATTCAGTTA
ATTCTGTGTAAGTTTGCAAAACACAACCTGTGTTTCTGCTCAAAACAACCTTCTCTGTAAGCG
CCTCATTTATCATCATCTGTAGCTGTGACGATATTCAGGGTAGCACCTTCTCAAGAGGGCCA
CAAGCTCAGTTTCCGAACATATCTAGTATAGTAACCTAGTGCAACTAATGCTGCCCAATATG
CAACGAGACTTGGGTCACTTCCAGAAGTTCTTCCGGGGCGCTCTCTCTCAGCTGTGT
CGCAATCTGTTCTGAATTCGTTTATAGCCGTCAACACCGACGTATCTGAACCTCAGTTA
GTAGCACAGCCCATACCAAAAGGACACCGCCACCACTTCAGTAACCGCCTCAGAAAGTA
TCACCTTCGGAACCTGCTCAGGCTTCAAGTTCAACAGAGAAGAAATATTAGTAACAGCGCGC
CCACTCGAGTAGCATTTACTCCAACAGTGTCTTGTGTGAGGACACGGTGTAAACATACG
CTGCCGAATACGGCAATTACATCCGAGCAATCTCTGCGCTTGCCACATCTGTGCGCTGCTA
CAAATGTCTCTAGTATCGTGAAGACCACAACCTTTAGAAAAATTCGAGTACCAACACATCA
CAGCAATTTACTAAGAGTACTACAACCTTGGCCACTACTGCTAACAACTCCACAAGGGCAG
CTACCGCAGTAAACCATAGATCCACATTTGGACCCCTACCGCAACTCAGCTAGTCCAAACCG
ACAATGCTAAACACACTTACATATGGATCTTCTTCCACAGCGCATCTTCTAGATAGCT
TAGGCACAACCCAGTATTAGTGTCTCAAGCAACACCACAGTTAGTCTCTACCTGCTA
CTTCCGAGAGCGATTATTCCGATAGTCTAGCTTTCGCCATCTCCAGTCCCAACCACTG
AAGCAATCTTGATCAACAAACCATCACAGCTTCTTGTAGTAGGATAGTAATTTCCCTA
CCTTCGCTGCTCTCTCTCAGATGAGACGGCTTCTACTAGAACAACTCTGCATCTTTGTA
GCACCTTTGAACCGCGCTCAACCCAAACAGTAGCTAACCATCTGCCCTATGAAACCA
ACACGGTGGTTTCAGCTTCTTCTTCCCTTCAACTACAAACCACTTGTCTAGAAAAATGATG
ACACTGCTTTTCTAGTATCTACACTGAAGTCAACCGCGCAACTCATATTAAACCCGAG
AAACATCTCTCTCGCTAGCGATTTCGCGCACATCTGAAAAAGCCAAACGAGCCCACTTCTG
TCAAAATCCACTCTCAACGAAGGCACCTCTTCCACAAACCAACCTACCAACAGACTGTG
CTACACTGTATGCCAAGCCCTCCAGCACAGCGCTAGGTGCAAGAACAACTACTGGTAGCA
ACGGTCTTCAACTACCAGCCCAACAGACGGGTCTGCCATGCATACGCCAACTTCTCGA

FIG. 1 - 52

TCTCACTCACTAAAAAGAGGCACATCAACCACCGCAAAACTTTCTGCATACGAAGGTG
TCGCAACACCTCTTTCCATTTTCCAGTCAATAGTCTAGCTGGAAACGATTGCCCGCTTTTG
TCGTAGCTGTTCTGTTCCGCTTCTAG

YJL078C, 881 aa (SEQ ID NO 150)

MLEEPIFVLLGCLVAVKAQTTFNPFESDVLNEHNKFRALHVDAPLWSDTLATYAQNYA
DQYDCSGVLTHSDGPYENLALGYTDTGAVDAWYGEISKYNSNPGFSESTGHFTQVWVK
STAIEIGCGYKCGTWNIVCSYNPPGNLYGEFAEVEPLISTVSSSSSSSTSTSD
TVSTISSSIMPAVAGQYTTTVSSAASSSSSLKSTTINPAKTATILASSSTVITSSSTSVGS
TVSSAASSSTVTSYATSSSTTVSSDATSTTTSSSVATSSSTSSDPTSSSTAAASSSDP
ASSSAAASSSASTENASSSSAISSSSSMVSAPLSSSTLTSSASSRSVTSNSVNSVKFAN
TRTFSAQTTSVSASLSSSVAADDIQGTSKEATSSVSEHTSIVTSATNAQAATRLGSS
SRSSSGAVSSSAVSQSVLNSVIAVNDVSVTSVSSTAHTTKDTATTSTVTAESITSETAQ
ASSSTTEKNISNSAATSSSIYSNSASVSGHGVYAAEYAITSEQSSALATSVPATNCSSIV
KTTTLENSSTTTTITATKSTTTTLATTANNSTRAATAVTIDPTLDDPNDNSASPTDNKAKHS
TYGSSSTGASLDSLRITTSISVSSNNTQLVSTCTSESDDSDSPFAISTATTTESNLTIN
TITASCSTDSNFPSTAASSSTDETAFTRTISTSCSTLNGASTQTSSELTSPMKNTVVPAS
SPFSTTTTLCENDDTAFSSIYTEVNAAITINPGETSSSLASDFATSEKPNPSTSVKSTNE
GTSSTTTTYYQTVATLYAKPSSSTLGARTTTGSGNRSTTSQQDGSAMHQPSTSSITYQLKE
GSTTAKLSAYEGAAATPLSIFQCNSLAGTIAAFVAVLFAF

YJL179W, 830 bp, CDS: 501-830 (SEQ ID NO 151)

TTGCATTATCAACTATAATCCATTTCCTAGAGGAGTTTTATAGTCTGCCATCTAATT
GTAGAGCAATCTTTCCCTTTCTCAACATCCCTTATTAGTGACACCTTTTCCCAAAACTCTT
GTGAAGTTTGTCTCAATCTATTGTGTTCCGTAGGAGTGTATTCTCAATCGTGTGTCTG
TCCCGCATGGCTGGGCATTTAATGAGTAGAATCGGGGCAGTTTCAATCTTATGGAATTCA
CAATGAAGCATCCCTTCCCTTAATGATGGCAGCATTCGTATTCTCTTTGTGATGTTTCTG
TTTGCTCTCAAGTGTGTTGTCTTATTATGAGCTTTTCTTTTACCTTTAAATTTTTTCTTTT
CTCTGAAGAAATGAATGAGTTTAAAGATATAGCAATTAAGAAAGTAAACAGTGAAGAAAT
TCTCAGATGAGCAGATGGGAATTAAGAACTATCTACAGAGCTCTTTACTAAATGGAATC
AATAATACATACTTTACAAACATGTCACAGATAGCACAGAAATGACAGTGAGCTTAAGAA
ACGCCAGGACACAATTTGGATATGGTCAATCAGCAGCTAGCATATTTGGACAGACAAGAAA
AGCTTGCTGAATTGACAAAGAAAGAACTAGAGTCTTATCCAACGGGACAAAGATGGAGAT
CTTGGCGTAAATCGTTTATCTTACAGGATAAATCCAAATACGTTAATGATTTATCACATG
CGCAAGACTGTCTCTGGAATCAAGAAACAAATTAAGATTAAGAAAGAACTATTAGAAA
CTCATGTTGAAAAAACAATAGACAATCTAAAGGCATTGATGAAGAATTA

YJL179W, 109 aa (SEQ ID NO 152)

MSQIAQEMTVSLRNARTQLDMVNNQLAYLDRQEKLAELTKKELESYPTDKVWRSCGKSFI
LQDKSKYVNDLSHAETVLLDQRKTLKIKKNYLETTVEKTTIDNLKALMRN

YJL180C, 1478 bp, CDS: 501-1478 (SEQ ID NO 153)

AATAGTCTCTTTATCTTTAATGTTTTCTTTGATCCAGAAGAACAGTTTCGGCATGTG
ATAAATCATTAACGTATTGGATTATCTCTAGATAGAACTTACCGCAAGATCTCC
ATACCTTTGTCGGTGGATAAGACTCTAGTCTCTTCTTTGTCAATTGACGAAGCTTTTCTT
TGCTGTCCAAATATGCTAGCTGCTGATGACCATATCCAAATGTGTCCCTGGCGTPTCTTA
AGCTCAGTGTCATTCTTGCTGCTATCTGTGACATGTTTGAAGTATGTATTATGATTCA
ATTTAGTAAGAGCTCTGTAGATAGTTTAAATCCCATCTGCTCATCTGAGAAATTTC
TTCAGTGTACTTTTAAATGTCTATATCTTTAAACTCATTCAATTTCTCTCAGAGAAAGAA
AAAAAATTAAAGTTAAAGGAAAAGGCTAAATTAAGAAACAAACACTTGGAGGCAACGAAAC
CCTACAAAGAGAAATACGGAATGCTGCATCATTAAGGAAGGGATGCTTCATTGTGAATT
CCATAAGATTGAAACTGCCCGGATTCTACTCAATTAAGTCCCAAGCCTGGGGAACAGACA
ACACGATTGGAATAACACTCTACGGAACAAATAGATTGAGCAAAACTCTCAGAAAT
TTTGGGAAAGGTGCTCAATAATAGGAGTGTGAGAAAGGAAAGATGCTCTACAAATTAG
ATGGCAGGACTATTAAGAACTCTCTAGGAAATGGAATTATAGTTGTAATGCAAGTCTC
TCTTAGCATACCTATTAAACTGGAGTGGTGGTCTCTATCCAGTCTTTTCCATCAAACTC
ACTCTTTGCCACTAACTTCATTAGTGGCAAGATGCATAGATTTCACAAAGTACAAATGAGC
CTGGCTGTGACCTCTCAATTAGTTGCAAGATTGGAGGCAACAGTGATGTTATAAAAAATC

FIG. 1 - 53

AGTTGTTAAGATATTTAGATACCGGATACTTTATTGGTCTTTTCCCTTATGAATGAGTTTG
AAGGAAGATTACGCAATGCGCAAAATGAGTTATATATACCATCAAAAGGAATGGGAAG
AGTTTTTACGCAACTTTTCATCCGAGTCTAATATTCGACTACAATTTTAGATGCCGACA
TCCATGGGTTACGAGGCAATCAGCAGTCGGATATCGTTAAGAAATGCAGCAAAAAATATA
TGAGCAGCTTTACCATCGGGATCTTGCAATTTCTGAAAAAATCTGATTTAACCAAGT
CCTTCATTTGCGGCGTGCTATTATTAGAAAAATAAAAAAGATCTCGGAATCTAATTCGCG
CTTTGAAAAATATAGGATAATATTTGACGTGCCGCCACCTTAGAAACAATCTTCCAAG
TTGAAAAAGTGGGAGAGGTTGAAGATACTCATGACGTTGACAAAAGAGACATCAGAAGAA
AATTCATACCTGCTCGATGCTGCTTTTAAGCAATAA

YJL180C, 325 aa (SEQ ID NO 154)
MLPSLRKGCFFIVNSIRLKLPRFYSLNAQPLGTDNTIENNTPTETNRLSKTSQKFWEKVS
LRDVEKGKIALQLDGRITKPLNGLIIVDNAKSLAYLLKLEWSSLSLSIKTHSLPLTS
LVARCDILQMTNEFGCDPQLVAKIGGNSDVIRKQWLLRYLDTDLLVFSFPMNEFGRRLNA
QNELYPIIKGMEELFRNFSSSENIRLQILADHIGLRNGQQSDIVKNAAKTFFKMGSSLS
DLAILEKTVLTTKSFICGVLLLENKKDTANLIPALKTMDMNVIRAATLETTFQVEKGEV
EDTHDVKDRIRRKIHTAAIAAFKQ

YJL181W, 2336 bp, CDS: 501-2336 (SEQ ID NO 155)
GCAAGTCAGTACGATGCATCCTTGGAATCAAGAAGGTGAGTCTGGAACCGGTGCTTCTAAT
GGCGATGTTTACCATTTAATGAAGGGGACTTGGCTGCCTCCTTCAAGGGGATGTAGATCA
AGAGGTCAGGTGCTAGTGAAATAGGTACATGTACCCAGAAAAATCAAGAAATCTTAGATCA
TTGTTAATCTTGAATTTAGTTTCAAAACAAGATCTCTGTATTATATAAACAAGATATATA
ATTTTAAAAAATAATGAAAAAGCAATATAATTCAAGTCCCACTTGGAAATATGGCA
CTGTATTGATGCTATTTCCTTATGCTTAGTGACGCGTTTTCGCGCGTCAGTTTCAAGTTT
TTCTTGGCTTTTTTTTTTTCAATTTTCGTAAGGGTCTTAAAGAGATTAATAAATGACGTA
TTGAAATAAAGACAATATACGAACGGTGAAGCTGCTATTTTGGTTATTATATACCTCCAG
GACAGTACGCGCAAACTATTATGGAGATATCAAGGAAGAAGAAGAAGCTTTTTCGG
CGATAGAGGTGATAATATATGCTGTGAGGTGATGACCCGTGATACCCGCTCATTTACATA
AAAGCAAAACAAAGATCATCAATGCTGCTAAATTAATTATAGAAACCGCATTTTTCATATT
ATACAATACTCAATAACATTTAGATATACAAGCTATCTTTCTACTTGGCTTAGGGATC
TTGGAACGACAGGTCCATACCAACAATTTCTTCAAGAAAGTATTCTCTCATGTTTGAAC
GCATCTGATCTATCTTCAGGAAATGTACGATAGAGGGAGGTTTTCACATTTGATCGCAC
GTCTTTATCTCAGATTGAAAGCTACCAAGAGCTCTTAAACGATGACAGGATTAAGAAT
TTTTTCAAGCTACGATTATGCTTTTCGGGTTGTCATACAACCTTGTAAATTTGCTCTGAAT
ACAGGTATGACGAAGTTCATTACATATCGAACCGGCACCTTACTCATTAGTTCGATCGATGA
AGATAGATCCTGTGAAGTCAATAAAGGGAACAATTTTAGGCTTACAATTCGCAAAATTTA
ACATATCTAATATATTAATGAAATTTTTCATTTGCTCGATGGATTAGCATTTTTTAAGG
TGAACCTGATAGTTTATCTATATCTACAGCTTCAGCAGAAACAATCTTTTCGACGATCT
CCGAAGGTAATCATCAGGTCTTGAATTTGGGAGAAAGTTAATGTTTCCATTGTTGAGGA
CTGGAGATTTTGAATCTGTGCTATTGACGACGCGGGAGCTGTCAATCAATTTACAGAAG
CGAAGGATGTAAACTAGAAATAATCAGTCTGGATGAAGTTTCTCGGTAATGCAAGTGA
AATCTTGTCTTCAAAATATGAGAGAAGGGCAGCAATGACAGTTCAATTTATCAAAAGCA
ACCTCAAAATTAAGAAGGCCAACAATTTCAATGAAGATAATAAGGGCTAGGACATAATG
TAGACAGAAATATTTCAACAGATGATTTTACGCTAGCTTCTACAAACCGTCAAGTCCCC
CGCTTCAAAATCTGGTTGTTTCAATACACAGGCTTAAACCTTGCATATCTCTTATCAT
CTGTTATTCTGTAAGACTTTTATGATAGCTTCTAAATGAGCGTATCTTAAAGACGGAG
ATAGCAGTTGTGAATCCTTTCAGTGGCGCGAAAGTATCTTATCAGACTACGATTTTCATG
ATAATGAATTTTAAACAACCGTCAACCTCATTTTTCGAGAACACATAGACAATAACT
CGAGAGAGGTGGTAATAACAGATGAAAAATACGATAATATCTTTGGAATAATACCAAGTAA
GTCGGTGGTCAAAATCTCATCTAGGCAAAAAATTTACCGCATCAATTTACAGGTCTCTATT
TCCAATGCGCATGGGAACTTCATTGTCGCTTATGATTTGATTTAATACCTTTCATCAGT
TCAAAATTCGTTTGTGTGACGATATAAATGTATACAATCCACAGCAAGACATACAAA
TACGCTGTCGCTCGGCGCAATAATGTGACGCGTCACTGGTATCTTGAATATTAGGACGA
AGGACGCTGACAAAGTTCGTTTCGGGTATTAAAGCTTTTATACCACTGACCAACGGAAGCTG
TATCGCATCAAAACAATCAAGATGCTACTGCAAGTCCACTTTCGTCAGTTTCTACGAA
TGGATCTCAAGCATTCATTACAGAAATGTTCTCTACAATAATGCCCAAGAGTTGACGC
AGGACGTCATCGGTTCAAAATCAGACCTAATCAGTAATATTGCTCAAAAAATATAA

FIG. 1 - 54

YJL181W, 611 aa (SEQ ID NO 156)

MEIFKEEEEFSAIEGIYACEVYDVPVRHLHKSCKTIINAAKLIIETHLSYTYILNNI
SDIOAYLSTWLRLDGLTGPYQITLSEISLMFDRPTVSI FRKCTIEGGFPHLIARLYRLK
SYOKLLNDAGLKNFFSSDYAFGVAYNLVNCSERYRDEVHYISNGTYSLVASMKIDPAEV
IKRHFRLTTPKFNISNLIEIFHLLDGLAFFKVPNDSLSISASAEIIFRSISEGNHQV
LELGRSLMFLPLLRITGDFEICRIDDAGAVITTEAKDVKLEIISLDEVSWVMQWKSCLQNY
ERRAANDSSPKTHLQFKKANFNEDNNGLLIVDRNIPDDFTLASTNRRQSPSPNTGC
SLHRSKPLHLPLSSVIREDFYDSSLNERISKDGDSSCESFSGAESILSDYDFHNEFFNN
QSPHYFSEHIDNNNSREVITIDENTIISLENTQVSRWSNYSWQKISPHLOQVSIILQRMGN
FIVAYDSYDNLHGFQKIRLCDDIKIQSTEQDIQIRVPLGAIMCSVTGILNIRTKDADKLL
RVLSEYTTDHTAEVSHSNQDATASPLSSVSSAMDLKHSLOKCSSTIMPQELTQDVIGSK
SDLISNIRKQI

YJL187C, 2960 bp, CDS: 501-2960 (SEQ ID NO 157)

TCTTGCAACCATCGTCTCTAAGGAAGAAATGTGGCACCTTTAAATAGGTTCACCTCA
CAGATGCCAACATGTGGGAGATAGGGGGCTATTTCGCAATTTATTAACTCTCTAGTACTG
TAGAGCTTTCTAACATCTCTGTGGTCACTGATGTGTATGTTCTTTTTTTTATTCTCTC
CGGCTGTATACGACGCGAAAAATATTTTTTCATTTTTCTTTTAAACCATCACAATTTTGGCA
CGCAGCGCAAAAAATGCGAGAGAAGTAAAGAAGTGTGGTAAGAAAAATCAACACACAG
TTGAACATTTGGCGTGCCTCTGTATTAAGTAAAGGTGTGCAAGAGAGCTCTTTTTTGTA
TGATTCGGTGTGTGTTAACTATCTCTGCACATCATCTTGCAGTAGTGTGCTTGGGAAAAAGTAAACACAC
TACTACTGAAAGAGTCTTACTATTTTTGTATGCGTAGTGTGCTGGGAAAAAGTAAACACAC
ACAGCGGCACACGAGAACAGATGAGTTCTTTGGACGAGGATGAAGAGGACTTCCGAATGC
TGGACCGGAACCTCCAGTTTATGGGGAAGAAGATGTTTGGCAACACGAGCGCGGAAG
ACGAGATGTGATGTTTGCTATAGGGGTAGCACCCCGACCAATAACTGAAATTTTATC
CATATTGCAACACAAATTGACAAGAAGTACGGGGACCTTGAACCTGTCTTAAGTAATA
CAGCTTTTGCAGAGCTAACTCCAATTTCTTGGGAAAATGGAAGAGGAAGAGG
AGGAAGAAGCGAGGATGAGGAAGCGGTGGATTCTCGTATTAAGAAGTGGTCTCCGTTC
ATGAAAATGAAAGTGTACTACTCTTATTACAAAAGATCTCGCGAAAAAACGACAGCT
CTATTTCTCTCAACAAATGGAAACGAGCGATGGTTTCCGAAAAATGATGCTCGCACTGAA
ACCATCTCATCTCTCTCATATAGCGTCGCTAAACCTTAACCAATCAGCCTTTACGCTCT
CGCGCCTCGTATCTAAAAATGCTATGGACACTTCGTTATACCTCGCAAAATGAGGATAC
CAGGAACACCGAGTAAAAAATCACCTTAGTGGAGGGAAGAGACCATTAAGCATGTCCACC
TTTCGAGTTTCGAAAAATGCATCGCTCTCTAAGTGTTCCTTTAAATTTTGTGTGAAG
ACAATAATTTACAAAGAAGACCTTTTATTTTCAGATTCTCCGCTCTTCAAGATCTTTACCTT
CCATCATCTGTACCAACCATAGACTCATCCCACTGAGCGAGGCAAAATATCATCGACATG
ATCGTCAACAATACACAGACAAACATCTCTGTCTCCCACTAATAGCTTGGTTACCAACAGCT
CTCCACAAACATTTGCATTCTAACAAAGTTCAAAAAATCAAAAAGACGAAGGAATTCGGTGA
TTTTGAAAAATAGAGAGCTAACAAACAGTTTCAACAATTCAAAAGATGATTTATACGGCA
CGGACGAGAATTTCCACCTCCAATCATAATATCAAGTCATCATTTCAACTAGAAAAAAC
CTCAACCTTATCAATTTCTGTGGACGCTATGACAATGACACTGACGAAGAGATCTCCACTC
CAACAAGACGAAAAATCTATTATTTGGGGCAACATCTCAAAACATAGAGAAAGCAGACCAT
TGTCACATCTCTCTCGCCATCGTGACAAACCAACAAGTGCAGAGACGCAATTCATATCTT
CCACGATCTCTTCGCGTTTAAATTTCCAAAAGGCGTCAATCTCTTCAAAATAGATTATCAG
CAAATTCAGATTCCTCATTTTCGAAAAATTTACGAATGTGCATTCATTTGCTAAAGGCC
AGTTTTCCTCGGCTTACCAAGTTACGTTTTCGCCAAACAAACAAAAAGATGCAATCAAG
CCATTTAAACCAAAATAATATCTTGAACGCAATATTACTGGAATTTAAATATCAAT
ACGAGGTAAACAAACAAATTAACAATGGATCAAGAAGGGAAGGAATACATCATCGATTACA
TCAGTTTCCTGGAAATTTCAAATTCATCTATATTATGACAGAATTTGGCGAAATGGTA
ATTGTTGGATTTTACAGAGCAAGTTATTCGAAGAAAAAGGTTTGAAGATTTGGA
GAATTTGGAATACTCGTGGAAATTAAGCTTGGCTTATGAGTTTCATTCATGATTTCTGTG
CAATTGTGCATCTTGGACTTGAACCCGCAACGCTATGATCACATTTGAAGTAACTCA
AATAGGTGACTTTTGAATGGCTACTCATTTACCGTTGGAGGATAAAGTTTGAATAT
AAGGTGACAGAGATATATTGCACAGAAATCATTTCTGATTGTACGTACGATTACAAAG
CAGATATTTTTTCCCTGGGTCTGATGATTGTGAAATTCAGCGAACGTTGTGTACCTG
ACAATGGCAACGATGGCATAGTTGAGATCGGGTGATTTATCGGATGACGGAAGATTAA
GTCCACAGATATTCATTCGAATCATTTATTCAGACATTACGAAAGTACGATCAAAAT
ATTATTTGATTTTGAAGAGACAATATCAGTGGTAATAGTAACACGCTGGCACCTTCA

FIG. 1 - 55

CTGTTTCATAACAATAGTAATATCAACAACCCCTAATATGAATAATGGCAACGATAATAATA
ATGTCACATATCGCCGCTACCAAGAATCGTCTTATTTTCATATAAAGTTCTTAAATATCCCG
CATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAAATAGTACGATGGATGA
TAGAGCCCAATTTATGAGAGAAGGCCACGGCAAAATCAAATCTTACAAACTGAGGAATGCC
TGTATGTAGAAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTTTGGACCTA
AGCCAAAATTTTTTATATGA

YJL187C, 819 aa (SEQ ID NO 158)

MSSIDEDDEEDFEMLDTENLQFMGKMFQKQAGEDESDDFAIIGGSTPTNKLKFPYPSNNKL
TRSTGTTNLKLSNTALSEANSKFLGKIEEEEEEEEGKDEESVDSRIKRWSPFPHENESVT
TFITKRAESKNSPISLKQWNRWPKNDARTENTSSSSSYSAKPNQSAFTSSGLVSKM
MIDTSLYPAKLRIIPETFPVKKSPLVEGRDHKHHVHLSSSKNASSLSVSPNLFVEDNNLQED
LLFSDSPSSKALPSIHVPTIDSSPLSEAKYHAHRHNNQTNILSPTNSLNTSSFPQLHS
CATGKKIKRARNVSLKNNRELTNSLQKQDDLYGTDENFPPIIISSHHSTRKNPQPYQFR
GRYDNDTDEEISTPTRRKSIIIGATSQTHRESRPLSLSSAIVTNTTSAETHSISSTDSPL
NSKRRLISSNKL SANPDHLEKFTNVHSIGKQFSTVYQVTFQAQTNKKYAIKAIKPNKY
NSLKRILLEIKILNEVTNQITMDQEGKEYI IDYISSWKFNQSYIIMTELCENGNLGDFLQ
EQVIAKKRIEDRWIWKIIVELSLALRFIHDSCHIVHLDLKPANVMITFEENGLKLGDFM
ATHLPLEDKSFENEEDREYIAPEIISDCTYDYKADIFSLGLMIVEIAANVVLDPNGNAWH
KLRSGLDSADGRISSTDIHSESLSFSDITKVDITNDLDFFERDNI SGNSNAGTSTVHNNS
INNPNMNMNNDNNVNNTAATKNRLILHKS SKIPAWVPKFLIDGESLERIVRWMI EPNYER
RPTANQILQTEECLYVEMTRNAGAI IQEDDFGPKPKFFI

YJL188C, 809 bp, CDS: 501-809 (SEQ ID NO 159)

AATTCCCGCATCGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTAGC
ATGGATGATAGAGCCCAATTTATGAGAGAAGGCCACCGCAAAATCAAATCTTACAACTGA
GGAATGCTGCTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTGT
TGGACCTTAAAGCAAAATTTTTATATGATAAATGGAAACAAAACCTTGTGTTTTATAC
TACTTTTTTCCCAACAGTGCATTATGGGCGCATTTGTATAAATAATCCAATAACGAAAAAG
AGTGTAAATTCAGTCCGGTAGTAAATACCATGTAAACCTTAGATGAGTTTATTTTAAAGTA
CAGCGCTTCAAGCATTTTTATTTTTATTTTACAGATGTAGCAGATAACCAACCGTTAAAT
TATATTTATATATATATATATATATATATCAAATACGACGATATACATATATATTGAGAA
AAGGGAAGGATGGAAGACAAATGACAAAAGTTTGAAGCATAAATATGTTCTCGCTTAG
ATGTCATCTTGTGTTCTTCCAGTTTCTTCTCTTAGCGTTGTAAACGGATAGTGTGTTG
GTTCTCAATCTGATCCATTGTGGCAATGGTCTGTTTGTCTTCTTAGCCTTAGCCATTTT
TGCTTGATCTGAAAGACTTTTGAGCCTAATTAAGGGAACATATCGTGACATACGTA
AGTGACAAATGTAAAAAATGTTAGTAACAATGTTCAAACATCAATATGATGACATCA
CGGATCCAAGGCAATACCACCTGACATAA

YJL188C, 102 aa (SEQ ID NO 160)

MTKSLKHVYLRLLDVHLGSSPVSSLSVVTDSVVGSDPLWQSVLLLSLSHFLDLSERL
LSLIKRETYRAHTKCTIVKNVSNVQTHQYDAFTDPRQYHLT

YJL189W, 1042 bp, exon1: 501-506, intron1: 507-892, exon2:
893-1042 (SEQ ID NO 161)

TATTCAAGAATTATTTACATCTTCCAGCGAGTAAACATGCGCGTGGTAATCGCGCGTCC
TCAATATTTGAGTTTTCAAATAGTGAGGTGTTGGATGTATAGAGAAATTACACACTTTTA
AGTATGTGATGTATGGGCGCACAGTACCAATTTTCTTTTCTTATTGTTTTCAGTTTTCAG
TTGATTTTCAAAAACCTTATGGGCGTTTATGGCTCCGGCTCAAACCTACCCACCACGCG
CGAGGCGGAGGCAACAGTACGCTCTTGGCGGGGACGCCGAAGCGCACTCTTGTGTTCCAA
GCTCAATGGTCTTGCCTTACGCTCGCGCGTGGGCTAACTAACGCAATTCGGCTTTTGG
GCTGTCGAGAACCAGAAATTAATCTTCGCTCTGATAGATACCTTTAAACCTCTCATCTTAAT
ATACCTTCTACAATTTTGGTACATTCATATTATACTGAAAATTCGAAAAAGACAAGCAA
ATAAACACAGATAGATCAACATGGCTGTATGTTAGAAAGATATTATAATCCAGTTTGA
TGCTGAACGTATCAATAGCAAAATTAATAACCATCAATCTAAATGACCTTACCACCTAC
AATTTGATGATTAATAAGCAATGTGTAAATATAGGGAAGGATTAGGATGCTTTTCAAC
CATACTAAAATTTTCTTATCCGAAACAGAAATCTAAAGTGCCTACTACGCAGATTAAAA
TATGGTCATAAACTGCTTATCTGAGAACTTTTGGTGGTCCAGCGTGGTTTATGTCAGGT

FIG. 1 - 56

GGTATTCGCTTGGATCCGTGAATGCATCATATTGATGAGTTTGAACATTGTTACTAACAT
TTTTTACAAATTGTACACTTCGTATTGTGCAGCATATGTTTCCTCTTTAATTAGGCTCAAAA
GTCTTTTCAGAAATCAAGCAAAAAAATGGCTAAGGCTAAGAGCAAAAACAGACCATTTGCCACA
ATGGATTCAGATTGAGAACAACAACATATCCGTTACACGCTAAGAGAAGAAATCGGAG
AAGAACCAGATGAACATCTAA

YJL189W, 51 aa (SEQ ID NO 162)
MAAQKSFRIKQKMAKAKQNRPLPWIRLRTNNTIRYNKRNRNRRTKMMI

YJL190C, 893 bp, CDS: 501-893 (SEQ ID NO 163)
TCTCGACAGCCCAAAAGCCGAATTTCGGTTAGTTAGCCACGCGGAGCGTAAACGCAAGG
ACCATTTAGACTTGGAAACAGAAGGAGTCGCTTCGGCGTCCCGCCAAAGGCGTACTGTTTGC
CTCGGCTTGCCGCGTGGTGGTGGTAGTTTGAAGCCGAGCCTAAACCGCCATAAGTTTTT
TGAAATCAAGCTAAAAAATGAAAAAATAAAGTTAAATTGGTACTGTGCGCCCATAC
ATCACATACTTAAAAAGTGTGTAATTCTCTTATACATCCACACCTTCACTATTGAAAAACT
CAAAATATTGAGGACGCGGATTACACGCGCATGTTTACTCGCTGGAAGATGTGAAATAA
TTCTTGAATATTGGGTTTCAGTTAGTCAATTTCAATCTAAATAATCTTAATCGACTATT
AATTTCTAAATTTGAAGGTTTTTAAATGGCCTTCAGTTCTAGTATTTTTATPAAACAA
GACCAACATACATATCAAGATGACCGAGCTTCCTGTTTAGCTGATGCTTTGAAATGCCA
TTAACACAGCTGAAAAAGACCGTAAAGCGTCAAGTTTTAATCAGACCATCTCCAAAGTCA
TTATCAAGTTTTTGGCAAGTTATGCAAAAGCACGGTTACATTTGGTGAATTTGAAATACATCT
ATGACACAGATCTTGGTAAGATTGTGTTCAAATTGAACGGTAGATTGAACAAAGTTGGTG
TTATTTCCCAAGATTCAACGTTAAGATTGGTGACATTGAAAAATGACATGCCAACTGT
TGCCAGCCAGACAATTTCGGTTACGTCATCTTGACCACCTCTGCTGGTATCATGGACCATG
AAGAGCCAGAAGAAAGCACGTTCTCGTAAGATTTTGGGTTTCGTTTACTAA

YJL190C, 130 aa (SEQ ID NO 164)
MYRSLVADALNAINNAEKTGRQVLRPSSKVIKFLQVMQKHGYIGFEFYIDHRSGK
IVVLNGLRLNKGCVISPRFNKIGDIEKWTANLLPARQFGVVILTTAGIMDHEEARRKH
VSGKILGFVY

YJL197W, 4265 bp, CDS: 501-4265 (SEQ ID NO 165)
CTTCTTCGGGGTTCCTCAATGTCACTGCCATCTCTAAAGTAGATAGAAAGGCGATCGCT
ATTTAAAGTGTCATGACTTCTTAACGAGAGGTGTCCAGCTTCTATTTTGGCTTTCCCTAT
GTGTCATTACTCTAGGTTATGGTATCATGGCATCTGTTGTCAAGGGTAAACGCAACCTCTG
CGTAAGAGATACGCTTACGATAGCATGTAAACAGCGTATATATAATCTATATGTATTTCGAT
TAATCCAACACTCTCTGTTGTGTAGTCTAATGTTTCGAAAAAAGGTACGCTTCCCTGTTAT
AATCAGGTATATTTCTGTTATCTTATAAGCTAAAAGATTAAAAATTTTCCACTTTCCCT
GAAATTTGGTTCGGTTCTGTGAAAAATATATTACGTATTGAAGAAGTGCATGAAGATAAA
AGATGGGATTACTGAAAAATAAAGGGAGGAAAAATCTGCAGAACGTGTGTGTTTCAATC
GAAGTTTCTTCAATCGAAAAATGGGTCTCTCAGATGTTTCAAGTCGTGAATGTTTCAATGG
TTTATATGAAGATTCCGATTTTCAACGATGGCACAACACCATGTGATCGGTTGGGAGTGG
ACTTGATGAATGTTCTAGATGACAAGGATGAAATAACAGCAAGTCTGTCCAGTCTCAG
ATCGTGAATTTAGGATACGGAATCCGATGCTTCCGCTTTTCTTCAATTTGCTAGCGCTA
ATGAGTTAATAGCTGAGCCACACGCTCAAGTGAACATAATCTTGAACATAATGGTCAAG
ATGGAAGAAATGTTTGAACACCAACAGACAGCTGGTTGCTAGACTAATAGAAGAAAAACA
AGGAAACGCAAAAAGAGGGTGATAAAGTCTGTATTGTTCCCAAGGTTTGGTACGATAAAT
TTCTGACCCCGATGTTACCGATCTGAAGATATAGGCCCTTAATTAACACGATGATTT
GCAGAGACTTTGAAAAATTTTGCTTGAGGATTACAATAGATGTCCTATCTGCTTATTTG
CAGAGCCTGTTTTCAATTTTCTATCAGAAATTTACGGCATGACAAGTGGCTCTTACCAG
TGGTAACATAATTTGGTTATCAACCAACACAGGGGAGTTAGAGACGAATAACAATAAAT
GGTTTTTCAGACTACATTACCTGACCGAAAAACAAGACGGGAGGAAAGAGGACGATGGCC
AGGACGATTCAATAATGTACCTTCGATGCTTCGGTTGAATTTAGTACGTGATTTGGTTG
AAAGAGATTGAATCTGTTTTTTGAGAAAGCTGATCATCTAGACGTGAATGGCGTGGATT
TTAAAAATTTGGTTTGTGTGTCAGAGGATCTGATATTGCCACAGATAGCAATGTTAGTACT
TTTGAATTTCTCATATGAATAAATCCGCTTCAATTTCTCGAATCACCAGATAAGAGAAC
TACTAAATACGACATGTTTGAAAACCGTTTAGACAAGATAACTTCAAAATCCGAGTGACC
TTGTCATAGAAAAATAAACCTATAGAAGGGAATCACCATTGGCCTTCAAACTATTTTGCTT

FIG. 1 - 57

ATAATAAACTCGAACCGAGCATCAGGTACTACTGGTTTGGTCAATTTGGGAAATACATGTT
ACATGAATTTCTGCGTTGCAATGCCTGGTACACATTTCCGCGAGTTTCGCTGATTATTTCCCTTT
ATGATGGTTTATGAAGACGAAATCAATGAAGAAATCTCTTGGGTACACCGGCTATGTGG
CTAGGGCATTTAGTGACTTGGTTTCAGAAAGTGTGTTCAAACACAGGATGAGCATTAATGCGAAA
GAAATTCGCTGCTTTCCCCCTTCAATGTTCAAATCCCACTATCGGGCACTTTAATTCGATGT
TTTCTGGTTTATATGCAACAGGATTTCTCAAGAAATTTTTCAGCCTTCTCTGTTAGACAGTTTAC
ATGAAGATTATGAACAGGATATAAAGAAAGAAATACACAGAAAACCATCAITTTATCTCTCG
GTGATGACGTTGAATGTGGAATGTAGTCAAGAACTGGCAGACGATCATTTGGGAGATGTC
ATTTAAAGAGAAATTTGTTCCGTTATAACGGATTTTATTTGTCGGGATGTACAAATCAACGC
TATATTGTCGGAATGTCAAATGTTTCTATAACGTTTTCACCGGTATATAATGTTTACAT
TGCCGCTTCGCGTTGATACAGTGTGGGATAAACTATAAAAAATTTTCCATGAGACTTTC
CACCCTTCTCTTGAAGTTGAGTTAAGCAAAATCGTCCACTTATATGAGACTTGAAGATT
ATGTTGGTAAATGTGCGGCCCTAGATCCAAATACACTATTTGGCTGTGAGATTTCCTGATA
ATCAAACTCTATGTTAACTATGAGTCAACAGAGTTCGAATGCTCAATTTTAACTTGTGCGAG
AATTGATCAAAACCTGCTGATGACGTTATTTTATGAATTACCAGTAAACAAATGACAAAT
AAGTAATTTGTTCCCGTATTGAATACTAGAATTGAAAAAGGCTACAAAAATGCAATGTTAT
TTGGAGTCCCTTCTTATTACGTTAAAAAGAGTGAATTGAATATCCAGGTGCAATAA
GAATGAAATTCGAAACAGGTTTGTCCATTAAAGTGGTGGGTATATCCAGTTTCTCGAACC
CTGTGAGAAATCGAACCGATTGTTGCTGATGCTTTTCCATTATTAGTAGAAAAATATCCAG
ATGTTGAATTTGCAACAATATAAAGATATACTACAGTATACGTTCTTAAGGTGACTGACA
AGGATAAATCTCTTTTTCATCAAGATTCTGCTGTAGAAAAAGACGCAATTTTGCTA
TGAATAACCGAACAGGCTTAATTTCTGGACCCCTATCTCCAGTTAAACCTTTGACAAAGC
CTACAGATATAGACGATAAACTTGAAGATGTGGTGAAGGATATCTACAAATATCCAGCTCT
TAGTAGATTGCTGTGAAGGGTCTTATGCAAGTGGATGATGAGGAGATACGAGGGTA
GTGAAGCAAGAAATTTTCCAAAGCCCTTCCAAATCGGAGATGATGAAGAAAAAAGAAAA
CTGTACAAATTAATGAAAAATGTAATAAATACTAATGATCGGATGAAGATATGGAACATAA
CAGATGATGTTTGAAGAAGATGCAAGTACAGAGCCAGAATTAAACAGATAAGCCAGAGGCGT
TAGATAAAATTAAGGATAGCTTTGACTTCCACTCCGTTTTCGATCTCTTCTATGAATGATAT
TTATTTGTTTGTGAGTGGAGCGAATTTGGGTTTCAAATGAGGCAATTTCCGATGAATAATAT
ATACTCGGAAAAATCCAGCTACTTTGCCCTAACAAAGAGTGTGAGAACCGCTAAGTTTGGAAA
GATCTAACGCTTAAGGAAAGAACCAATAAACCCTTGGACGATTTGCTCCAATTAATTTCCAAAC
CAGAAATACTAGGATTAACCGATTCGTGGTACTGCCCTACATGCAAGGAACATCGTCAGG
CTACCAAAACAAATACAACTTTGGAATACACAGATATTCTGCTAATTCACCTTAAAGGT
TTGAAAGTCAAAGGTCTTTTAGCGATAAAATTTGATGCCACGGTTAATTTCCCCATTACAG
ATTTGGGATCTGTCAGGTACGTTGCTATAAAGATGATCCAGAGGTTTAATCTATGACC
TGATGCAGTAGATAAACCACTATGTTGGTGGTGGTGGTGGGCATATACCGCGTACGTAA
AGAATTTTGCCGCAACAATAATGTTACTATTTGATGATTTCTGAGTAACTGAACTCGC
CAGAAAAATAGTATAGCTGGATCGGCTTATTTGCTATTTTACATTTCGCGGTACATAAAGATG
GCAATTGGATTAGCGAGCTCTAAACTACAGGAATAATCCAAAGTCAAGCCACAGGATATG
ATGAGCGTATCAAAAGATATACGATGAACAGATGAAGTTGTATGAATTTAATAAGACTG
ACGAGAGGAGATGTTTCTGATGATATGATAGAATGTAATGAAGATGTGACGCGCCCTG
AATATAGTAACTGTAGTTTGGAGGTTTGGGCATATTGAAACTCAGGACTGCAACGACGAAG
ATGACAATGATGATGGTGAGAGGACAAATTCAGGTAGGAGAAATTAAGATTGTTGAAA
AAGTCTACAAGATAAATCAGGCTTGGGTTTATCGAGTACGCTGAAATATCTGAGGAT
GCCCAGAAAAACGAGTCGCTGATTTGAATTTAAAAAATGGTGTGACACTAGAATCGCCAG
AATAA

YJL197W, 1254 aa (SEQ ID NO 166)

MGSSDVSSRECSLVYNEDPDFDTGTTPCDRLGVGLMNVLDKDEIKQESVPVSDREIEDT
ESDAVSVSFASANELIAEPHAASETNLGTNGQDGRNVLEQORDVVARLIEENKETQKEG
DKVCIVPKVWYDXFPDPDVTDPEDIGPINTRMICRDPENFVLEDYNNRCPYLSIAEPVFN
LSEIYGMTSGSYVVTNLVINQTTGLELEYNKWFFRLHYLTKQDGRKRRHGQDSDIMY
LSMSALNLVRDLVEKSMNLFPEKADHLVDVNAVDFKIWFVSEGSDIATDSNVSTFLNSSYE
ITPLQFLELPKLLIPDMFENRLDKITSNPSDLVIEIKPIEGNHWPVSNYPAYNKLEPA
SGTTLVNLNGTGYMNSALQCLVHPIQLRDFLYLDGYEDEINEENPLFGLHYGVYARAFSDL
VQFLQNRMSIMORNAAFPFSMFKSTIGHFNSMFSGYMQQDSQFLAFLLDLSLEDHLNRI
IKKEYTEKPSLSPGDDVNDWNVVKLADDTWEMHLKRNCSTITDLFVGMYSSTLYCPEQ
NVSITFDYNDVTLPLPVDTVWDKTIKIPFMNSPPLLELVLSKSSSTYMDLKNVYVKRMSG

FIG. 1 - 58

LDPNLTFGCEIFSNQIYVNYESTESNAQFLTQLQELIKPADDVIFYELVPTNDNEVIVPVL
 NTRIEKGYKNAMLFVGPFFPITLKEDELNPNPAIRMKLQNRVHLSGGYI1PFPPEVGNRTD
 FADAPFLLVKEYPDVEFEQYKDIIQYTSIKVTDKDKSFFSIKILSVEKEQQFASNNRTGP
 NFWTFPISQLNLDKATDIDDKLEDVVKDIYNSVSLVDCAGVLMQVDDGEGTEGSEAKNFS
 KFFQSGDDEENKETVTNNENVNNTDRDEDMELTDDVEDASTPELTDKPEALDKIKDS
 LTSTPEALLSMNDIIVCEWSELGSENEAFSDDKIYNWENPATLPNKELENAKLERSNAKER
 TITLDDCLQLFVSKPEILGLTDSWYCTCKEHRQATKQIQLWNTPDILLIHLKRFESQRSF
 SKDIDATVNFPIYDLDLSRYVYKDDPRGLIYDLYAVDNHYGGLGGGHYTRYVKNFADNK
 WYFFDTSRVTFETAPENSIIAGSAYLLFYIRHKDGNGLGSSKLQEI1QKSRHYDIERIKKI
 YDEQMKLIFYFNKTEDEEDVSDDMIENEDVQAPEYSNRSLVGVHIEQDNCNDDNDGGE
 RTNSGRKRLLLKKVYKNSGLGSSTSEISEGCPENEVDNLNKNVTLLESPE

YJL198W, 3149 bp, CDS: 501-3149 (SEQ ID NO 167)

TGTCGTATTCCACTGATTGGATGTATGTTGCATGGTGTAGATTTGTAATAAATCATT
 TCCACTGGTTTCTAGCAGAGGTAAGAAAAATCAGTAGTAGCGGCAGCAGCCAAAGAAAAATG
 CGAGCTGGCAAGCAGCGAAGGCCATCTGTGCTGCATTTCACACTCCTTGTATGATCGC
 ATACCGTAAAGAGGTGCCTTGCTAGGCGTATATGATCTCAAGCAACAGAGAACCAAC
 GGTTCTCTTCTCTTCTTATTTCGTATATGTCTTCCCTTTTACTATGGGTAAGTGCGCC
 TAAAGCGGGCGCTCACAATATCGCCGACGTACAGCGCTTTTCTTTTCTTTTGTGTTTTT
 TTTGCGCTGCTTCTCGAAGAAATGAATGGCTCACTGAAAAATTTTGATTCATCGATATAAA
 GAACACTGTTCACTTCGATGTCATCCGCCCAATAAAGTTGTTTTAGGATAAACAGTAA
 GTGGTAGCTCGTACAGGATCATGAGATTTTACACTTCTTGAAGTACAATGCTGTCCAG
 AATGGCAAAACCATATATGGAATACAGCGAGCTGAAAAATCTTATTACACAGCTCTAAAC
 CAGATGAATCTCAGGTTGGTGATACGAAGAAGGATTTGCGCAGGAAGAGCTCTAAACA
 TTACAGATAGGTTCAAAAAACAAGTTTCTTTAAAAAATGCGAAGGAAGATGCTGTCTCCG
 GTATGAACAAGAATGCGAGGCATCGTTGAGGAAACCATCGAGTTGCGAGAGTGGCTCATG
 CTCAGACGGTGCCTGCCAAACCTTCTCCTTTCAGAAGAATGAAGGAAAAGATATTTTACA
 AAAGAAGGTGCTCTCCGCATCGTCCGCTCTCTCCACGGCCAAACGAAAAATCTGCAATTAG
 ACACCTTATGATACGTTTGTGGTGATTAAACAGCTGAAAAACAGAAAGTAGATGATTTTT
 ATAAGAGGACAGAAGCGAAGTTCTACGACAAAATTTGACGCGCTGGTGAAGGACCTGAAGA
 AAATCGGAGTTATAGAATACGATATCGACGATGATACTCTGTTAAACGAACCGATTGGCA
 GCACAAATGACGAAGTTCCCCCACTAGACTGGATGATGACGAAGCAGACGACGAATTTT
 ACGATGATCAATCTAATATTGAAGATAAATACTGCTTTGCTGCATCATTCGCGAGTATAACA
 TTAAGTCTCAGAAAAAATCGCTGTGAAGAAGTCGATCGTAAACCTATATATCGATCTTT
 GCCAGTTGAAGTCGTTCAATCGAATTGAACCGCATTTGGGTTTGCAAAAAATACAAAGAAAT
 CAGACAAAGTTCTTCACTTGAATACAAGAACCGAACTGATCGAATCGGAGCAGTTTCTTCA
 AAGACACATATGCAATCCAGGCAGAAACGATCGAATGTGCTAAATTCGCAAAATTTCCGAGC
 TAGTCACATTTTATGCGCGCATCACTGACCGGCTCATAATATCTCGCATAGCAAGCAAG
 AGTTGGAATCTTACCTGCATGACCACATTTGTTGGGAAAGAAAGTAACTTGGAAAGACA
 TGTGGGAGTGCTATCGCAAGCTGACGAGTTGACACCAAGGAACAGAAATATAATGCGAA
 ATAAGCTGGTAGGCAAGTTAGATTGGAATACTACAGATGGCCACTACCCAGACCGATAA
 ACTTAAAAATTCACGTAGTATAAACACAGTTGCACTACCGAAATTTTTCACCAAGAAAAG
 CATACAAGATTTACTTTATTATTTAGTCACTGGACTCTTGTAGGAATAAAGACCTTCA
 ACGAGCTGTCTCAGCACCGCTGCATGGCCCTTGTGAGTGTGTGCGCTTTTGTGGGGTCA
 GTAGGGCCATCCCATACACATTACAGCATTCCTTGTACCACTACTTGTAGTCTTTTCA
 AAGTCTTAAAAACTCCGACGGGGCTATAATGAGTGTGCAAGCGCTTCATCAGAAATTT
 TGGCGCCATGTGGTCTTCTACAATTATGATTCGTCTGGCAGGTTTACTTTGGGTGAAG
 TACTTGCACAAATATAACATCGCCAAAGTTCTTGCCCTGGTGGTTGTGGCCTTCTGGGT
 GTTAAACCCAGAAAGTCTTTTAAATGCGAATGTGTGCTGTTCTTCTATCAATGTGGA
 GTTCAATGTGCGCAGCACTGTTCTAACATATTCGTTGTTATCTCCCATTTGGATGCCA
 TGGATGCGAGATAGCCCATTTGCGCAAGCATTTGGTGTAGGTGTAGCGTTGGCTGCAAAAT
 TACCGTGGTATGCTCTTACCAATCTCTTCACTCAAAACCATATTTCATGTCTGATCTGA
 ACCGTATGGTATTTGGCTGGGGCCAAATCTTTGCTGTGTCATTTGCAATCTGGTATCTGG
 CCAATGCTTTTGGTTTGGATTTTATGTTTCACTACTTTCAGATGAATTAAGACCAAAATGG
 AAAAATTTAAGCCTATTAAAGACGAAATTCACAGTTAAGCAGTATATATCACTATTGCTGA
 CTGTGGCCACTATTTTGTGTGGTGTGTGGAAAGCCAGATTGAAGGTGCTTTTGGGTCA
 CAGTCAAAATTTGCAATCTTCCCATCGTTTGTGTTTTTGGTACCGGATTTACTATCAACAC
 AAGATTTTAAATGCTTTCCGTGGTCAATCGTATTTTGGCAATGGGAGGTATTGCTTTGG

FIG. 1 - 59

GGAAGGCCGTCTCATCTCGGGTTTGTCTATCAACCATTCGAAAAGCATTACAAAAGAAA
TGTAGAAATGATGGTGTGTTTTGCCATTCTATGTATTTTCGGTATCTCGATGTTGGTGTGGG
GTACTTTTCGTCTCGCATACAGTATCCGCTATTATCATCATCTCCCTTGGTGAAGAAGTTG
GTGACAAGCTTGGCAACCCAAAGCTGCTCTATCTTGTTCGCGTTGTGCATTATTGT
CATCTCTGGTGTATGGGACTAGCTTCTTCGGGGTTCCCAATGTCACTGCCATCTCTAAAG
TAGATAGAAAGGGCGATCGCTATTTAAGTGTATGACTTTCTTAACGAGAGGTGTTCAG
CTTCTATTTTGGCTTTTCCATGTGTCTATTACTTAGTATTGGTATCATGGCATCTGTG
TCAAGGTAACGCAACCTCTCGTAA

YJL198W, 881 aa (SEQ ID NO 168)

MRFSHFLKYNAVPEWQNHMYDSELKNLIYTLQTDDELQVDNEEFGAGKSSNITDRFKN
KPSFKNAKEDTSSGMNKDAGIVETIELRELPTAQTVAAKSPFRRMKEKIFKYRRSSSA
SSVSSTANENLQDITDYDTFVGDLTAEKQKVDDFYKRTAKFYDFKDALVKDLKKIGVIEY
DIDDDTLFNEPIASTNDEVPLDLDDDEDDDEFYDDQSNIEDNTALLHHSQYNIKSQKS
LLKKSIVNLYIDLQKLSFIELNRIKFAKTTKSKDKVLHLNTRTELIESEQFFKDYAFQ
AETIELLNSKISQLVTFYARITDRPHNISHSQELKSYLHDHIVWERSNTWKDMLGLLSQ
ADELTLPKETEYNANKLVGKLDLEYRWLPRLPINLKFTSINNVALPKLFFTKKAYKIYFI
ILVTGLLLGIKTFNDQHRCMALVECVAFLLWASEAIPLHITAFILVPLLVFLVKLTSD
GAIMSAAASASSEIILAAWSSITIMILLAGPTLGEVLAQYNIKVLASWLLAPAGCKPRNVL
LMAMCVVFFLSMWTISNVAAPVLITYSLSPLLDAMDADSPFAQALVLGVALANIGMSSP
ISSPQNIISMSYLPKPYGIGWQFFAVALPSGILAMLVLWILLFTTFKMKNTKLEKFKPIK
TKFTVPKQYIIITVTATILLWCVESIEGAFSSSQIAIPIVLVFPFGLLSTQDLNAPP
WSIVLAMGGTALGKAVSSSGLSTIAKALQKRIENDGVFALLCIPGLIMLVPGVFLVSH
YLSMTIIPLVQEVGDKLGNPKAAPILVFGCALLSSCGMLASSGFPNVTAISKVDRKGRD
VLSVITPLTRNGPASIILAFLCVITLGYGIMASVVVGNA

YJR049C, 2093 bp, CDS: 501-2093 (SEQ ID NO 169)

ACTGCCATCTCTTCCATCTCTTGAAAGATTATTAAAGTTCGTCGTTAAGTTCGCGCAATCT
GCTTTTCATTTAAAGACGGATCATATATTCTGTGCTTTTGTGTTTATCTCTTTACTTA
CTTGTGCTTCCATTCGTTGGCCTCTTTTATGGATTTTACCTTAGACACGTTCTCGGGCC
TCTGTAAACGTGAATAATCTTGTATCCACCTGCCGACTCTGCTGTGCTGCTTTGAAAGT
GTACCAGAACGTAGTTGGCCTTATCTACATTTCTACTCATTTTGAATGCACAGGTATCTG
ATTACTGATGTGGTGCGCCTTGCGATATAACGGTGTGTACATTTTATTTGTCTTTTAC
CATCTGAAATTATTTACCGCACTACGCAAGAAACGGAGAAAGGTATAATAGGGC
AAATGAGGATCATCGTGATCGTAAGCAAAAAAATAACAATAGGCTCCCTCAAGATAA
GTAGAGTAAAGCTCTTGAGATGAAGGAAATGACATGAATAATGGCGTAGATAAATGGG
TAAATGAGGAAGATGGTCAAAATGATCATCAACAACAATAATAACTTGATGAAGAAGT
CCATGATGAACAATGAGCAAAATGTAGTAACCTCAGGATATCGCAACGCCAAAGAAATGT
TGAGGAAAAATCAAGTGAAGCAGCTCGCGCAGAAGCTCCCTGTTGATAAAGATTATCAT
CTCTCGTGAACGGCAATGCAACAGTGGCGGGTGTACGAGCATTAACGGAACAAGAGGAA
GTTCTAAGAGTAGTAATACACACTTTCAGTATGCCTCCACGGCGTATGGTGAAGAAGTT
TGAGTAAAGATATATCTAATACCAGTGAACCTGGAGTGTGGAATAATTGATGATTGTTA
CGAACTCAACGATGTCTCACTGATTTCTTAAACAAGAGATTGGTGAAGTGGGTTTTGG
TACATTTTCCACGTGTGACTGTTTATGTGGATTCCGAATTGAAACACAGCAAAAAAATTG
CCGCTGGCGAGTTGTGGAAGATAGTAAATGTAGAAGATCAAGGATCAAGTATTGGACA
AGGATTTTCATCAGGGAACATGATGTTTTCTTCGATTGTGAGTGACTTTGGGTGGCCAGC
GTACTGTCTTTTGTGAAGTTCCATTTTTCAGAGACATGTACACCCGCTTATGTGCTTTT
CATTAGGGTCTCTAGGATTTTAAACAAATTTTAAAGTTGAACATTTCAGGGAGGATTATC
CTCGGATTATGAATCATAAATCAAGACAAATTTACGGTGTAGGTTGGAGTGCACAAATTT
ATCGTAGACACCGCCCTGAAGTAGACCCAAACAGGGGAAGAAATATGTGTGGTGGAAA
AATCAAGCACACACCACATTTTGAACGAAGTGACCATCGATCGTGTGTCGAGCTTCTTTC
TATCCATGTTAGAAATTGTATGGTAGCGGCTCATTAATGACCGTTCCGCGACCGGACGAC
TGATTGCTGCTACTCGGACTGGGTCCACGGCTTATCTTTGAGTGCAGGTGGGTCAATTGG
TATGCCAACCGTCAATGCAATTGCTTTTAAACCCATTGTGCCACATGCATTGAGTTTCA
GACCCATCATCTTACCAGAAAGTATAAAATTTAAAGTGAAAGTTCGATGAAGTCAAGGG
CTCCAGCATGGCGCGCTTTTGAATGGGAAGAGTGAAGTTGAATTGCAAAAAGGTGATTTTA
TAACCATATGCGCCAGCCCATATGCTTTTCAACCGTGAAGCGCTCGCCGATGAGTTTA
TTAACAGTATCAGTCGACAACTAACTGGAATGTGAGGGAACAACAAAGTCCCTTTACGC

FIG. 1 - 60

ATATTTTGTCCAAAAGAACCAAGAAAAATATGCACATGAGGCGAACAAAGTCAGAAATC
 AAGCAGAACCCTTTAGAGGTAAATAAGAGATAAAATCTCTCTGGAAGCAGACCGCTACTAAGG
 AAAACACAACGGAAGCGATGATGAGAGCGACGATGAGAGTGTAAACTGCGGAAGCTTGCA
 AATTTAAAGCCTTCGAGCGTCCCAAAACCTTCTCAAGCAAGGTTTTTCAGTATATA

YJR049C, 530 aa (SEQ ID NO 170)

MKENDMNGVDKWNNEEDGRNDHNNNNLKKMMKMNNEQIDRTQDIDNAKEMLRKISSE
 SSSRRSSLLNKDSSLVNGNANSNGGGTSSNGTRGSSKSSNTHFQYASTAYGVRLMSKDISN
 TKVELDVENLMIVTKLNDVSLYFLTRFVWVHLVHFPRVTYVDSELNKSKFPAAGELCE
 DSKCRRESRIKYWTKDFIREHDFVDFDLVVTLLGGDGTFLVFSSIFQRHVPVPMVSFSLGSLGF
 LTNFKEHFHREDLPRIMNHKIKTNLRLRLLECTIYRRHRPEVDPTNGKKICUVEKLSLTHI
 LNEVITIDRGSPFPLSMLELYYDGSLSMTVAQADGLIAATPTGSTAYSLSAGGSLVCPVTNA
 IALTPICPHALSFRIILPESINLKVYSMKSRAPAWAADFQDKRIELQKGDFTITICASP
 YAFPTVEASPDEFINISIRQLNWNVREQQSFTHILSQKNQEKYAHEANKVRNQAEPLEV
 IIRKYSLEADATKENNNGSDDESDESVNCEACKLFSSVPKPSQARFSV

YKR094C, 1255 bp, exon1: 501-508, intron1: 509-876, exon2:
 877-1255 (SEQ ID NO 171)

AGGTTGTGTTCTTCAATGATGGGCAATGCAATTTGGCGTTAAGCGCCTGAGCAATAAGGT
 AACACGCAAAATTTATGACATATTTATTTGCAACCTTTTCAAACTAGTAGATTTAGTGATT
 TATTACCTATTGGCATTTCATTTCTGTGTTCTATATGAGATGAGGATAGCGGCTTCTCTCT
 CATCGGAGGCCATATCATCTTTTCGCAATCTCTTTTAAATACTATTTCCATCCGTGCGCTC
 TAATAGATTTGTGTAGTTGCTGGGTGCAATCTTTCATTTTGTCTGAACCTTTTTTTTTTT
 TTTTCATGTTTTTCAGATTCTCGAAGTACCGCAATAGCATATGGCGGAATAATCGCCATAT
 GATCTCGCCTCATACTAGCCATTACCCATCTATCCAGGCAATTATGGGTATGCAACICTATA
 ATCTCAAAATACACAAATAAGAGCAACCTTATATATCATCTTTTCCGTTTCAGCAAGAGGT
 AAGGCGACCAAGAGTTCAAAATGCAAAATGTATGTTACGCGCAATACAGAAATACTATGTTTC
 GAAATAATATGAGGATTATACGATAGCAAAAAGCGATAAACGAAAGACATAAATGGAAA
 ATGATGACAGAGCTCACAATTTATTAACAAGTAGCAATTTGAGAAAAACTATTACTCGCG
 GCAAGCTTCTGAGTTTACATTTAAATCTGTAGAGCAAAATGAAAAATGTCGCATATGTGCTG
 AAGGGTTGTGTTGTTCCATCTTATTTTGCATAACATAGTTATATTTTACTTGGTGCATAA
 AAAATATTTTTTACTAACGTGAAGTTTCTTTCTTTATGATGTACGCACGACCGTCTGTGC
 TTACTCCATAAATGAATCTTATTCCAATTTTGTACAGCTTCGTTAAGACTTTGACTGGTAA
 GACCATCACTTTGGAAGTTGAATCTTCTGACACCAATTGACAATGTCAAGTCCAAGATCCA
 AGACAAGGAAGGTATCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTTGGA
 AGACGGTAGAACTCTATCTGACTACAACATCCAAAAGGAATCCACTTTACATTTGGTCTTT
 GAGATTAAGAGGTGGTATCATTTGAACCATCTTTGAAAGCCTTTGGCTTCCAAATACAAGT
 TGACAAATCTGTTTGTGCTAAATGTTACGCCAGATTACCAACGAAGCTTACCACTGTAG
 AAAGAGAAAGTGTGGTCACACCAACCAATTCGCTCCAAAGAGAAGTTGAAATAA

YKR094C, 128 aa (SEQ ID NO 172)

MQIFVKTLTGKTTILEVSSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYN
 IQKESTLHLVLRLGGIIEPSLKALASKYNDKSVCRKCYARLPRAITNCRKRRCGHTNQ
 LRPKKKLK

YLR040C, 1175 bp, CDS: 501-1175 (SEQ ID NO 173)

AGCTCTCAAAACCACTAATACTATAAGTTCAAGTACAAGCACAGGAGGTGTAGGTTACGTC
 AAGCCATGCTCTTTACTTCGTTTAAATGTAGAAAACATCGCTTATTTGTTTCTTAAACA
 AATATATTTAGGTTCAAGGCTCTCGCAGGTGTAAAGAAAACCGGTGGTCTCCATATCTTTAA
 GPATGATAAATAAAAAAAACCTAATAAATTTAATTTGCTTCAAACTCTTTTCTTTT
 TAGTTTAAATAATTTCAAAAGCTTATCTTCATTGAACGCCCAATAGGAAAAAATCTCGGC
 AAATTTTTTATTTGCTGTCATCCAAGGCTATGCTAGAAAATTCAGAGCTTGGATGATTTA
 AAAAGACACTCTCAATCGAAGAGTTTATCTTCTGTTATCTGCTTTACCTGATCATCAATT
 CGCGCGTATGTTTCTAATCAAGTGATTTTCGATATCCAGTTACGAACCATTTTACACATT
 CCGTAAAATATTCGCTATCAATGATATTTGCTCCTCTCTTTCTCCTCATTTAAATATATC
 TCGTGGTAAGCTTCTTAAATCAGCCACAGTTTGTCTGCCAAAACCTTTAAGCTGTAGTCCA
 ATGACGATACACTTTCGAGGTCGCGAGCTGCAGATGCAGACATGGCATTTCTCACTGGAGT
 TTTTAAAGCATTTTCGACACCGCTTTTCCACAGTATACCTCATACATGATGCAAAACCAT

FIG. 1 - 61

TAACCTACCTCAACCTGTTGCTGACTACTACTATCACATGGTTGATTGGCCCTCAACAG
CAGATTTCACAACTGATATGCTCAGAGTTTTCGGTTCACCTCAATTCCAAACACTTCATTA
CGGCCTTTCCATGGTATACCTCTTTGCTAAACAAGGCCGCCACCACCATATACCTTTC
CCCAACACTTCAATAACAGGTGAGACAGAAGCTACCATGACTAATCATCTTATGCCAGCC
AAAAAACTCCGTTTCCAAATCTGTTCCCTTTCTCGACAGCGAACCGCCAGCTCCATGA
TTTCATGGCTTAATGAAGAAAAAGTACAAACAGCACTTATATCCGCATCAAACCTCTCTT
CAACATCCGAACCTAGTCAATCACAGAATGGTGCCCATGCCAAAAGCTTATATTTCCCA
TGGCGTTGTTGCGGAATCTTTGCAAGTTGCCCTTTAA

YL040C, 224 aa (SEQ ID NO 174)

MIFAPSFSLIKNILLVSLISHSFAAKTLTSSNDDTLARSAADADMAFFMEFLNDFDT
APFOYTSYMMQNLTLQPQVADYVYHMDLSTADLQSDIAQSFPTQFQITAFWPYT
SLLNKASATTYLTPHFITGETEATMTNSSYASQKNSVNSVFFSTANAGQSMISMANEE
NSTTALISANSSSTSRTSQSQNGAHAKSLYFPMALFGIFAVA

YL048W, 1618 bp, exon1: 501-590, intron1: 591-949, exon2:
950-1618 (SEQ ID NO 175)

GCACCCTTTTCTTTTCAATAACAAAAAGAGCTTGGGCATTACGTTTTCACACATTTT
AATATTTCCTTTTACATCCGTACATATAAATGTAACCCATGCATTCATGACAATTT
TACCTATTCTTTAAAGCCCTTTGTCACTCTTTATGGGAATGGCGCTACTTTAATTTTCC
GCTTACTTTGAAAAATTTACCAAGGCGAAATTGAGTCCGCTAGGCGGAAGTTCCAGGGCA
CGGTCAACGAACTTTGTGCTGTTTCGAACGAGGTCCTCGTGGAGGTTGACGACGCGG
GAGGAGCTGGAAGATGGAATGGAAGGACTGCAACACTCAGTAAGAAGGTTTCGTGGTAGG
GAACACTCACCTCTCTAGTTCCTGTAAATAATATGATCAAGTTTGAATCTCGTATTG
AAAAATCGCGAGTTATTAAGTGTGTAATTTAGAATACCGAAATAGCACAAGAAGAGATAA
GATAGATATCTGATAGGATAATGTCTTTACCAGCTACTTTGATTTTGACTCCGAGAGATG
CCCAACTTTTGTGGCCGCTAACACCCATTTAGGTGCTAGAAACGTTCAAGTATGTACAC
ATATCCCATACGATTATGTTCTATAGATGATAATAGGCTCGAAAGAAATATGTCCCCGA
TTTAACTATTTGGAGGTGAGAGGACCAAGGTAATTTAGAGAAATTTTGAACACGCC
GGGTTTGAAGAAGTTAGAAATTTCACTTCTTAGTGAGGTAAGGAGAAGAACTCAATAAG
AATATACACTCTCGACTCTCTCAAGATTATGAACCTCGATCAACACGATAAAGCTCAAA
AAATTCACCGGATATAATTCGTACTTTATGGATATGGAAGAAAACCTATATATGCA
CAAAATGAGCTCTTACTAAACATAATTTATCTTTCCTCTCTTTTGTAGGTCCACCAAGA
ACCATACGTTTTCATAGCTAGACAGATGGTGTTCACGTATCAATGTTGGTAAGACCTG
GGAAAAATTTGGTTTGGCTGCTAGAAATTTGCTGCCATTCCAAACCCAGAAGATGTTGT
TGCCATCTCTCCAGAACCACGGTCAAAGAGCTGTCTTGAATTTTGTCTGCACACTGG
TGCTACTCCAACTCGCCGGTAGATTCACTCCAGGTTCTTTCACTAATACATCAACCGGTT
TTTCAAGGAACCAAGATTGGTTATGTTACCAGCCCAAGATTAGACGCTCAGGCCATTAA
GGAAGCTTCTTACGTTAAACATTCAGTCAATGCTTTGACTGATTTGGAATCCCATCTGA
ATTGTTGATGTCGCCATCCCATGTAACACAGAGGTGAAGCACTCCATCGGTTTAACTGT
GTACTTGTGGCTAGAGAAGTTTGAAGACTAAGAGGTGCTTTGGTCGACAGAATCAACC
ATGTCATCATGCCAGATTGTACTTCTACAGAAACCCAGAAGAAGTTGAGCAAGTTGCA
TGAAGAAGCTGCTGCGCTGAAGAAGGTGAAGAAGAAGTAAGGAAGAAGTCACTGA
AGGTCAGCTGAAGCTACTGAATGGGCTGAAGAAAATGCACACAACGTTGAATGGTAA

YL048W, 252 aa (SEQ ID NO 176)

MSLPATFDLTPEDAQLLLAANTHLGARNVQVHQEPYVFNARNPDGVHVINVGKTIWEKLVLA
ARIITAIIPNEDVVAISSRTYQORAVLKFAAHTGATPIAGRFTPGSFNTYITRSFKEPRL
VIVTDRLDAQALKEASYVNIPIVIALTDLDSPSEFVDVAIPCNRRGKHSIGLVIWYLLARE
VLRLRGALVDRTPQFWSIMPDLYFYRNPVEVEQVAEEAAAEEGEEVEKEVTEGQAEAT
EWAENADINVEW

YL088W, 2345 bp, CDS: 501-2345 (SEQ ID NO 177)

CTTCCCATGTAGAATATCATTTGTCAAACATACTACTACCGTGAGAAATCCAATCTACTAA
AAGACCCAGCTAAAGTCCTTTTGGTGTGCTAATGGAACACACCGCTAATTTGGAATAGCT
TTCATCTGCTAAGCTTATTAACCGTCAATAGAAGACTTGAGTCAGGTGGCTTTAATGAGT
ACTATCTCTTTTTCCTTCCAAAGAGCACTATGTTGATAATACCGCAGTAATTTTTCG
AGTATCTCTGAGCCTAGAAAGGTTGAAGCTTATAAAACCGTGCAACAGCTTTATAGTGG

FIG. 1 - 62

GGAGTTTGGCTTCCCTCTATTGTATATTGATCGCCATCCCTACGAAGTTATTGGGAACG
CATCGTGAACTCTCACTTTAATGCCAGCGGTAGAAAAAAGTCATAAACCAATACACGC
CGGCTACACTTAGAAAAAATGACATTTGGCTGTCTTATAAAAGGACTTGACAGACCAAG
ACGCGTATAAATACACCAAGAAATGGCCTATTGGAGAAGTTGCATCGAAGGATTGTTGATA
TGGGGCTTGTCCCGGTATAATCGCCTATTACCAGTTATTTCATGCTATGCGCTCTAT
TTGGGTTTATTTCCTATAGCTATTCTGCTTATGGATGGACAGTACAGAAGAATCATATTT
CTGAGAATTGCTATGATGCTTCAACAAGCGTATAGTTACTTTAGAGAATCTGAATGGAACA
TPTTGAGGGCTATTGCATCTCAAAATTAAGAAATGGTAAACATGACTTCTATTGGAAGAA
ACAATTTGATGGGTCTTGGTTACAAGAATTGGTACTAAGACTGCTATTTCAGAAATG
AACAATTGGAGAACAACATTGTACGGTGTAACTGACCGCTCTAGGGGTGATGGACAGAG
CGATGGTGCTTGGCGTTCCATGGTTTAAATTCAGATGATGAATTCATATTGGCGGCGCAG
CTTTGGGTGTATCTTTAGCAAGATTTTCTCAGCTTGGCCAGTATGGTCCAGAAATATAA
TTGTTGCTCTCAGCGAAAAATCTCGTGAGCATTAAGATCATGGGTGAGGCATACCATTA
CTTCCTTAGATTGACTGGTGGTTCCATGGAAGCTGCTGTTGTTGGATTATTTCGAGTA
CGGAAGATTCTCGAGTAGTAGAAAACTCATACGACGGTCTGAATGGTGAGCTGCCCA
ATTTCGATCTTGTCAACATCGCTATATCCATTACGGAACATGAAGGTATGAAAGTTCTCT
TGCACGGCTCACCCAGTGATCAGTTAACTAATAATTTCTGGTCAAGATTAAAAATG
TATGCTCGGGAATAAGGGATTGGCGGTGTGTCGGTGTAAAAAGCCCCATGGTAACGAGG
CATTTAGCGGCTGGAGGATCAATCTGTAACATTGAAAGCACATGGAAAAAGTGGTCATG
TATATTACTACATTTGGACGTATACCCGAAGCAATGTTTCGCTCTATTAAATACCTTTTGG
AAAAATTTACCAATCGTCTCTCTTTATTGTTATTAGCACACAGCTCAGTTTCGTATCCA
TTAGTAGTATTTTGCCAAGCGCTGTGGCTTTATCTATTAGCATTCGCCATAAGTTTCATTAA
ATGCATTTATAAACAATGCTTATGCAAAATATATCTTATTTCAGATATAATTGTTGAG
CGTTTGTGGTTTGGTTCTGTCATTTGGTGATATCATTTGTTGTTTACACAGGCTTTCTTC
TAATACCTTCATCGGGATTATTGATGACAAATAGCATGGCATCTTGTGTTTTTACCTTTGA
TACTTTCCAGAAAAATTCACATCTCAGAACCACTATCATACAGTTGAAAAATGTGTGCT
TTTTATTTTCAGTTTGGTTTCAACATCTTTGCTAATGATAAATCTTGAATGGCTTTTAC
TGATCGGCACATTTGCCATTCTCTATGACATTTGTGAAGACCATTTGTTGAAGTTCTAGCG
AACATGAGGTGACAACTCAATCTCTTAACCCAAATAAACTGAGCGCAAGAGATGAGATG
AGCTCGTCGAGAAATCAGATGGATACAACGCCAGCAACCCCCAACACAGAAACAAAAAC
TAAAAAATTTAGTACTATTAAATTTGACAAATCCATTATTTCATAAACCCTTATTCGGAG
TATTTTGTGATGATGAATTTTCATGGATTGATATAATAAACAACATGGTTTTCAGCATGGT
TGATTTGAAATGTGGAGTTGGTTTGTACTTTGTATAGGTTGGCTTCCAGATTTGGCTAT
TGGATTATACCGTCACTGTTTGAATCTAAATCTGTGCTAGTAGAGTCAAGGAGGATGAAGA
GTTAG

YLR088W, 614 aa (SEQ ID NO 178)

MALLEKLHRRIVDMGLVPRIALLPVISMALCFGISIAILPMDQGYRRYISENALMP
SQAYSYFRESEWNILRGYRSQIKEMVNMNMTSMERNNLGMSWLQEFGKTAIYENEQYGETL
YGVMHAPRGDGTAMVLAVPWFNSDDEFNIGGAALGVSLARFFSRWPVWSKNIIVVFSEN
PRAALRSWVEAYHTSLDLTGGSIEAAVVLDSSTEDFFEYVEISYDGLNGLPDLNLVNI
AISITEHEGMKVSLLHGLPSDQLTNNFWSRLKILCLGIROWALSGVKPHGNEAFSGWRI
QSVTLKAHGNSGHDITTFGRIPEAMFRSINLLLEKFHQSPFFYLLLPARQFVSISSYLP
AVLSIAFAISSLNARINNAYANISLSEYNLVALLVWFVSLVIFSVVQAFLLIPSSGL
LMTISMASCLPLILSRKIHISEPLSYRLKNVAFVLSLSTSLMLINIFAMALLIGTLAF
PMTFVKTIIVESSSEHEVTTQSSNPDKTEPKDEIELVENHMDTTPATPQQQKQLKLVLL
ILNTFFISITLFLGLFFDDEFHGFDIINKLVSAMDLCXWSWVFLCIGWLPCWLLILASSF
ESKSVVRSKEKQS

YLR159W, 845 bp, CDS: 501-845 (SEQ ID NO 179)

TCCGTCCCAAGATAGCTTGATCATCTTAAGCGGGTCGATTTTACTATCCCCAGTTCGG
AAGAATAACAGAGCTCAATGCATATGCTGTTTATCGTCTCACAAGGCGGTATGACGTTT
TTAGCAATGTAATTTATATTAAGAAGATCTTCAGTCACATGAGTGGTGTATGTCGCCATTA
GAGAGCTATAAGCGCAGCTGAAAGCTGCTGGTTCCAGTTCGCTCATGCTGCACCAAGTC
ACTACTCATTGCTCGCATTCATTGCTACTCATCTGCGAGTGAGCATATTTGAGATCTGA
CTTGCCCAAGGAGATTAGAATCAGTAAGACTCTGATCTCTAGAGATATTTCTGACAAAG
AACCACCTAAGCCATGCAAGTTTATTTTTCATTGTTGGTGGCGCAAGAGGTGATGAAG

TTTCTTCTTGACAAACGCCAAGCCCGATAGGTGAGACAAATCTTGAAGTAATGGACCTC
TGAGTAAGCATATCAGTCGAATGAAGTTCCAATATCGGTTGGCCCAAGGAACAGCTAGGCA
GCAACTCGCGCAGTGGCGCTCAAAAACTAATAAGTAACACCACCTGGCTTCCGGAATACT
ATTTCTCTGATCTCTCATTTTCTGTTGTACAGCAGTGGGACAGTAGAGCCATTGAAAAAA
CTACAAATCATATCTTGTATGCGGCCCGCAAAACCAAGAGATTATCTCTTTGAGACATTGTG
AGCTCCCTCCGTTTCGCAACCGTGCTCTCTGTTTTCATCACTATATGCAACGCTCTTTCCAAA
GACCTCGACATTTGCACGTGGCGGAGCCATCGCCCGGCTTCCATATGTACGGCTGCCACA
CCTAA

YLRI59W, 114 aa (SEQ ID NO 180)
MKFGYALAKEQLGSNSRSGVKLISKHWLPEYYFSDLSFSVVQWDSRAIEKTTIISCM
RPAHQEIYPLRHCETLRSQPCSLFSSLYARSFQSSCTLHVAEPPGFMHYGCHT

YLRI67W, 959 bp, CDS: 501-959 (SEQ ID NO 181)
ATCAAAAGAGTGTTTCAAGTAAGTAAAAACATTTGAGCCTCCCCATTTGTTGAAAGGAGA
GAAATTAACCTGGTTGGGGTTAAATTAATTTGATGGGTATATTAATTTGCAACCGCAAGGT
ATCGATAATAAATATTCTACAAAACCTTTATCAAATAGTGGTGAAGTCTTTAGTGCGATCT
ACCTGGGGTTAAATGGAACGAGAAGTTCTTGAGATATCTTTCCTGTTTACCTCCGTCGATCTC
TGTAAGGAATTTGGGTTTATCATTTATCATTTATTTAGTACAAAATTTTTTTTTTGGCCC
GGGCGCACTTTTCAAGCGTGGGAACTCATCAAATGAAAACTAGATACCTTTTAGACT
TATTAATGTGGTTAAATATTTTGTAGATGTTGCTTATATCAGAAATCTCCTTACTCTTATC
TTTTTATTTCCAAATCAAGAAGTCACAAGATTACTTGGTAAGAAAGAACGACGTAAATTTT
AATTTTGGCCGACAGCAAGATCAAATTTTCGTCAAGACTTTAACCGGTAAAGACTATTA
CCTTGGAGTTGAATCTTCTGACACTATTGACAAATGTCAGTCCAAGATCCAAGACAAAG
AAGGTATTTCCACTTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTTGAAAGATGTTA
GAACCTTGTCCGACTACAACATCAAAAGGAATCTACTACACTTGTGCTTTGAGATTGA
GAGGTGCTGTTAAGAGAGAAAGAAAGAGGTCTACACACCCCAAGAAAGATCAAGACACA
AGCAAGAAGGTCAAGTTGGCTGTCTTGTCTACTACAGGTGCTGAAGTAAGG
TTACCAAATTTGAGAAGAGATGTAGCAACCCAACTTGTGGTGTGGTGTCTTCTTGGCTA
ACCACAAGGACAGATTGTACTGTGGTAAGTGTCATTCGCTTACAGGTTAACGCTTAA

YLRI67W, 152 aa (SEQ ID NO 182)
MQIFVKLTIGKTTILEVSSDTIDNVKSIQDKGIPPDQRLIFAGKQLEDGRLTSDYN
IQKESTLHLVLRLLRGKKRKKRVYTPPKIKHKHKVKVLA/LSYKVDABGKVKTLRRE
CSNPTCGAGVFLANHKDRLLYCGKCHSVYKNA

YLRI232W, 848 bp, CDS: 501-848 (SEQ ID NO 183)
AGCCACCAATTTCCACCAGGCCCGGCATTCAAGTACTTGTGAAGAACACCAACAGGCAAAAGT
CAACACCCCAATCATAGAAGTTGCAATGGGACGTTCCCTACAGCGTGTGCTAAATCCCCTC
CAACCAATATGTCTGGGGAATTTGGTGGGCAATGAGGTGATTCGGCCAATATCGAATATTT
GCCCGGTGTAATACTGAACACCTGACAAACAGACCAGCGCCAATTCATCTTGATTACCT
CTATGGTATCCAGGATATCTTGAGTTCTGATATAAGTCTCTCCCTCGCGTGGCTCGATCT
GAATAAAAACATCTTCCAGGTTCGAAATTCATGAATTTTGCACTGGGTGTGAGAAAGCAT
AATAGTCTGATGAAAGGAGCCCTTTTCAAAAAGGACTCTTGAATCTTTTCTCAGTAGGTT
TATAAAGCGTAATTAACAATGAATTCAAATTTGCACTGAGACTATTCATTCTGCAACTT
CATTTTCTTGAGCACCCAGCATGGGCGCTAGTAGTGAAGAATAGTTAAGTCAATGCTGA
CCTCAAGGCATCTTCTCTGGCTTCTTCAGGATGTTTGAATGCGATTCCACAGCACAT
CGCTCCACGCTATAGCTCAGCATTAAATGAATTCCTAGTTGACTTCGGCATCAAAACCTA
AAGAATTCGCCGATATAAGTACGTACAGGCTATTCGTCGGAGCATAGTCCATGGAATTTAA
ATGTAGGGATGTTGAATTTATCCCTCAGAGATTCGGGATATCTCCGTTCAATTCCAAAG
CTTCTTCCATAAATTACCAGTTGTTTCTTTTTCACAGAATATTAGGCTTAATATGTA
CGTATTGA

YLRI232W, 115 aa (SEQ ID NO 184)
MGASSGRIGKSMLTQGTFFPLASSGCLKCDSTAQSLHASSSALIEFLVDFGIKPKFPHKY
VTGLSSDDSPMDLNVGLMNSLSDSGYSPNSKAFSIITSLFLFSTEYGLICTY

FIG. 1 - 64

YLR233C, 2600 bp, CDS: 501-2600 (SEQ ID NO 185)
 GCGCATTTTCCCCACCCATGCGAATCATGGCTGAAATCAATGCCTGTTAGGTGCCCTGCA
 ACACATAGTCATGGTTAACTTCGCGAGTTAGCCCCATTTCTGGCAAACGGGGAACCCCATCAAAAC
 ATGAAATCATAGTTCTTTTACATACATGTAGCGGAAATCCCTTGAAGTTGATCTGCCTCCT
 CCTAGGATCTGTGAAACTGCCTTCGCTATAGAAATTTTCTCTCGCACACATAGCACTTTTC
 ATTATTGTCTATTAATACACCTTTACGTAGCTGAAGCGAGCGCACAGACGAAAGGTGCTTTC
 AAAAGCGAATGCCCTCTTTATTTGACAGTTACTAATTCGCCAAACTGCTTTTATTTTCAATCAAT
 GTGATTTTTCGGTTCTCAGCCATTATCAATGTCAAAAAGGATAATGGAAATGTGTAACATG
 CTTGTATGATGTCGACCGCTTTTATAGCAAACTTATCAGGGGAAAAGTATATTTCCATTAAAT
 GACACATGCCACCATAGATAATGGATAATGAAGAAGTTAACGAAGAATGTATGAGATTAT
 TTTTCAAGAACCTCTCGCGCATCTCGGATAAACATCTAAATCAAGGTTCACATGCGATG
 AAAATGCAATATACAGTTTCAGATGCTTCTCGATGGAATACATCGCAATCTACTAGGT
 TTCTCGAAGAGCTACTTTTGAACAAGAAAAATGTACCATTAATAACAAATTACGAAACGCA
 TAAATGATTCCGTGATACCATTGGTTCTGAAACTTTTATGGCTTCAAAATTCACGAACCTA
 CACTCCAATGGTTTGAGCACTGGTTCCATGATATCATGCGACTAAGTAAACAGAAAGAAAT
 TCAGAGTTTATAGAAATTTTCAAAAAAAATGATTTCAATTTTTCAAAAATTCACACACAGGT
 ATTATGATGACATCATCGAACACCTATGCGCAAAAGTACGATATGAATTCGGTTTTCGTTTCAA
 ATGCTCTCTTCGCCAAGTTGAAATTTAATGCAATACACAGATGGACTTTCAACTCATGAGA
 AAATATTCTTAAACACGAGTAATCCACTGACGCTTTTCCATGTAACTCTCACTACAAAGAT
 GCGTGATTAATCTAGGTTCACACATTTTATAAAACACTACTAAACAAAGCGGTCTAAACA
 AACCCAAAGAGTGTGGAAGGTTTGAAGAAGTCTATTAGGTACTTGAATATTGGCTCACTCT
 ATCTCCCAAGCGTTTGGAGATACTTATTTTCAACGAGCGGAAAATTTACTTGATCACTGGGA
 AATTTCTCACTGTTTCTTTTGAATTAGTAAGAGGAGCATTTGGTAAGGATTCGGTCTAAAT
 TGGCTGTAAACAAATTTGAAAGATTTTCAATTTTGACTCTCTGATTTTTCGGGAAAGAACGCTG
 TGATGAAAATAATTTGCAATTTCTGTGTCAAAGATCTCAAAGGTGAGAAATCATTTCTTTG
 AAGGTCAAATTTGTTGCAATTTCTATCGATAGTAGAACACACCTTTGGTTCACAGCTCAT
 GGAACGCACTCAGCTGCTTCTTAATTTGTTGGTTATTGAAAGAGCATTTACAAATGGCTGATC
 TAAAGTATCATCTCAGGTAATATTAATGTTTATCTTGAAGAACTTGGCTGCCACAATGGGAA
 GTTTGATGCTTTATGTTTACAACTCGAAAAAGTAAGGAACAAAAGAACAACTCAAATATG
 CAGATTTGATGTAGCGCCAGGTTTCTTTTGTAGCTTGAGCTTTGATTTTATTTGCTAATA
 TCATAGACGCTGCTCATCAAAACCTCTCGCAAAAACATCGAAGACTTTCGATATCTAG
 CCATTATTCGTTTCTTATGTGCTGGATTAAGTCATATAGATCTATTTTCCAGTACACTC
 ACAGACACAGGAAGTTTTCACATTCATCTGCCTTGTGTGCTGAACGACTTGATAAATAGTC
 CACTGAAATTTTCAGGAAATATATATAGCCACAGGCCGAAAAGAGCTATCTTTTATAGAG
 AAGATGATTATTTTCAGGGAATTTTCTTGCAATTAATTTTGCACTAACAGATTTTATGAGC
 ATTATGTATGATGATTCTCCGACATGATTAAATAATATAAATGGATGCCCTACATGTGACTA
 AAGTGCTTTCTCCAAAAGAGAATGTGTTCTGCGAATTAGATCAATAATATTTTCTCGGCA
 TGAATTTTATAGAAAAATGACACCGCGCTCATATGGAATGCCAGCAAAATATAAGTTTG
 ATTTAATAAGCCCAAAATATAAATAAAACGCAAAATAGCATTATCGGAAATTTCTCTCCA
 AAATAAATGTA AAAACACAACAGGAAAGAGTAGTCTCTCGAGAAAAGTTGAGGCCCAAAA
 GAGATGAACAACACGCGCAAAAGAGCGGAAAAATAGCTGTGACAGAACTGGA AAAACAAT
 TTGCAAAATGCTCCGAGAGAACAAAAAATTTGCTCCGCTCCAGAAAAGAGTGGCGTTTCTT
 CTGAGTTGGTAAAACATGCTGCTTACAGAGGGAGAAAAACTATCACTTGCCCCACTATCTCT
 CTGATTTTCTCTCATACCCAGCAAGCAATTTGATGCTGATGAGGACATCACCCGTCGAAG
 TGCCAGATACTCCTACTTGA

YLR233C, 699 aa (SEQ ID NO 186)
 MONEEVNEECMRLFFKNARAHLDKHLTSRLTCDENAYITFRCLFDGIHRKSTRFLEELL
 KQENMYHNHNNYERINDSVIPLVLKLLWLQIHEPTLQWEHWFHDIMRLSNRRKFRVFRIF
 QKMTQFFKITHRYYYDIIEHLCAKYMNSVSNALFAKLNLMQYTDGLSTHEKIIILNTS
 NPLTFSIVISLQRCVINLGSFHYKTLNKNPSNPKSVVEGFEKSIRYLNIAISLYLPAVGD
 TYFORAKYLYLTGVFSLYFFELVRGALVRIPSKCALNNLKDFILPTDFPERRRLMKKLAI
 LVSKDLKEKESFFEGQIVLQFLSIVEHTLVQPSWNASRASNCNWLKEHQLMAALQKHYSGN
 INVILENLAATMGSFDMFTTRKSEKQKNLKYADLSERQVFFLDLSFFDIINIDVVIK
 PSWQKNMEDFRYLAIRLLMCWKSKYSRSLQVTHRHKFKCTSFALLNLDLINSPLNCSGN
 IYSHRPKRYSYLFREDIIFREFSCINFALTDNDYVVDSPDMNNIIGCPTLTQVLSPE

ECVLRIRSIIFSGMKFLEKNDTGVIIWNASKYFDLISPNIKIRQIALSEISSKINVKTO
QERVVSSRKVEAKRDEQQRKRAGKIAVTELEKQFANVRRTKKLSPLPEKDGVSSELVKHA
ASRGRKTTITGPLESSDFLSYPDEAIDADEDITVQVPDTFT

YLR234W, 2471 bp, CDS: 501-2471 (SEQ ID NO 187)

AATGGTATCACGGAATCATTTATGCGTTTCGTAATTTGTTATTTATGGTACATATTTTCTGT
TTCAAAAAGTAGCTCTTCGAGAAAACCTAGTAGATTTGCGATGTATTTCCATCCAGGAAGCAT
CTGAACGTGATATATGTCATTTTCATCGCATGTCAACCTTTGATGTTAGATGTTTATCCAGA
TGCGCAGAGCGCTTTTGAAAAATAATCTCATACATTTCTCGTAACTTCTTCATTTATCC
ATTATATATGGTGGCATGTGTCAATTTAATGGAATATACATTTTCCCCGTGATAAGTTTGCT
AAAAACCGTCCGATATACAGGCATGTTAAACATTTCCATTATCCTTTTGTGACATTTGATA
ATGCGCGTGAACGCCGAAAATCACATTGATAAAAAAAGCAGTTTGCGCGAATTAGTAACTGT
CAATAAAGAGGGCATCGCTTTTGAAAGCACCTTCGTCGTGCGCTCGCTTCAGTACGTA
AAGTGTATTATAGACAATAATGAAAGTGTCTATGTGTCGACAGAAAAATTTCTATAGCGA
AGGCAGTTTTCACAGATCCTAGGAGGAGGCGAGATCAACTTCAAGGGATTTCGGGCTACATGT
ATGTAAAGAACTATGATTTTCATGTTTAGTGGGTTCGCCGTTTCCGAGAAATGGGGCTAACT
GCGAAGTTTACCATTGACTAGTGTGTGACGGGCACCTAACAGGCATTGATTTACAGCCATGATT
CGCATGGGTGGGAAAAATGCGCCATCCAAGAGTTTATTGATGCGCCACTGAACGAGATTA
TGAATTAACAACAAAAAAGATAGCAAGCAACATCAAGCGAGAAAGCGAGGAATGCAGACT
ATCTGATGATATGGACAGATTGCGACCGGGAAGGAGAGTACATCGCTTTGGGAGATATGGC
AGGAGGCCAGAGAGGCAACAGGCTCATACAAAATGATCAAGTATACCGGCAGCTCTTTT
CGCATCTCGAAGACAAACACATATTAAATGCGACGAAACCCAACTGATTTGGATGATGGA
AGAGTGTGCGAGCTGTAGGCACCGGATTTGAATTCGATCTTCGAGCAGGCTGTACATTTCA
CCAGACTCTTAAACAGAAACGCTACGAAATAAACTGAGAAACCAAGCCACCTACCAAGG
ATGTTGCAAAAACACCGCGGTGGTAAACAAGAACGACTCAAAAGTCGATACGTAATGGTACAT
GCCAGTTTCCAACCGCTCGGCTTTGTAGTAGACAGGTTTGAAGAATTCGAAATTTTGTTC
CCGAGAGTTCCTGGTATATCCAATTTGGTAGTCGAAAACAAAGACAACGGCGGAACAACAA
CGTTCCAGTGGGACAGGGGCCACTTGTTCGACCGGCTGAGCGTGTAAACGTTTTCACAGA
CATGCATCGAAACCGCGGCAATGTTGCTCAAGTAGTAGACTTGAAATCAAAGCCAACAA
CGAAATACAGACCTTTACCTCTGACCACAGTGGAGCTACAAAAAACTCGCGCCCGGTACC
TGCCTGTGAACGCCCAACAATCACTAGACGACGAGAAAAAGCTATACCAAAAGGGGTTCA
TATCGTATCCAAGAACAGAGACTGTACTTTCCACACGCAATGGACCTAAAAATCCCTTGG
TCGAAAAGCAAGCTCAATTGGACCAACTCGCTGACGGCGGCAAGAACCCGCTGGGCATCGT
ACGCGGCATCGCTGCTCCAACCCGAAAAACAAAGTAACAAATAACAAGTTCAGATTTCAC
GAAGCGGCTCCCATGACGACAAAGCGCATCCACCAATCCACCCCATCGTAAGTCTGGGGC
CTGAAGCAATGTTCGCCAGTGGAAAGAGAGTATACGAGTACGTGGCCAGGCATTTT
TGGCAGCTGCTCAGAGGACGCCAAGGGCCAATCGATGACCTTGTGTGTGGACTGGGCGG
TTGAACGTTTCTCAGCTTCAGGTCTCGTAGTCTTAGAGAGAAATTTCTCGATGTTTACC
CTTGGGCGGATGGGAAACACCAAGCAGTTACCGCGGCTTGAATGAATGCCCTCGTAGG
ACATCGCGAAGGCCGAAATGAAGGCGGGCACTACGGCGCCGCCAAGCCGATGACTGAGA
GTGAACCTCAATTTCTTCATGGATACAAACGGCATTTGGCAACAGCAGCCACCATTTGCGGAGC
ACATAGACAAAGTCAAGTACGTAATTTACGTTAGGAGCGAGAAAGTAGGCAAGGAAACCT
ACTTCAACACCAGACCCCTGGGTGCTCACTAGTGCACGGCTTCGAGGCCATCGGCCTCG
AAGACTCCTTTGCAAGCCCTTCCAGCGCAGAGAAATGGCAGCAGACTCAAGAAATCT
CGAAGGTCAATGCTCCAGACTGATGTTTGAAGGCACTAGTCGAGAAATATAGAAAT
ACTGGCACAAGACGAAATGCTTGAAGAATACTCTTTCGCAAGTTTATGACCGTGTCAAGG
CATCCATGTAA

YLR234W, 656 aa (SEQ ID NO 188)

MKVLVAEKNSIAKAVSQILGGGRSTRSDSGYMYVKNYDMFSGPFFRANGANCEVTMTS
VAGHLTGIDFSDSHGWGKCAIQELFDPALNEMNNQKIASNKKREARNADYLMWTD
CDREGEYIGWEIQEAKRGNRLIQNDQVYRAVFSHLERQHTLLNARNPSRLDMKSVHAGV
TRIEIDLRAGVTTTLLTETLRNKLNRQATMTKDGAKHRGNGKNSQVSVYGTQCFPTLG
FVDFRFRIRNFVPEEFWYIQLVENKDNNGTTFQWDRGHLFDRLSLVLTFTYETCIEAG
NVAQDTFVLDKSKPTTKYRPLPLTVELQKNKARYLRNLNAKQSLDAEKLKQYKFISYPRTE
QVDFPHMDLKSLEKQALDQLAAGGRTAWASYAASLLQPENTSNNNKLFQPRSGSHDD
KAHPPIHPIVSLGPEANVSPVERRVVEYVARHFLACCEDAKGQSMTLVLWDWAVERFAS

FIG. 1 - 66

GLVVLERNFLDVYPWARWETTKQLPRLEMMNALVDIAKEMKAGTTAPPKPMTESELILLM
DTNNGITDATTAEHIDKIQRVRYVRSEKVGKETYLQPTTLGVSLVHGFEGLEDSSFAKP
FORREMEQDLKKICEGHASKTDDVKDIVEKYRKYWHKTACKNTLLQVYDRVKASM

YLR238W, 1937 bp, CDS: 501-1937 (SEQ ID NO 189)

CTTCGTTACACATTAAATATTAATAACAGCTCTTCTTCTAATAATAACATATACACTAGAT
ATATAATACCAATAAATAAATAAAGAAAAACAAAAATAACGTAGCTTTTGTTCAG
TCGTAATAAAGAAACAATAAACCATTCTTATGCGAGCGTCTAACTAGCTCTTATTAT
TCCAATATATTAAAGGGTAAAGACTACTATTATTCGCCCTGAATTGAAGATCTTTAGAAA
GCACCTGCTTCTCTCTCTGGTGTCTTTTCTTCATCTATTATCTAAATTTCTTCAAGCTT
CGTTATTTGTTGTTATTCGCTAATCGTGGTCTCACTTTTGAATTTTCATTGTTTACC
ATAACCGGAACATAATTAATAATTTGTTCTTGAAGTCAAGCACTACGTGAACACAAAA
TTAAGCGCAAGAGTGACAAAAGTAACCCCTCACAGGAGCGTGTCTGTTTATATTTGGAAGC
TATAGATATAATCGAATCCAATGACTGGTCTCGGACCTGAAATAAATTAAGGAGGAGCACC
CCAGTTCCTCCGGGCAAGAAACAGATAACATATAATAGTATACCCAAGAAATGCAATCTAA
TTGATGGATTACGAATTCATCGAAGAGGCCAATTGAAAGATGACAAAGAGAAATAGCCG
ACCCAACAAAAGCTATTTCACATAGCATATCAAGAACCAAGGAGAAAATATACATT
ACCATCTAGTCTCCATCACTAAATGGAACCTTTGAGAGCAAAATGTGGTGTATACCAT
TAAACCAGAGTGGTTGAATTTGGGAAGGCCCTGTTGCTAATAGTAAATGACGAGCTCCAGTT
CATCGCTCAGGGGCGGTAAAGAGTGGATTACACACTTTTCCCAAGTAAGGTCGGATA
ATGGTAATTTGATTTCAAGTACTCTCCAGGAATCATGCATTGTTAAGTTGCCAGCCGC
TCACGGGTAAAGGTATATATACGAGACTTAAATCCAGTAATGGTACGTTTCATTAAACGGTC
AAAGAATTGGCTCAAATGACGTAGAAATCAAAGTTGGCGATGTGATAGACTTGGGAACAG
ATATAGATTACGAAATTGAGCATCTGAAATAAAGTGCCACAGTTGAAGAACAATTGTTGAT
AACCTTTTATAGATAACCGATTCTTGAATAAGATAGTAGTATGATGTCATACATAATTA
CAGAAAAGAGGAGGCTGCTGCCATAACAAGTACATATATGGTGAATTCACAACTACGAT
AATTGGAAGAGATTCTCTGGGCTGTGATACAGAAATCTGAGTGGAAATTTCTTAATTAATA
ATTGTATTTGGTACGAGCCCGACTTTATCTAATATCATCAAAACCCCTGGCAATGGAATTC
CATTTTCCAAATGCGATAATTTTAAATTCAGTCGATGGAAGATTTCTTAATTAATTA
CGACACATCTAGATACAGAAACAACTTTAGTGGAAAAAATGATCAGCACTGTGTAA
ACGCTGCAAAATGATTAAAGAAGCAAACTGTCGGGAAATACGAAAGAGATTATCGAACAA
ACAGAAATCAAGTAAACAGTTGCAAAAGGACCATATGTTTTTCAAAAAGTCATTGTAAG
TGAAGAAAAGAGAAATATGAAAAGCAAAAAGCATGGAAGAGGAAATAGAAGACTTGA
AAACTAGGTTAGAAGTGGAAACGATATAAGAAATTCACAAATGATGAAGAGAACAAACAGA
AAGAACAAGAACTCTCAACTGCATCTAAAAAAGACTACCGAATGACATAGAGGGC
TCCCGGCATGAATCCTAAGGGTACTGACAAATTTAGCATCAAGAACACGCTATGTAATC
ATTTACACATATTAACATTGGGAATTTTCCATCGGGATTATAGCTATTGTCTTCAAGA
TCCTTTCCCCCACTAG

YLR238W, 478 aa (SEQ ID NO 190)

MTGPGPEINKEEHPSPGKKQITYNSIPKNNALIDGSTNSSKRPIEKYDKRIADPTKSYF
PHSISRTFPRRKYTYILVLTSLNGTFESKHVVIIPFKPDGLKLRPVANSSSSSSSLRGGK
RVDSHTFSQVRSDNGNFDRLVLSRNHALLSCDPLTKGVYIRDLKLSNGTTFINGQRIGSD
VEIKVGVDVLDGPDIDTKIEHRKISATVEELFVQPLLESPIFENEDSDDCHTITEKEEAA
AITSHIYGDNSNNLEEVILGSDTEILSGIFINNCTGTSPTLSNIIKLAMEIIPFSKCDN
FKLQSMENFLINVTTHLEYTNKLLVEKNDDQLVKLQNLRRRLSGKYEKIIEQNRNVQK
LERDHMFKFSFEVKKRRNRNEQKSMERIEIDLKTLREVERYKNSQMKKNQKQKQELST
ASRKKTTHEHTRVSPGMNPKGTDKFSIGNTLKNHTLLTFGYSIGIIAIVFKLLSPN

YLR241W, 2849 bp, CDS: 501-2849 (SEQ ID NO 191)

CGAACATACCTGATATCAGAAATAGATCCCAATGGTGTCTATATTACGTGTAAGAGAGAGAT
TTAAATTTGAATATGTCCGAAGAAGATGCCACAGTGCATTTCAGAACTTAATCAATGATA
GTGTAATAGCTTTGCTGCCATCTCGTGATTGATCATTTACATATCTGGCACAATCTGCG
GGACTGATGGTTGTGATAATTGGTGTCTTCAAAATTTAAATTTCTGCATCTTAATATATCT
TAACATATAAATGGTACCTTCAATATATCTTCTTAGTAAAAAGTACGATGATTTTGCTGT
AATTTCGACCTTTTATTTTAAAAATAAAATACAGTTAAATTTTCTATGATCTTTCGAA
GACCGCCTCCCCCTAATGTGGCATATATACAAATGTGAATCAGAAAAACTCAACACTT
TAACATAATGGCGGACGAAGGCTAAACAAACAAGATTAGCATTTGAATGCCCTTTTGTG

FIG. 1 - 67

GTACAATGAGACAGTACTGAATGACATCATATATCGAAAGGCTCAAGTCGGCAGCATCGT
 ATCTTGTATACAGTTCAGATGAGCATCATGATTTTCAGAAAAACCCACCGCCAGGTTGTAA
 CGAGCAACTGACTATTGCTACTTCACTAGGTATTTTGGCTTTGCTTTCCGTTCTCAATT
 TACTAAAAAAGTGGCCCTAGATTATACGCAAGCAGACGATATAAGATGACGGGAAACCTTC
 GCTTACCGTCTCGGAATCAGTCAAGTTTATTTCGGCTGGTTAAACAGTGTGGTATAAGATAC
 GGGAGCAACAGATCTGGAATATGCAAGTTTAGATGCGTATGTGTTTTCAGTTTTCATCA
 AAAATGTCGATCAAAATTACTTTCTATTTTTCGTTCTCTCTGCTGGCTTATATCTCCAG
 TAAGATATCATTTTACTGGAATAATTGATGACGGCAACGATGATGATGACAGTGAAAGTT
 CTTTAAATACATCTGGTAAAAAGAAATGTGGAGGGAAGTGGCGATGGTGACCAATCATTCAG
 CTCCCGAACGTACAAATGTGTACCTCTGGATGATGTTCTCTTCAACATTTCTTCACTCT
 TCATAGCAATTAATAATGGCAGTTGCGGAACAAAGCAGCTCGTAAGTACTGAGCAAGCTT
 ATCTTGGGAAGCAAAATACGATTACTGATAGAACGATAAGGCTCTCAGGCATCCCGATAG
 AGCTTCTGTGATTTCGGAAGCCTTAAAGACCAGAAATGAACAATTAATAATCCGCAACCGTTT
 CATCAATCATGATTTTGTCTGAGAGTGGGGTCTTTGAACAAGCTATTTTATTTGTGGAAGA
 AAATACTCAAAAACCTGGAATTAATAATTCAGAAATGTCCAAGGGAGCTCCGTACTCGAC
 AACCATATTCGGAGAACTATCATTTTATGGGAACGAGCAATCAGCGCAGTTTACACATG
 GAGAAAATGTTTCCATCAAGCAATAATAATGACGAGGATACTATACTATTCTCAAAATTT
 CTTCTGGAGAGAGACCAAAAATGAAAATTTGGATATCGTGGTATCTTTGGGAAGCAAGTAG
 ATGCCATAGAGTACTCTGGAGCAGCAATTAATAATTTATGATGCTGAAATTTATGAAGCTAG
 CAACAAACACACTACTCCGCAACACCTACGGCATTCTGTTACGATGGAAATCTCTGTGTAAG
 CGCAAAATGGCAGCTCAGGCGGTATTAGATCTTAGAGTACATTACTTCAATACCAAGATTGG
 CTCTCGACCTCAGATATCAAGTGGGATCATGTTTGTCTTTCTAGAAAGGACCGGTTAA
 CAAAAGTTTATCTTACTACCGCTATTTATAGGCCCTTCAAGTTTGTTTTGTATCTCTCTG
 TATCATCTATGCAACATGCTTAAATTTGAAAACACTTTCGAAATTTCTGGCAAGCGTAG
 GGCAGCTACTAAAAAGATCACCAGTGGGCCGCTAACATTTGTAACGGGGCTATTACCAACCT
 ATCTCTTCACTTGCCTTAACCTTTGGAATCCCTATTTTTACGAGTATTGACTTCTTATC
 AAGGATTGGTATCATACAGCGAAGAGGAAATCTCACTTGTTTCAAAAATTTCTTTTATA
 TTTTGTGCAACCTTTCTCTAGTTTTCACATTGGCAGGTAACAGCATCTAATTTACTGGGCGT
 ACCTCAGCGATACCAACCAAAATGCTTATCAACTTGTACATCTGTGGAAGGAGTTCTCCT
 TATCTATGTCGATTGATTAATATGCAAGGTATTGGTATGTTCCCGCTTTAAGTTGTTAT
 TAGTTGGTAGTTTGTAGCGCTTTCCTCTAGTGAAAATCAAGGCTAAGACACTCAGGCAAC
 GGAATGAACCTTTAATCCACCGATATTAACTTTGGACTACAATTACCACGAGCAATTC
 TGATTTTGATTATAACGTTGATCTACAGTGAATGAGCACGAAAAATTTTGACTCTAGGGC
 TGGCGTACTTTATATTGGGTTTTCAGCTCATATAATATCAATTGATTTTGGCCACAGATC
 ATTTGCCCATCTCTACAGGAAAGTATGGCCATTAAATTTTGAAGAATCATCGTTGGAT
 TGTATTTGTTTCAATTAACAATGACAGGAACACTGGCAGGATTCGAAGGAGGATGGGTTT
 TGTATCTTGCCTTTTCCGCTTCCAGTAGTGACATTATGTTTCTATATGATTTCAGGTA
 AGAATCTATTGCGGTTGTCAAATATATCGCATTTGAGTTCAATTTCGCGAGTACGAAAGAG
 ACAATCTACGGTGAATTCGCAATGAGGAGAGTCTGATGCATACCTTTACGCTGTGA
 GTGAATTAGAGGTCGATGTTGGATTGA

YLR241W, 782 aa (SEQ ID NO 192)

MTSYIERLKSAASYLDTVPDEHDFRKPATKVVTTQLTIATISLGLIFALLSFSILLKKWPR
 LYASRRYKDDGNLRLPSWNQSSSLFGWLTVLYKIRDEQILLEVAGLDAYVFLSFFMKCKILL
 SIFCFVSVCVISPVRVYHFTGKIDDDGDDDESSLIHVKKRIVEGSDGDMNSHAPERTNV
 LYWMYVLFTYFFTFIAIKMAVAETKHVSTQAYVLGKQNTIDRTIRLSGPTIELRDSGA
 LKTRIEQLKIGTVSSITICREWGPLNKLPHCRKKILKNLELKYSCEPRELRTOPFYSYEN
 HLLGNEQSGAVTHGENVPSNNNDEDTLLYSQISLGERPKMKIYGRYFGKEVDIAIEYLE
 QQLKFLDAEIIIEARKQHSATPTAFVTMDSVANQAQAVLDPRVHYFITRLAPAPPHDI
 KWDHVCLSRKDRLTKVYSTTVFVIGLSSSLFVIPVSYLRLNLKLTLSKFVPSVGLKLDKH
 QWAANTVTGLLPTLYLFTLLNFGIPYFYEYLYTSYQGLVSYSEEEISLVSKNFFYIFVNLFL
 VFTLAGTASNYYWALSDTTKIAAYQLATSVKEFSLFYVDLIIHQIGMFPFKLLLVGSLIG
 FPLVKIKAKTPQRNELYNPPIFNFGQLQPOPIILIIITLIYSVMSTKILITSLGAYFIIG
 FYVYKYLIFATDHLPHSTGKWPPLIFRRIIVGLLLFQLTMTGTLAGFEGGWLLSSCLFP
 LPVVTLCFLYDFEKNYLPISKYIALSSIREYERDNSTVNSANEESYAYPYAVSELBGM
 LD

FIG. 1 - 68

YLR321C, 1781 bp, CDS: 501-1781 (SEQ ID NO 193)
TTCAGTGCATCTTTGTAAGGAAGATTACAAGTCTCCAGTGGTCACAAACTGTGGCCAT
TATTTTGTGGATCGTGTGTTTGGCCAAAGATATGAAAAGGGGCACCAATGCTTTATATGC
CACAAAGGAGACCCACGGCAGTGCACAAAGTAGCATCTGACTTACAGAAGATGCTTAAATAAA
AGGAAAGATTGATGGAGAATGCCATATCACCCCAAAATACACGCACCCGATGCTTAATG
TACAGAAATATAGAGCACATGACCCATAGATTTATCGAGCATTGTGCAATTTCCGAAG
ACTCTTTACATAATAAAGTATGTAACTATATAGATAGAAGATCTCCCGTGCTCTTTTGT
TCTACTAAATGATGATCTGCTCATTTAAAGTCCGCCGACTACTTTGACAAAATAAAAAA
ACTTAGAAATAACGACAAATAGAGATTATGAAATGAAGTACATTGAAAAAGAAAGAAGA
AAGGCACATAGCAGCACCAATGTGCGACCAAAACCCAGCTTATTCACCAAGCTTTATATTT
CTAACTTTCATAACAGATTGACAAACGAAGATGATGGTATCCCATCTTTTACAAATGGCTC
ACAAACCAAGGCAGCATAAAGGGCTAAAGTGGTCAACTATGCGGAATATGACCAACGATC
TCTTTGATGAATTCATATGAACGGTCTTAATTTCAACAAATGCTGATACACACTATAAAG
ATAATGCAAGTGTCTCATGAAAATACTCCGGCATTACAAATGGTGTACCATTGGACGGGT
CCGAATACAATGTCCCTAGAGAACATGAATGGAGCTGATAGTATTATCTCTAACCAACAAAT
ACGATGCGGGTTCAAACATGGTTGTGGAATCTTTATCCGGTTTGAATAGCAATAACCAACG
CCAGCAATGGTCCGAGACAACAAAGCGCAGGCACAGGATATGGAAACCGCGTCTTACCGG
ATCTCGAAGACCAACACCACAACCCCTTCAACATATTGAGATACCCCTAAAATAAGAGATA
CTTTCAATTAAACGAAAGTGGTGTCTCATATAGACTCAACACTGATCAAGAAACGAAGG
CAAAACGCCAATTTGAGAGAGGCAATCATGATACCAATTACTTTGGATATAGAACAATATGG
GTCATACCAATAAAGACCGAGTTTCTCGGAACTACAATGACGACTCCATATCTCCGGAGG
AATTTGGCTCTATATACTGTAAGATCTTGATATGACTTCCGCTACCTTACAACTCAAA
TGGCGAATATAAAGAGCGAGTTGAAAGACCTCGAAATATTTGCGCACTGAGATAA
TGTCTGACCTCCAGCTGATAATCAACCTAACCTGCAACTTACAAGACAGATTTTGTGAAG
ATAACTTCCAGTGGCACTTGAACGACAAATCACTTACTCCAGAAAGATTGCTACATGCA
TTGTACAGGACCTTGGCTTAAACAGAGAGTTCATCCCTTAAATATCTCAATCCGCTTCATG
AACTATCTTGAAGATAAAGAGGACTGGGTAGATGGCCACTTGATTCAGGACCATGTCC
CAACAGATGCGGCATTGGGTACTTATCTGGTATAAGGCTGGATATTGATGAACCTGGCT
CCAATTGGTGGCCCAAGGGTGGAAATATTAAACAAAGAGAAATACAAAGAGAGAAATTG
AAAAAGAAAGAAACTTAAGAAGATTGAAAGAGAAACTGATAGATTATCTAGAAGGGGCA
GGAGAAGATTAGATGACTTAGAAACCAATAGAGAATGTAG

YLR321C, 426 aa (SEQ ID NO 194)
MSHQQLIPQAYISNFHNLINEDDGIPIFTMAQOQTRQHKRAKVVNYAEYDNDLDFEFNM
NGSNFNADHYKIDNAVSHENTPALINGVTMDGSEYVNLNMGADSIISNNKYDAGSNM
VVESLSGLNSNNNASNGPSNKAQADIGNAVLPDLQDQHHPFNILRYPIKRDFTFNGKV
VSPYRLNTDQETKANANSGEAIMIPITLDIEHMGHTIKDQFLWNNDDSIISPEEFASIYC
KDLDMTSATLQTIQIANIIKEQLKDLENIAATEIMSDLHVIINLTCNLQDRFEDNPOWNL
NDKSLTPERFATSIQDLGLTREFIPLISQSLHETILKIKKDWVDGHLIQDHVPNDAAFP
YLSGIRLDIDELGSNWCPVEILLTKEILQKRETEKERNLRLKRETDRLSRRRRRLDDL
ETTMRM

YLR322W, 815 bp, CDS: 501-815 (SEQ ID NO 195)
GTCAATCAAGATCTTTACAGTATATAGAGGCAAAATCTCCGGAGATATGGAGTCGTCA
TTGTAGTTCAGAGAAACTGGTCTTTTATGGTATGACCCATATGTTCTATATCCAAAGTA
ATTGGTATCATGATTGCCCTCCAGAAATGGCGTTTGCCTTCGTTTCTTGATCAGTGTG
AGTCTATATGGAGACACCACTTTCCGTTAATGAAAGTATCTCTTATTTTAAAGGTATCTC
AATATGTTGAAGGGGTGTGGTGTGGTCTTGCAGATCCGGTAGAACGGCGGTTTCCAAAT
TCCGTGCGCTGCGCTTGTGTGCTCGGACCATTGTCTGGCGTGTGTTATGCTATTCAAACCG
GATAAAGATTCCCAACCATGTTTGAACCCGCATCGTATTGTTGTATAGAGATAATACTA
TCAGCTCCATTCATGTTCTCTAGGACATTGTTATTCGGAACCGTCCATGGTAAACACATT
GTAACTGCGGAGTATTTTATGAGACACGCAATTCCTTTATAGTGTGATCAGCATTTG
TTGAAATTAGAACCCTTCATATTGAATTCATCAAGAGATCGTTGTCATATTCCGCTATG
TTGACCACTTATGCCCTTTTATGCTGCCTTGTGTTGAGCCATGTAAGATGGGATA
CCATCATCTTCGTTTGTCAATCTGTTATGAAAGTATGAAATATAAGCTTGTGGAATAAGC
TGGTTTGGTGCACATGTGTGCTGCTATGTGCTTCTCTCTTTTTCATGATAC
TTCATTCAATAATCTTATTTGTCGATTTTCTTAA

FIG. 1 - 69

YLR322W, 104 aa (SEQ ID NO 196)
MRHCIIIFVICISIVEIRTVHIEFIKEIVVIFRIVDHFSPFMLPCLLSHKDGDITIFVQC
SVMKVRNISLWNKLVLRVHCVLVLCFAFLSFFNVLSIISICRIF

YLR325C, 737 bp, CDS: 501-737 (SEQ ID NO 197)
CCACATGTGACAACTACTTTGTGTAAGTGTGCATGCGGTGATTAGTATTATAAAACATCATA
GCCTTGGCCAAATAAACTCGCTTCCAGAAAAGACGCCAAATTAACAGCCGCTGTTATGTG
ACAAAACAGGGCATCTCACATATTCCGGTACTGGTGTCTTTTAGCTCAATTCGGATATTA
TTCCAAGACGGAATTTTCATCTAGAGAAAATGCATCCGTGCATTTCATATAAACCCACACA
ATTAATAATGCCTTGGGAAAAGGAGGACTCGTCCGTGCACTGTGAAAAAATAGACAGGA
GCATCATACGTTCCGAGTGGAAAAATATGAGAGATTTCCAAGCTCTATGGCATGTAGAGT
CGTGATTGCTGCTGTCACGCTTTTGCACAAATATTGAATCTTCAATCTAAAGAAATTAATTT
TCTAATTTCAATGTAGAAAATATTCAACTGTTAGTTTTTTATTTCAGGTGAATATGATA
GCACAAAATATCAAGGAAAATGGCTAGAGAAAATCACCAGACATCAACAAATTTTGGAAAT
TGACCAGAAAGAGCTGACGTTAAGACCGCCACTGTTAAGATTAAACAAAAATGAACAAGG
CCGGTAAGCCATTGACACAAACCAAGTTCAAGGTTAGAGGCTCTTCTTCTTGATCACTT
TGGTTATCAACGATGCTGTAAGGCTAAGAAATTGATCCAATCTTGTGCCACCAACTTTGA
AGGTTAACAGATTATAA

YLR325C, 78 aa (SEQ ID NO 198)
MAREITDIKQFLELTRADVKATATVKINKKLKAGKPFRTQKFKVRGSSSLYTLVLINDAG
KAKKLIQSLPPTLKVNL

YLR344W, 1331 bp, exon1: 501-519, intron1: 520-966, exon2:
967-1331 (SEQ ID NO 199)
TAAGGGCTGTCAATTTTTCATTTCCCTCAAAGTTAATGCGCAAGAGTTAGGATGATCTTG
ATTATATTGTTATTTGTTTGTTCATCAATTATGCGGACGTCCTAAGTGCTATTGAAATGA
TCGATTCTATTGCTATCTATTGTATTGTAGCGCGGCGCTAGTAAACAAGACAGCATAC
CTTTTCCAACATCCGTACATATTGATTATTGTATCTATGATTTTCATGTAAATGTATGGGTT
AACTAATCCTTCTCTCTTTTCTTTTCTGAAAATCAGTAGCTAGAGGAACCTGTTTC
GTAAAGATATGGAATATTCCGCTAGGGGAAGACCGAGAGCTGAGAGCAGTATCCGATC
GATGGAATCTTGCTCGGATGCGTAACGACGACAGCTTGCTAGAGGCGAAGTACAAGAT
ACTAAGAAGACTATAACAACAGAGACAATTTTGTAGTCGATCTATATATTATGACAGTA
ACCAACAAAAAGTATCAGAATGGCTAAACAATCATTAGGTATGTGCACAAATGCTAAAT
CACTGAAACCCGTAGAGCTGGAATTGAAAATATAGTTTGTACCTTTTTCGCTAGGGCGAG
AATGACTCAATGTTATCTTAATTCGATTAGAAAAAGAGGTGCGTTATCCAAGGTTGAAA
CTTGTAACACTATTTAGGTGATGCTCATAACTGCAACCACTGGAAAAATGACGCAAAATC
AAAATAATAGGGAGATAAAGTCTCAGGACATGAAAAATCATAGAAATTATGTTTCAATTT
CTCTAGCCGATATCTTACCTTATGAAAAAAGTGTGAATATGTTTTTCTAAATCGAGCTTCC
AGCAAAATCTACTATATTATGTCATCCGTGATACATCTGAAATTCAAATCTTCTCCAAGG
TCTTGCTTACTAAGAGGGTAAGATTGTTGAAACTCGAAATCTAACATATTATTTTCATTA
TTTGTAGCGTTTCTCCGACAGAGAAAGGCTAGAAAAGGCTATTTACCAGCCATCAACCTCT
CCCCAGCTCGTGTGTTGCTATCTGCTCCATTATCTAAGAGGTTGAGAGCTCAATACGGTA
TCAAGGCGTTGCCAATCAGAAGAGATGATGAAGTTTGGTTGTTCTGGTTTCCAAGAAAGG
GTCAAGAGGTAAGATTTCATCTGTTTACAGATTGAAATTTGCGGTTCAAGTGTGACAAGG
TACCAAGGAAAAGGTTCAACGGTGCTTCCGTTCCAATTAACTTGACCCCTTCAAGCTTG
TCATTACTAAATTACATTTGGACAAGGACAGAAAAGCTTTGATCCAAAGAAAGGCGGTA
AGTTGGAATAA

YLR344W, 127 aa (SEQ ID NO 200)
MAKQSLDVSSDRRKARKAYFTAPSSQRRVLLSAPLSKELRAQYGKALPIRRDDEVLVVR
GSKKGQEGKISSVYRLKFAVQVDKVTKEKVNGASVPINLHPSKLVITKLHLDKDRKALIQ
RKGKLE

YLR367W, 1376 bp, exon1: 501-633 intron1: 634-1116, exon2:
1117-1376 (SEQ ID NO 201)
ACTTTTTGTCTGCTGCTGGTCGTTTGTCTTTCGTTTTAAAATTGCGCTAGACAAATGAAAC
AGGGATTGCTTAAGAATCAAAGTAGCTTAACCTCAAAGATATATTTTCTCAGTTGTGGG

FIG. 1 - 70

CCCATGTGTTGGAGGGAAGGAATATATTGAAATGTAAATGTTCTTAAAGTTCGGTTGAACT
 TGGATATTGTTACAAGAGTTCTAGTCTTTGATACCATTTTACGCAATTACAAACCGCAT
 ATTTACCTTTTCATCTTCAGTTTACGGTTTCAGTTTATTCTGTAGCAAGAACTATGTT
 GATTCAAGGCGAAGTGCAGTAGGATTGTAACCTCATATTCTTTAGGATACCTTACAATTTT
 GTACTGTTTCAAGACCACTGTAAACCGATAATAAACCGGAGGACACATTTTAAACCCACTA
 TTTTTTTTCAAGAGTCAGATGCGAGAGCTCGAAGCATAAAGTATAAATACTAACGTTTCAAA
 ACATAGTAATTAAGTTAAAAAATGACTCGCTCTTCGGTTTTCAGTGTGCTTTGAATGGCA
 TTAATAACGCCGAAAGACCGGTAAACGTCAGGTTCTATTGAGACCTTCTTCCAAGGTTA
 TCATCAAGTTTTCACAAGTTATGCAAAAGCATGGTATGTTTCCAACATTTTTCACATATT
 TCACATGTGTTTCAATTTCTGCTTATTTTAAATGTTACCAACGAGGTTTGTCCAAAGTTCA
 ATGTTGCGCAACTCTAACGAAGAATAATTTATGCCATTGTTTTTACTCCGGGCTGATA
 ACTAGAGTGGTGTGATCGGGCAGTATACATAATTTATACGGAACAAAGACTCGTAAAGATG
 TCTTTTGTGCTTAGTCCCATACTGTTTTTAAAGTGTCCGGGATATTAACTCCCATGTGGGA
 AATGCTTCTTACACGGTTATGGATTACACCTCATGTGTAGCTACTATATCCATTACCGTT
 TACTTTTCCCAAAATCTCACTCTTAAATTTTCAATGGCAAAATCTTCCGCAACAAT
 AGACAACATTTTCTGTGTTTTTATGAAGTAAGCAAAATTTTCAATCAACAACCGTCCAT
 GAGATTCTTCAATACTAACATTTACTCCTTATTTAGGTTACATTGGCGAATTCGAATACA
 TTGACGACCACAGATCTGCTAAGATTGCTCCAACTGAACGGTAGATTGAACAATGTG
 GTGTTATTTTCCCAAGATTTAACGTTAAGATTGTGTGACATTGAAAATGGACCCCAACT
 TATTGCCAGCCAGACAATTCGGTTACGTTATTTTGACTACTTCTCGGGTATTATGAGACC
 ATGAGGAGCTAGAGAAGACAGCTTTCGGTAAATCTTGGGTTTGTCTATTAA

YLR367W, 130 aa (SEQ ID NO 202)

MTRSSVLADALNAINNAEKTGKRQVLLRSPSKVIKFLQVMQKHVIGIEFEYIDHRSKG
 IVVQLNRLNKNCGVISPRFNKIGDIEKWTANLLPARQFVILTTTSGIMDHEEARRH
 VSGILGFVY

YLR393W, 1340 bp, CDS: 501-1340 (SEQ ID NO 203)

CCCTCAACCCCGCATTTGCTGAGAATTTTCACCAAGGCCCTAGGTGATATTAGATTCCAC
 CTGACTAATTGCATTACAGCCGACCCCAAGGCAATATCAGTTTAAATAAAATATCATGTAT
 TCACCCTCTCTTGTGATATTAGTAAAGAGACGCTGATCTGTAAACAGTGGTGAAGATTGT
 ACTAGAGCAGAATCAAGAATTTAAAAAGTGTAAAGGCAAGGCAGAGCCGATGTACATAAAA
 ACTTCGAAGTAAGAAATATTAAATAGTTCTCGCCACATCACTATGCAGCTATATAAAAAAC
 TACTATAAACGTTTGTGTTGTTCTTACGCAAAATATCCTTGCTAGAAATCGTTTGTGA
 AATTTAAATTTTATTACCATTTATTTGATTGCGCTTCAGAAAAATATGGAAGAGTGCAT
 ATTTAAAAAGGACTATTTACGATATAGTAAAGTCAGGTTATTGTTTATTGTCGATAT
 CAGAGTAACTTAACTAACTATGCGAGGCACTTTTAAAAAGGTTTACCATCCACGCTTA
 CGCGGATGCTCTTCTTGATAAAATTCCTCAAGCCTATGATGGCAACCGCTTCCCCAAAGG
 AATACAGATCAAAACAACTGGTCAAGCCAATAGGCTTAAACACAAGCAACCAAGGAAAAAGCA
 CCAAACTCTCCAGGGGAACCTTTGAGGGATATGTTTGTATTCGAAAAAGCAAAACCA
 GAGTTAAAGGTTGGCCGTGAATTCAGCAAACTTGGACTTTATGACGTGCAAGCTTCTCC
 AAAAGCAAAAGGGGAAATGTTTATAGCTCCAGTTTTCATATTGGAAGAAGATAAAGCTT
 TGTTTTTCCTCATTTGATAGGAACGGCAATGGATGGTACGAAACAACAGAAATATCAGG
 ATATGTTAAAGGGTAAACCAAGTATAGTGAGGTTATTTAGTACAGCATCTGGCGATAAGT
 TGAGTAGTTCACTATTCGAAGAACTGTAGACGATAACAAAAAACTGACTACTTGACTG
 AAGCTGATGCGGCTTTAAGTTTAAATGACAGTAAAGCTTCAAACTCATCGAGGTTCAATCTTG
 TAGAAAAAGCTGTGAAAAGTGCTCTAGTGAAAACGCTTGCTCGTTGGGCCAATTCGGCTCA
 CACTTGGCGCAGCCATTTTATTTTCAATGTTCTAGAGGCCAATGGCCATTTTCCGCTCA
 GGGAGAGCTCTTTTGCATAATATGCTTTTCTGGATACGCTTCTTCTTGTGACACAGAGT
 TAAAAAATTAAGTGGCAGCTTTCGCGGGAGGCTACTCCATCTGAAAAGGAAGCATTGTGGA
 AGTTTGCCAAACGCTGTGA

YLR393W, 279 aa (SEQ ID NO 204)

MQGTFKRFYHPTLRMSLDKFLKPMATASPKKEYIKQLVKPIGLTQAPRKSTKYSQGN
 SLRDMFDSKTNHRVKELAVEFSKSLGYDVQVQFKTKGLFIAPVSYWKEDKALFFPHLI
 GTAMDGKQNTIEDMLRGKTSIVRLFSTASGDKLSSSYFQGIVDNKKTDYLTADARLS
 LNDNSVQITVNLVENA VKSALVKTLARWANRVPWSRQFPYFECSRGQWFFSVRELFCN
 NVFSGYVFLVDQQLKIRWAAACGEATPSEKALWKFAKRL

FIG. 1 - 71

YLR423C, 1754 bp, CDS: 501-1754 (SEQ ID NO 205)
 TTCTATTGGTGTAGTTATACCAGAACCCTCCCTCCCAAGGCCTTTTCCCGCAACATATCC
 CATACTCGAAAGTAACCTTCGCACCAATACCATATGTCTTCGTTAAATTTTGAGATCGTTGG
 GGCATTGGCCGTACTAGTTTTCGAAGGCATCATTAGTGTATGTATGTCACTATTTCATGCT
 TGAATTTATTTCTTCCATCGCTATAATTTATAGGAATCGATTCTTCTTTTGTGAAAAA
 GAACTTTTATCTTGTGTGGAGTCCGAATCTCCATGTTTGTGGCGTACTGGAAGGCTTAA
 GTCTTCGACCTCTCTCGGTTGTACTATTTCGAAATTTGGGATTTTGGTATTTTGTATTTGAC
 ATAAATGTAAATACTAGATGCGCGCTCTAAGGCCTCAGTATTTAAAAATTCGACGATATCCC
 TAACTTGATAAATTTTGAAGTCGCATAACGTACGATAAATTCGATACCTCGAGGATAT
 TATCAACGTATTTAAACACCTATGAACGAAGCAGATGTTACAAAAATTTGTTAATAATGCCA
 GGAAACCGCTGACCGATGCTCAACTTTTATGTTCAAGTGCTAAATTTAAGGATTTGATGATA
 TTAAGAAAAAATTTGTCATCTTGGCAGTTGAGTATTTCAAACTCAATTTTCTAATAGTTG
 GCTTGAGACAGCAAGGAAAGTTTCTTTACACTATTTTAAAGGAAGGCATTTGGGACAAAGC
 TAATTCGAGAAACAATGGAATCAAGCTGTCTTAGTGGTCTTAGTTGATGAGATGAAGTACT
 GGCAATATGAAATCACTTCTAAAGTACAAAGGTTGGATGGTATAGTAAATGAATTGAGCA
 TATCAGAAAAAGATGATACCGATCCCTCTAAACTAGGAGATTACATCTCGAGAGACAACG
 TTAACCTTTTGAATGACAAACTGAAAGAAAGTGCCAGTAATTTAGGCGTCAAAATTTGAAAAA
 CTTAAGCTTCAATACGAAAAATATGGTCAGAAAAAGTTAAACAAGAACTGATTTGATACCAAGT
 TGACGGACGTAACTCAAAAAATCCAAAGTAAATTTGGTATAGATAACCTTGAGTGGAAACAA
 ATGTTTCGAGACGACTTTAGCAGGGAACCTAACCGACTTGAAGAAAGATTAGCAGAGATAA
 TGAATTCATTCGACACGACCTTTGATAAGACATTTGCTGTTACAGATATAAAAAATTTGATA
 ACGATGAACGTTGAGGAGCTGTTTAAAGTGGTACAAGCGACGACAAAGAACTATACAACA
 TTTTCAAACTCTGCATGAGGTAAATTTGATGACGTGGACAAACAATTTCTTAACCTGGGCT
 AATTTTTCGAGGCAAAAAATAAGGAAAAAGACAGAATACACAGCGAAGTTCTTGAATAA
 TAAACGATTTCAATAGAAAATTTGGAATATCTATTAATCTTTAAAGATATTTTCCAATCTGA
 TTGATAGCTTCAAAAAATCTCTGTACACAAGATATTTCAAACTAAGGAACTTTTGTGAAT
 TTTATGATAATTTTGAAGAAAGCTACGGTAACTTAGTTCTAGAAGCAAAAGAGGAAAAAGG
 ATGTGGCAAAACAGAAATGAAAACATATTTGAAAGATTGTGAAAAGCAGTTGCAGAAATTTAG
 ATGCTCAGGCAAGCAAGAACGTCAGAATTTTATAGCGGAAAAATGGAATTTCTTCTCTCG
 AGACAATCTCGCCCGGTAAAATTTAGAGATTTTCTTCCCTGTACACTTTAAATTTACAACG
 TGAGAAATCTCTTAG

YLR423C, 417 aa (SEQ ID NO 206)
 MNEADVTFKPVNNARKLTDAQLLCSSANLRIVDIKKLSSWQLSISIKLNFILVGLRQQK
 FLYTILKEGIGTKLIQKQWNAVLVVLVDEMKYWQYEITSKVQRLDGIYNELISIEKDDT
 DPSKLGDIYSRDNVNLNLDKLEKVPVIERQIENIKLQYENMVRKVNELIDTKLTDVOTQK
 PQSKFGIDNLMETNVAEQFSRELTDLKDLAEIMNSLTQHFDKTLQLQDKKIDNDEREEL
 FKVVQGGDKELYNIFKTLHEVIDDDVKLILNLGQFLQAKIKEKTELHSEVSEIINDFNRN
 LEYLLIFKDISNLDISFKNSCTQDIQTTKELCFYDNFEESYGNLVLLEAKRRKDVANRMK
 TLLKDCERQLQNLDAQDQERQNFIAENGTYLPETIWPGLIDFSSLYTLNYNVKNP

YML026C, 1342 bp, exon1: 501-547, intron1: 548-948, exon2:
 949-1342 (SEQ ID NO 207)
 ATCTGTAAATATAAGCCCATGAAATATCAATCTCACAATGAAAGAAATGTGATAATTCAG
 ATGATTTTGACGTGAAAGCAAGTCTCATTTCAAGAACTGTAATAATCCGTACACACTACTG
 AATTTTACATCCATACATTTTGTGAAATTTTCATGTTTGTGAAAAATTTGGAAATAGGC
 TAAATTTATCCGTCCGGGTGCTCCTCTAGCTCGGCTCAACCTAGGCAATGCGTTTCTCTG
 GGCCATCCCAAGCTCATCTTCCAGAGATTTCGCCTTTCAGAGGCAAGAACTCGCTCTCCG
 AGGCCCTCTTGTTCGGGAGGAGGAGAAATTTTCGCGCGGAACTGGTGTAGTGCCTGGGCTA
 TGGTAAATCTGACACCTTTGCTATCTTAACTGAAAAGGTCCTTAGTAAATACAATATCA
 GGTACTTTAAACATTTGTTAAAGATATACTATTAGTGAAGAAACCGATCTTACGAAAGGCCAA
 TAGACGACGAAAGTGGTAAAGATGTCTTTAGTTGTACAAGAACAGGTTCCCTTCCAACACA
 TTTTACCGTATGTTTACGAGTACAGTGCAGATATGTTGAGAGAGTTTCACTTACATGAG
 GATAATAGCTTTAATATGCGATTGAAAAATATGTAGTGCACTCCGATGGAATAATAAAGC
 TCACGGGTACCAAAATACGAGGCCGAAATTAACCTACACGCTACTATAAAAAATATCACTAG
 ATTTTAAAGTAAATACACAGTTTATTGAAAAATACAAATATATGACTATGATCGGAATTTAAA
 AATTTTCAGTCAATACGACTTGACAAATTCATATTTATCGTCCCTCCATGTTTCGTAGCCCA
 TTCCAAAAATGATGCGCATGTTGAAAAATTTTCGAGAACACTAGCAGTGGTGTGAAATAA

FIG. 1 - 72

ATTACTAACAAATAAGATGTACAATTTTTGTGCGCCATTACAATCAGTTTGTGAACAC
CAATGTCGATGGTAACATTAATAATTTGTGTACGCTTTGACCCTATTAAGGGTGTGGTCG
TCGTTATCTCCAATCTGGCTCTGAAGAAGGCTGATGTTGATTTGCACAAGAGAGCTGGTGA
ATTGACCAAGAAGAAATTTGGAAGAATTTGTCCAATCATGTCAAAACCCAACTCATTACAA
GATCCAGGCTGGTTCTTAAACCGTCAAAACGACATTTACTGATGGTAAGGATCCACAC
TTTGGCTAAACAAGCTCGAATCAAGTTGAGAGATGACTTGGAAAGATTAAAGAAGATCAG
AGCCACCGCTGGTATTAGACACTTCTGGGTTTACGTGTAGAGGTCAACACACCAAGAC
CACTGGTAGAAGAAGAGCTTAA

YML026C, 146 aa (SEQ ID NO 208)

MSLVVQEGSFQHILRLNTNVDGNIKIVYALTTIKVGRRYSNLVCKADVDLHKRAGE
L7QEELERIVQIMQNPHYKIPAWFLNRQNDITDGDYHTLANNVESKLRDDLERLKKIR
AHRGIRHFGLRVRGQHTKTCRRRA

YML063W, 1268 bp, CDS: 501-1268 (SEQ ID NO 209)

TATATATTTTTTCCCTTCTGGGTCTTTTCTTCCTTTTCTTGTTTACCTTTTTTGCTTT
TTCATAAAATAATTTCTCTAGATTGAAGACAGCATTTTGTACATCCATACACATACA
CCATACACCATAGCACCCAGTACACTATATTTTTATGAATTTTACTAAGAATTTATTCCTGC
AGGAGCTCCACTGAAAAAAGAGCAGCATGGATGTCGGTGAAGTGTCTACTGAGTAA
ATTGGGAAGGACGCGGTAGATCCAGTGTGGAATCAAGGTGGTGC CGGTGTGAAGCCGCTC
GGCCGGCTGGAATCTCCAGGCGGAGTGATGATGCCACGCTGAACGTAAACACAGTTTCA
CAATCAAGTGTCTCTCATTAGTGAGTTCCAATGTATAGTTAGTAGTGATTTTGATATA
TGTTGAGTGGTAGCAGATTGAACTTAGTTAGTTGTATTGCGCTTTGAGGAAACCAAGCAA
AAAACCGATCTAGACTAATCATGTGCTGTGGTAAAGAATAAGAGACTATCCAGAGGTAAAGA
AGGTTTGAAGAAGAAGGTGCTTGACCCATTTACCAGAAAGGAATGGTTCGATATTAAAG
CCCATCCACTTTTGAACACAGAAATGTGGTAAGACTTTAGTTAACAAGTCCACTGGTT
TGAAGAATGCTCCGATGCTTTGAAGGGTAGAGTTGTCGAAGTTTGTTTGGCTGACTTGC
AAGGTTCTGAAGACCATCTCTTCAGAAAGGTCAAGTTGAGAGTCGATGAAGTTCAAGTA
AGAACTTGTGACCAACTTCCACGGTATGGACTTCACTACCAGCAAAATGAGATCAATGG
TCAGAAAATGGCAAACTTTGATCGAAGCTAATGTTACCGTTAAGACTTCCGATGATTACG
TTTTGAGAACTTTGCTATTGCCCTTACCAGAAAGCAAGCTAACCAAGTTAAGAGACT
CTTACGCTCAATCTCCACATCAGAGCTATCAGAAAAGTTATTCTGAAATCTTGACCA
GAGAAGTTCAAACTCTACTTTGGCTCAATTGACCTCCAAATTGATTCCAGAAGTTATCA
ACAAGGAATCGAAAATGCTACCAAGGACATCTTCCACTACAAAACATCCAGCTTAGAA
AGGTTAAGTTATTGAAACAACCAAGTTCGAGCTTGGTGCTTTGATGGCTTTGCATGGTG
AAGGTTCCGGTGAAGAAAGGCTAAGAAGGTTTCGTGTTTCAAGGATGAAGCTTGGAAA
CTGTGTTAA

YML063W, 255 aa (SEQ ID NO 210)

MAVGKNKRLSRGKGLKKVVDFFTRKEWFDIKAPSTFENRNVGKTLVNKSTGLKNASDA
LKRNVVEVLADLQGSDEHSFRKVKLRVDEVQGNLLTNFHGMDFTDCLKRSMVRWQTL
IEANNVTKTSQVVLRIFAIAFTRKQANQVKRHSYAQSSHIRAIRKVI SEILTRVONST
LAQLTSLKLEPEVINKEIENATKDIFPLQNIHVRVKLKLQPKFDVGMALMHGEGSGEEK
GKKVSGFKDEVLETV

YML128C, 2042 bp, CDS: 501-2042 (SEQ ID NO 211)

TTAATAGGGTTAGCCACCATTTGCTCGAACATGTTCAACAGGCTCGGAGCTTGTGGCGGGT
GCCTCGCTTACTGGAGTACCATTAGCGGGTGTGTTGAAGCTAACGAGTTCACTCTCAAT
CTTTATTTCCACTTCTTTACAAGCTTTCTGCTTTTCTCTATGACGCTCTTTCCCAAAACAC
TACCTCTTGACAGCACTTGTGTTTTCGTTTCTCTAAGAATATCCTACTATTTCACTTT
TTTCACTTTTCCACCATTAAGCTGCTGGTGAAGCAACAGCATTACGCCGGCTCTACCTTTAGAG
GGGAAGAATAAGGGATCTTTGGAAGTGAAGGAAAATAGGGAGAGGGAGGAAACAAAGAG
CGCGTGAAGGGGATCGACAGGTTATTAAAGCCACTCATGGAGTCTGATTTCTAGCATG
ATTAGATTACCGGAGTTTGAAGAGGATCTGCAATAGAAGAGGAGACAACTACAAAAGAA
CTGTTAATTGAAGAGAAGAAGATGAAGCAATTCAGTTGGTTAATGCGGGTTTCCGATCAT
TTGTGCTTATTGGCTTAGTGTGGCCAATTCAAGTTCAGTGTTCGACAAAGTGGAGCGAGG
AAGACCTTGGCGGATTTATACGTGATAATAAGAAGAGCTTGGAAAAGTACGCTACAGACT
CCATTGAGGACTTGAACCGGAGGATCGCAGGTATGGGACAAACACGCGACGCCAAAC

FIG. 1 - 73

CATGTTGGCAGGTGTGGTCTAGTGACAGCAGTAGCGTGAGCAACAGTAACCCCGGATGTT
TTGGTTATACCTAGGGTTCTTCGGATCAACCCAGTTTCTGACTGGCTCTTTGACACCTGGTCCA
CGGACAGTCTACGTAACCTTCTTGAAGAAAAACGGCGTGGATGTTGACGACGCTAAGGCTT
CCAAGGACTCGCTGGTGAAGACTGCTAAGGAGAACTTCAACAAGATTTCCAAATCTTTGA
AGTCGTGGGATACCTATCCTTCTAGCTCTTACTTTGATAGCTGGTCAACCAAGAGTTTGC
AAAACTGGTTGAAATGACAAATGGTATCGACTACGACAGGCAAGTTCAAGCAGGACGAGC
TAGTTTCAGAAAGTCAAGGAAAACTCTACCGAATTCAGAAAAAGGCAAGAACGACGCTC
TGGGTTTCTCTAGAAAGCTTGGATTGGCTCACCAACAATATTAGACACATCGGGACAAA
TAAAGACACTGTATTGACAAAGTGGTCTAGTGATCAGTTAACCATTGGTTGGAGAGCC
CAAGGCTCAATTATTGACAAAGAACATGGCCCAAGAACACGACTATTGGTTTGAAGTTGGCCA
AAGAAAAATTCGCCCAATTTGAAAGATGATATCTACTGGTACCTGGACTATATGAAAAAGAG
AGTCTTCTCCATTTTTGACCAAGACCCGGAATACGTTGGTTCCGTTTGGGACTCTTCTTA
AAAAATTTCTCCCAAAATTTGTAATCTCAAGTTTCAGAGGTAAAGCTGCAATGTGATCAATG
ATACTTTTTTGGTTGGCTAGACTCTTGGCCAAAGGACAAATTGAAAAATCTTTTAGATG
CTCGGGTATTAAGTACTCAATGCTGTCTACTGAACATCAATTGAGAGAAATTAGTCAAAA
AATCCAGAAAAACGAAAACTCAAGATCCTGCCAAAAGACTACCAAAAATACTTTGACAACA
GTAACTCGTCTTTGGATGACATAAAGGGTTGGTTTGTGACAAAAAGGACGACTTCCAAG
ATTCTCAGACTTATCCACAATATTGACGAGATTTTGACAAGGTTTCCAAAAACACAAATG
ATGCTAAGGACCAATCGCTAAGACCTGGTCAAATACCTTTACAGAGCTGGTCTCAAGAAG
ACCTATTTCAGTACTCAAAATCATTCGGTGTTCGGTTTAAACAGACTTCTACGAAGACG
ACTTAATCAACTTGGCCAAAGCAGAATACGCAATGGTTGTTTCGGCACTGTTAAGGAGCCTG
CTTACAAGAGGTACCTACATAACGTTAAAAACTGGTCGAAAAGCATATTAGGGTTCAACT
AA

YML128C, 513 aa (SEQ ID NO 212)

MKQFKLVNAVSAFVLVGLVLANSDSVFDKWTQEDLADYLRDNKKSLEKYATDSIEDLKT
EASQVWDKHAQPKFWQVWSSDSSVSNSNPGWFGYTGSSDHPVSDWLPFTWSTSLRNF
LKNKGVDVDDAKSKDSLVTAKENFNKISKLSKSSGYYPSSSYFDSWSTKDLQNLWIND
GIDYDKAVQSKDELVLQVKENIYRTSEKAEQORLGLLESIDLHQQIILDTSGQIKDTPVD
KWSSDQLTNWLESHKVNIDKNMAKHHDYLVLRMAKENSANLKDDIYWLYDYMKRESSPPLT
KTPPEYVGSVWSSKNFLTNLYSKFRCKTNDVINDTFLVLGDSWPKDKLMFLDARGIKYS
MLSTPEHLRELVLKKSRIEKLKILPKDYQKYFDNSNWSLDDIKGWFADKKDDFQDSQTYST
IMQDFDKVSKNTNDAKDQIAKTWSNTFQSWSQEDLLYLKSFVGVVVKQTSTKDDLINLAK
QNTQWLFTGVKEPAKYKRYLHNVNKNWSKSLGFN

YML130C, 2192 bp, CDS: 501-2192 (SEQ ID NO 213)

ACGAGATCATTTTCTTATCTATCTATTGAGTAATGCTTACTTTTTCATATTTTCAATGAAC
AATAGGATATGTAGGAGAAATGATATATTTCACTGCGTATCAGAGAAAAGGCTTACTGACA
TTTTATGGCAAAATGTAATTTCTACACAAATCGAGAATACCCAGACAAATGGTACAAGACATA
CACAAAGAGAAAGACTGTTCTAATTAACAAATAATATTAGCTACCTGCTAAGTATGTC
TTTTCCCTTTGTCTTTGGTTTCTCTTATAGAAGACCTGGAAATTTTTCGATTTTTC
GGCTTTGGGCTTAGTAGAAGCAAAAAAGAAAGAGAGAACAAAAAGAACGATACCGGA
GTACGTGTCTATAAAAACTTGTTCATCATCTCTTGAAGCTAAGTATAAAGAGCTTGA
GTTTACCACTTAACTGGTTATCTACTTTTCAAGAGTGTAAACATTTTATTGCTATATACCA
CAGTAAGCTGTCAGTAAAAACATGAGATTAAAGACCGCAATTCGCCACATGCTGCCCTACGG
CTTTTACATCTGCAACTTCAACAAATAGCTACATCGCCACCGACCAACACAAAAATGCCT
TTAATGACACTCACTTTTGAAGGTGCGACGGAATGATACGTTAGTCCAGTTGTGAACG
TAACATCTCAATGAATTAATTAATGCAATTAATGAAGCAATTAAGATGATCTTCGGCTTAT
TAAATCTCGATTCTCTCAATACTTTTCGGCTGGATTATACAAGCAATGTTCATTTTTGGG
ACGCCAACGATGGTCTGTGCTTAAACCGCGCTTGCTCTGTGTGATGCTGAGGAGCTGGG
ATACACTGCTCTGAGTACTGGCAGCCTGAGATCTTGGGTAGTTTCAATATGATACAAATGA
AGGAAGCGGATGATAGCGATGACGAAATGTAAGTTCTTAGATCAACTATGTCAAACCACTGA
AAAAAATCTGTAGATATCGAAGACACCATCAACTACTGTGATGTAATGACTTTTAAACGGTA
AAAAACCGCTTCTGATTTGATTAAACAGCAAAATCGGGAACGATTTACAGGTTATGGTGTGA
ACGAGCTGGTCAAAATTTGGTCTACTATCTACCAAGACAACTGTTTACAAATTTGGCGAAA
CTGTGTAATCATTTGGCCAAAGATGCATTTTATAGACTTGTATCCGGTTTCCATGGCTCTA
TCGGTACTCACTTATCAAAGGAATATTGAAACCGAAACTGGTAAATGGGAGCCCAATC
TGGATTTGTTTATGGCAAGAATCGGGAACCTTTCGTGATAGAGTGACAAACATGATTTCA

FIG. 1 - 74

ATTATGCTGTTGTAGCTAAGGCTCTCTGGAATAATCAACCATAATTACCAGAATTTTCAT
TCTGTGATCTAGTCAATAAAGAAATCAAAAACAAATGGATAACGTTATTTCCAGCTGG
ACCAAAAAAATTTTAAACGAAGACTTAGTTTTGCGCAACGACCTAAGTTTGACTTTGAAGG
ACGAATTCAGATCTCGCTTCAAGAAATGTCACGAAGATATTGGATTGTGTGCAATGTGATA
GATGTAGATTGTGGGGCAAAATTCAACTACCGGTTACGCAACTGCCTTGAAAAATTTTGT
TGTGAATCAACGACGCTGATGAATTCACCAAAACAACATATTGTTGGTAAAGTTAAACCAAT
ATGAGTTGATTGCTACTATTACAGACTTTCGGTAGATTATCTGAATCTATTGAATCTGTTA
ACATCTTCGAAAAAATGTACGGGAAAAGGTTAAACGGTTCTGAAAAACAGGTTAAGCTCAT
TCTTCCAAAAATACTTCTTCAACATTTTGAAGGAGCGAGGCAAAATCGATTTCGTTACACCA
TAGAGAACATCAATTTCCACTAAAGAAAGGAAAAAGAAAGACTAAACAATTTCTCAATCACATG
TATTTTGATGATTTAAAAATGCCCAAGCAGAAATAGTTCCAAGGCCCTCTAACGGGTACAG
TAAATAAATGGAAGAAAGCTTGAATACTGAAGTTAAACAACGTTTGTAGAAGCATTCAGAT
TTATTTATAGAAGCTATTGGAATTACCCAGGAACATCGGGAATTATCTTTGATGAAGG
TATACAAATTTTGAATAAATTCATCGGTGTTGCTGATTACGTTAGTGAGGAGACACGAG
AGCCTATTTCTATAAGCTAGATATACAAATA

YML130C, 563 aa (SEQ ID NO 214)

MRLRTAIATLCLTAFTSATSNNSYIATDQTQNAFNDTHFCVKVRNDHVSPCNVFTFNELN
AINENIARDLISALLKSDFFKRYRLDLKYQCSFWDANDGLCLNRACSDVDVEDWDLTPEYW
QPEILGFSFNNDTMKREADDSDDECKFLDQLCQTSKKFVDIEDTINYCDVNDPFGKNAVIL
L/IANPERFTGYGGQKAGQIWTSTIYQDNCFTIGETGESLAKDAFYRLVSGFPHASITGLHSK
EYLNKFTGKWEPNLDLFMARIGNFPDRVTNMYFNAYAVAKALWKIQPYLPEFSFCDLVNKE
ETKNKMDNVISQLDITKIFNEDLVFANDLSLTLKDEFRSRFRKNVTIKIMDCVQCDRCRLWGK
IQTGYATALKILFEINDADEFTKQHVIGKLTXYELIALLQTFGRLESIESVNMFERMY
GKRLNGSENRLSSFFQNNFFNILKEAGKSIRYTIENINSTREGKKKTNNQSQSHVFDLLKM
PKAEIVPRPSNGTVNWKKAWNTEVNNVLEAFRFTYRSYLDLPRNIWELSLMKVYKFWNK
FIGVADYVSEETREPI SYKLDIQ

YMR022W, 998 bp, CDS: 501-998 (SEQ ID NO 215)

AACAGTATTGGCTGTTGATTTCATTGCGCTGCAGCAGTCACCTTCAATTTGTGCACCATTT
TCGTATTCTGTACTTTGCGATGTAGAGTCTACTAAAAATAGCGTCTCTGTAGCCATGGGT
GAAGGTCTTCTCTAGTTCTCACCTTAATTAGCATTTCGGTGAGAAATGCCTGCATGTTGAA
GAGCGATGCCCTCTGATGCACGATGCACACGCATATTGTTCCCAATAAATATTATCATC
TCTGATAGACCTTGAAGAACTTACCAGACTGTTTCAAGTTTAAAAACAAGGCGCCTCATCG
CATCTACCTCACGAAAGATGCAGCAGCTTATTGTCTCGAGATCCTTCTTATAACTCCTTTT
CGCCATTACCCGAAAAACGAGATTACAGCCTCTAAACCAAGAGCTCGAAAAAGCGCCAAAGT
AAACTCTGGCGTTTACGCTACGAAGGAGATTATCTTAAAGGAACTTCCCTAGTAAATAGT
GTAAATTTGGAAGGGCATAGCATGTGCAAAAACCGCTCAGAAACGTCCTCCTCAAGGAGCTTC
AACAGTTAAATTAAGATTCTCCACCTGGTATAGTGGCTGGTCCCAATCGGAGAAATAACA
TATTCATTTTGGGACTGCCTAAATTCAGGGCCTCCAGATACGCCATACGCTGATGGTGTGTT
TTAATGCTTAAGCTAGAGTTTCTTAAAGACTATCCGTATCTCCACCTAAACATTCTATTCTAC
CACCCAGCTACTACATCCAAATATTATCCAAATGGGGAAGTGTGCATATTCATTCTAC
ACTCCCTCGTGTATGATCTCAATGTACGAATTAGCGGAAGAAAGATGGTGCAGGATGC
AAAGTGTAGAAAAAATTTCTAATAGTGTATGAGCATTTGAGTGAGCCCAATATCGAAAG
GTGGTGCCACATTTGATGCTTGCATCTTGTGAGAGATAATAGACCTGAATTTGAGAGAC
AGGTAAAGTTATCCATTTGAAATCATTAGGATTTCTGA

YMR022W, 165 aa (SEQ ID NO 216)

MSKTAQKRLKELQQLIKDSPGIVAGPKSENNIFIMWDLIQGPDPFTFYADGVFNAKLEF
PKDYLPSPKLTFPTPSILHFNIPNGEVCISILHSPGDDPNMYELAEERWSVPQSVKIL
LSVMSLSFENPIESGANIDACILWRDNRPEFERQVKLSILKSLGF

YMR118C, 1091 bp, CDS: 501-1091 (SEQ ID NO 217)

GTCTCTCCGCTTTATATGTTTCGTTATCCTATCACAATTACAAATGACTTTGTGCCACTG
TGTCTTGACAAAAATTAAGTGAATATAATCAATAGTATTACATGTTTGACAGAAAGTAC
TGTGATCGCATCCAGTTCTCATGCAATATAGTTGTATACCATGTCGTTGAAAGGAACACAG
AGTAAACCACTTCTACCAAGTATTCTTACGGTTTCGGATCAAAACCACTCATCTCGCTG
ATTCTTACCGTAGATAAAACCAATTAACAGGAAAAGTATCCCTAATTAGAGATCACTGC

FIG. 1 - 75

ATCCGTAATAGTATTTTTTCTATTTTGGACTTTTGTAAAAAAGGGATTAGGGATACGTTG
 CTCATAAAAAAATTGACGAAGATTTTAGATAATGGCAAATAAAATGAAATAGTATCAAT
 ATACCGAAAAATTAATCACACTCAATGCGACTGTGATAGCTGATAAGTGGAGCTCAGAAA
 TATTCAGAAAGCTAAGAATAATGAAAGCAACCATTCAAAGAGTAACATCTGTATTTGGAG
 TTTCCCGAGCATCTGTATTCGTGCCAAGAATCAGCACACCAATTTATTTGATCAATTATA
 TCTCTAATGGCAGAATGGACCTTTTTTCCAAAGAAATTCACAATGGCCGCGTATCCAAAT
 CTGATCTTTGGTCAAGCAACAAGGAAGAGGAGCTTTAGTATCTCAAAGGAAAAAAGAC
 CGATCTCTCTCTAATCTTTAACTGTTTACGAACCTGAAATGAGCTGGTATCTTTCCCTCTTAC
 ATCGTATATCTGTGGCTTTTACTGGCTCTTGGATTCTATCTTTCACAATTTACTTTGGGTG
 TGACGACAATATGGGAATGGATACGACTTTTCAGGATCTAAACAAGTGGTATACGAAA
 AGATGCTTAAGTGGTCCCAATGGGTGGCCAAAGGCTCTGCAGCATATCTGTTTGCATTTCC
 ATTTTGGTAACGGTATAGGCATCTCATCTGGGATATGGGCTACGAATTGACCAACCGTG
 GGGTTATAAAAACCGGATCAATCGTTTAGCCGGCACACTCGTCTTAGGAACGTATTTAC
 TGGCTCAGTAA

YMR118C, 196 aa (SEQ ID NO 218)

MKATIQRVTSVFGVPRASVFPRISTFFILHNYISNGRMDLFSKEFHNGRVSXKSDLWSSN
 KEEELLVSQRKKRPIPHLTVYEPMSWYLSLLHRISGVLLALGFYAFITLGVTTIMGDM
 DTTTFQDLNKWYHEKMPKWSQWVAKGSAAYLFAFHNGNIRHLIWMGYELNTRGVIKTGS
 IVLAGTILVLGYLLAQ

YMR143W, 1121 bp, exon1: 501-524, intron1: 525-713, exon2:
 714-1121 (SEQ ID NO 219)

CCGCTTAGCGCAAACACTATCTGTGAACCTCGTGCAACAACCTGAGAGGGCAAGGATATACATA
 AAAATTAGCCTACAAATTTCTGAACCTCTGTAAGGAAGCCTCATAAATAAAGGTAGATAGTA
 AAGTATACAAGAGAGAAGAAATCCCAAGATGTGAGCTGTCCCAAGTGTTCAGATATGTTTCA
 GTTCGCAAGATGATGTTTGTATAGTATCGATAATGGAGTGAGATCAAGAGAAAAAAGAT
 AATATGTGAGCAACCAAGTCTGAGTAGGCAGTAAATGAGTACGCATATGATGTTATTC
 CAAAGGAAAGAAATGTTATTTTCAAGCCGAATTGAGATCCAATTAGGCAATGTTTGG
 GGAGAGTATTTTGACAAGATTTGGTTAAACTACTACGGTCAGTTCCGTAAACAGTACGATT
 GTACACATAAAGGAAACCACTGTAAAGATAAAACAATAAGGGCTTCCAAATGCCATTGTAAGA
 TATCATATTTCCATAACAAAAATGTACAGCGAATATAAGGCCAGCGTCAGTGTCTTCTCGG
 AAGGTTGGCACAATAAAGAAGTTGAATTAATAATGGCAAGCGTACATTTTCATCCATTT
 TCACCTCATCAGATGTCCAAGATTTTCGAAAAATAAATATCTCATTTTCTCTCAATGAA
 ATAATTGTTTACATAACATTGAATTTCTCGTAACATATTGCATTTCTTTAGATTTTG
 GTAAGAAGAAATCAGCTACTGCTGTTGCCCATGTCAAGCCGGTAAAGGTTTGATCAAGG
 TTAATGGTTCTCCAATCACTTTGGTTGAACCAAGAAATCTTAAGATTCAAGGTTTACGAAG
 CATTATTGTTAGTTGGTTTGGACAAATTCPCAACATCGATATTAGAGTTAGAGTTACTG
 GTGGTGGTCACTGTTTCCCAAGTTTACGCCATCAGACAAGCTATTGCTTAAGGTTTACTGTG
 CTTACCATCAAAAAATATGTCGATGAACAATCCAAGAACGAATTGAAGAAGGCTTTTCACTT
 CTTACGACAGAACCTTGTGATGTGCTGATTCTTGAAGACACAGAACCAAGAAATTCGGTG
 GTAAGGGTGCTCGTTCCAGATTCCAAAAATCTTACCGTTAA

YMR143W, 143 aa (SEQ ID NO 220)

MYSEKASTFGKKKSATAVAHVKAGKLIKVNGSPITLVEPEILRFKVIYEPDLLVGLDKF
 SNIDIRVRVTGGGHVSQVYAIRQAIKAGLVAHYHQYVDEQSKNELKKAFTSYDRTLIIAD
 SRRPEPKKFGGKGARSFRQKSYR

YMR174C, 707 bp, CDS: 501-707 (SEQ ID NO 221)

GTCCCATCATCTCTTTACACCTCGTACTGTATTTCATGATCATCATCCATTTTACATACCG
 CTCCTTTAAGATACGTTTATTTCGTAACCTCCCATTTACCAATCACTATGAGCCGCTGCACG
 TTTCCAAAAAATCAAAACATATGATGCAAACTCCAATGAGACTCAACGTAAACATGCAAA
 GTAAATACAGAAAGGTTAAGAGATAGTTGCTTTAAAGGGGTACCGAAAGCAATTTAGGGGAG
 GCTTAAGGGAGGGTGCCGATCTCATGAAGTATTAAATACGTAATGCCAAAAGGAATTGTTG
 AACATCTGAAGTGGATAGATTAAATCGTACAGTAATCGTACAGTACTATTGCTTACTGATG
 TCGGGAATCTCAGGGGCGACCGCCCCGGCTAGAAATTTATATATAACGTTAAAAAGAAAT
 AAAACTCTATTCTAGTTCTCGCCATTTACCTTGACTTTAATGAACCAATAAAAAGAAATTT
 CTACAACCAAGACATCCAGAATGAATACAGACCAACAAAAAGTGAGCGAAATATTTTCAAG

FIG. 1 - 76

GCTCAAAGGAAAAATTGCAGGGCGATGCAAAGGTAGTGAGTGACGCTTTTAAAGAAAATGG
CTAGTCAAGACAGGAGCGGCAAGACTACCGATGCTGATGAAAGTGAACAAACACAACATATC
AAGACCAATTACAAACAGCTCAAAGGGGCGGGGCATAAGAAAGGAGTAG

YMR174C, 68 aa (SEQ ID NO 222)
MNTDQKQVSEIFQSSKEKLQDAKVVSDAFKKMASQDKDKTTDADESEKHNYQEYQYNKL
KGAGHKKE

YMR191W, 1877 bp, CDS: 501-1877 (SEQ ID NO 223)
GGTTCGATACAACTTGTGCTGGCTGGTATATCAACCATGGGTACGTCAGCATATTTGAT
TCGATGTGGCAGGTGACGAGAGCCATTCTGTATCGTTCGACAAAGTTGCAATGACTTCAT
GTGTGTTCTGTACAGTATTCGTGTGTCAGATGCAGGAATGCTGGTTTAAAGTTTGGTGT
TTCTCGTCCACATTCATCTTTGGATTGGCGTTGTGGTGGCGAATTTGCTTAGGCCCTTT
TGTTTCGCGATGTGCTTTTGGATAGCCTGGAAATACGAAATCTTTGTCTTCCTGTAAGAGTCG
CCGTTTCCTTTAACCAATTGTGTCTCCCTTCTTAAGTTATGTGACGGCTTCGTACCAATTA
CCGCCCTGTGTGTACGTGTATGATTTTAAATATATACAAACATAATCTGTATTTTTC
TCTTCTCTTAGCCAATGACTCCAAGCTGGCTGTATAAAAACAACTAAACGGTAAAGCCAC
AAATCCGAAATGTATCAACCAATGATCACCCAGCCTGCTAAGTGCCTCTATTGTATCCGTA
TATCAGCTTTTAGTACAGGCTCGAGTTCTTGTATATGTGCAATTCGAAAGCATATAACA
AATCTCGGACCGCGAAGCCGGGCAATCCACTTCGAAACCGCAGCGCTGAACATATATAAAT
TAAAGGACATGTGGAGAGAAGCTTCTCTTCTTCACATTTTCGCAATTTTCATGATCTAAAGT
GGTTCTTTTACAAATAGAAAGAGCACCAACACGAAATATGGCTCTCGGTGGTAAATACCTGGA
CGATGTGGCTGCGAATGTACCGGGTCCACCTCAGGCAGATACGAAAGTCTCTGACCGCAA
CGCTGATCAGTTTGAGCCATGGGAATTTTCCCAACCAATATAATCGCAATATTTTGTGCA
CTTGGTGGAAAGACCTATTGTAGGCTTCTACAGCTTTTAGGAGGGCAAGTGGTTTAAACGG
TATCTCTCTCTACGAGGAGAGGAATCGCAAGGTTTACCATTTTCAGACCTGTTCCCAATG
TCAGTAAATTTGCTTCTTTTCCAGAGTGCCCAAAGGAGCCCCAAGGGGCCCTTTTACCA
ACTGGAATATGACTACATCAAGAGATTTATAGGGCAGAGAGCTTATTCGACTTCCAGTA
TCAAAATTTACCAAGAAGCCGTGAATAACATGACATATCTTTGAGGTGTTTTCCTCAACT
CACTAGGCGGATTAATCAGTGTCTCCACTCTAATTCTCGAAAGCTTATCAGAATCGCT
CTAATGTTACCTCTAAACAGGATCACGCTCCAACAGTTGCGCTTAAAGAGTTATCTCAAA
AGGATATCAATTTTATTGTAATTTAGAACTATTAAAGATAATGAAGACCGAGAATGAAG
TCGTTGATGAAACAGCGCATATTACATGGAAAAACAGGTTCCCTATATTGAATTTACCA
TTTCAGAAATTTAACGTTAAATGGGACATTCTCCGACCTTTGTCAATTTTATGATCTTCTT
TGTAGCGGATTTGGATGAAATGATTAGAAATTACAAATACGAAATTAATAATCAATATACA
GTAGTGTGACATGATCTTCGAGAATTTATGGATCATTGCGGATAACTTTTTCATCGAAATA
AGATTGCAATACATTTTCCAAACTCAACTGTGTGTGGAACAGAAAACTAATTGCAAGGTC
TGAATATTGCTACGGGTGTTATTATACGCAGATACGCTCTCCGATATCAGTCTAGAAGGTA
CAAAATTTGAATGCTCTGTTAATGTGACAAATCAGGAAGCGTATGGTCTTTTGTAAAG
AGCCCTCGTTTCCCTCTAGGAGCGCTTTTACCTATTTTATCAGATGCATCTGATGATA
CTTATGAATTTGCTCTAG

YMR191W, 458 aa (SEQ ID NO 224)
MITQPAKCPLLLRISAFRSGSFLLVHCKSIWNQPKPNPLNRNLNRYINIKMDWRE
ASLPSHFAPHDLKWFPHNRRAPTRNMAVGGNNWMSRLMSRVHLRQITKSLDRLLSLSH
GNFSHOYNNRNIIVTWKSLFEASTAFRRASGLTWSPLTRRGIAFDHFRFPVNVKSFASF
PRVPKGAAPRGLTFNNMNTTSKRLLGQRAYSTSSIKFTQEA VNMNTTSLRCPFNSLGLGLNQ
KSHMSCKYQNASNVTSKQDHVPALKKLSQKIDINFRNLFLPKIMTKONEVVDSTSA
YYMEKPGSVILEFTISEFNVNQTFSAFLSFLDPSLLADLDEMIRNVKYELKSIYSSVDMILV
QNGYSLFIPTFHRNKRIRHFPNSTVVEETKLIAGLNIATGVVIADTSPDISLEGTNLNLV
NVNDSGVNSVFKPEFSFSSAFSPILSDASYDTYELV

YMR230W, 1228 bp, exon1: 501-552, intron1: 553-962, exon2:
963-1228 (SEQ ID NO 225)
ATCAAATATTGATCGAGTTCATATAAAGCTAAAGAGTAGGAAATATACCATCAATGGTGA
GCACTTATTTTTTTTGGATTAGATGTGAGACATACTAAAAAAGTTGCTATCAAGCG
TATAAATTTGGCTACGTTGTCTCCGGTGTTTATTAATTTGATTTAAGTTTACAACTCAAA
TCTGGGTAATTTGATCTTTTTTAAATAATTTATTTAGTGACATATAGTTCTTAGAGTTTCG

FIG. 1 - 77

AGATTATTTTGTGTCATTTTGGATCGGCGTCTTATAAAATCAAGACATAATACATCCGC
ACATCGCGCATGTGTGGGTGTATATGCCCTTTTCACGATTTTAAAGTTCGCTCTCAAAT
AGTTTCCGAGTTGGAAGCCTGAGTTTTCAAAACAATATAGGAATTTAAAGGTATACGTC
TTGGATACATGTTATTTGAAATGGGTTAGAACCTAGCACAACTGAAACCAAGAAACACAG
ATCATAACTAACGTTTCAAGATGTTGATGCCAAAGCAAGAAAGAAACAAATTCACCAAT
ACTTGTTTCAAGGTATGTTTGCATTTTTAGGTGAAATATGCGATGATATGCTCCGAAAT
GGATAGCAAGGATGATAAATGAAAAATACAATTAATTGAACCTTGAATCATTTAAAGTG
GTAGAAAAACCGATGTTTCAAAAAGATCTTTGTGGACAAGTACGGCAGTGATGAATCCG
AAGAAAAAGTGCACCTAAGCAGAAATTCATTTATTTTCACGCGTCCATTTTATATAGTTT
GAACTTTGTAGTCTTATAGAAATGCTAATATTTATGATCAAGCGATATATCATTTACT
TTTCAGTTTCCGGAGTTTCCGTATTATTGCAAAAGGACCACAAACAAATGAAATCATGAT
ATCGGTGAAGAAATATTTACTAACAAGGAGATCATTTGAATTTACGATCGCATATCGAAAT
AGAAGTGTGTTGCTCGCTAAGAGGATTTCAACCAAGCTAAGCAACGAAGAAATGTATAC
CAAGAATCTGTATGTTATCAAGGCTTTGCAATCCTTGACTTCTAAGGGTTACGTTAAGAC
TCAATTTCTCATGSCAACTACTATTACACTTTGACTGAAGAAGGTGTTGAATACTTTGAG
AGAATACTTTGAACTTGCTTGAACCATTTGCCAGGTACCTACATTCAGAAAGAAACCC
ATCCCAAGAGCTCAAAGAAGATACTAA

YMR230W, 105 aa (SEQ ID NO 226)

MLMPKQERNKHQYLFQEGVVAKDFNQAKHEEIDTKNLYVIALQSLTSKGYVKTQFS
WQYYXYLTLEGVEYLRLEYLNLPEHIVPGTYIQERNPSQRQRRY

YNL054W, 3998 bp, CDS: 501-3998 (SEQ ID NO 227)

CCCTTCGCTAAATCATTAAGAGGTGTCATGAAGTTAAATTCAGCACAAGGTTGGACTG
TTAGACACGAGATACACATTCGAGTCCAAATGTGCAGATTTTTCAGATAAATGTGCTGTC
ACAAGACTGCCCTTCCCGTCTCTCAGACGACACAAAATAGATTTTAGCTTTACATAAAG
ATGTACATAAATGAAAAACGTTAATCCCTCTTAAATTTAGACCTTGTAAGTCTTCTCG
GCCACTCTTTGTGATATATTTGTAGTGAATATATTGATTTCGTTCTTATTTCTTTGTT
CTTAGGCATTTTCGCTTTTAGAAAAATTCGTTGGGTGGTTTCTGCGACGGGTATCCCTTCG
ATTTTGCATAATGATCTTCAATTCACAACTAAATCAAGTAGATACAGGAAAAATATTCC
ATAAATATAGTGTAAATCGCCCTGTATACACCTTATCGTTTCATCTCAGGCAAGTTAAA
GCATTTGGGAAACGTGCTAGATGACAGAAGAAGTAGAAAGCTCACGTGAGAGACAGAAA
CAGTTGAGGCACCCGTGGCAATAATCTTTTATTGTGCAATAACAGTAATGTAGTAGAC
CTAATCTCTTATTTCCCTTCGCTCCACATCTACCTCTCCGCTACACAGGAAAAATGTTG
ATGATTTCTGTGCTACTGCTAACACCCACGCAACGTTGTACAGCATAAATTTGCCACCA
TAGATAACAATTTAATGGATTCGATGCCACGTCACATAATCAAGATCATTTGGCATTCAG
ACATAAACCAAGGAGGAACATCAATGTCAACGAGTGATATCCCAACAGATTTACATTTAG
AACATTTCCGGCTCTGTTTCACTCAACTAATAATAATAGTAACAATGCGCTAATCAACACA
ACCTCTGTGATCTCATCTTTCCAATTCGCTCATCTTCATTACGAAACAAGAAGAGCTCTT
TGTGGTAGCTTCTAACCTTCGCTTGTCTCAGATGTTGAACCTCTCGAAGAAGAAACCTG
CCGCTACTCCAATAATATGCTTACAAGTAACATTTGCCCTTTATCAACAGCGAGATCGG
CGAATATTCTAGTCCATCATCACTTCCGCTCTTAAAGCGTTTCAAGAAAGCTTCGGCTCT
TCTCCAATAACAGCGCACCCAGCACTAGTAATAACATCGGCTCGAATACACCTCCAGCT
CTCTTTTACCTCTACCTTCACTATCACACAAAATAAGCCAAAATAATAGAGAGGCCCA
CAATGACGTCACATAATTCAAGAGAAATACTTTTAGGTGAAAAACCTGTTAGATGATACAA
AGGCGAAGATGCTCCCGCAATTCACACACACAGATTAATGGTCCAGTAGCAAAATGATG
GGCTGCGTATACCGAATCACTCGAACGAGATGATAATGAAAAATACACAAATTAAGA
AGAATAAAACATTAATAGTGGGAAAAATGAACGTAATGATGACACAGCAAAATATGCA
CTACATCTACTAAACAGCGCTTCAACCGCACCTTTGGGCAGTACAGACAAATACTCAGG
CTCTCACTGCTAGTGTCTCCAGCAGTAATGCTGACAACTACAATAATAACCAAGAAAA
CCAGACGACACACACCGCAATAACAGTAAATAGTGCATCCAATAAAACCAATGCCGATA
TCAAGAACTCTAACGCCGACTTGAGCGCTTCTACCTTAACAATAAGTGCATAAATGACG
ACTCATGAGAGTAATTCAGAAAAACCAACAAAGGCGGATTTTTCGCTGCAAGGCTCG
CTACAGCTTATAGTGAATAAGTGAATTTAGTGATTCTGAGGAAACATTTGTTTATGAATCGG
CAGCTAATTCGACTAAAAACCTAATATTTCCTGACTCCTCCAGCCAGCAGCAGCAGCAGC
AACGACAACTCCAAAACACAGCAACAGCAACAAATCATGGAATTAACCTCAAGATAA
GCGCCCATTTGCTAAACATAACAAAAAATTAATAGCCGACTGAAAAATTCAGACATA
TTAGCACTGGTCCATATTGAATAACACAACTCGCATATAAGCACAAATCCGAACCTGA

FIG. 1 - 78

ATTCTAATGTGATGCAGAACAAATAACATCTGATGTCGGGACACAAATCACCTGGACGAGT
 TGAGCAGTATAAACAAGGAGCCACCGCATCAATTGCAGCAGCAGCAACCAATGGATG
 TACAATCGGTAGATTTCGTATACCTCTGACAAACCCAGACAGCAATGTTATTGGCCAAGTCGC
 CTGATAAGAGGTCAAGCTTAGTATCCCTATCTATTAAGCTTTCTCCACATTTACTTTTCATCCA
 CATCAAGCAACGGTAACACAAATATCGTGTCCCAATGTTGCCACAAATTCGCAGGAATTTGG
 AACCAACAATGATATTTTCAACGAAGAAATCTCTTTCCAATTTCTACTTTGGAGACATTTCTCT
 CTGTAATATAGAAATCTTAATTATGGTGACACAAAGAGCGCTTTAGAACACAAGTGTGCAA
 AGATATTTGATCTCAAAACCCCTAATGGAGCTCTTTACGGAGATACTCTGGGGTACCGGATG
 ACGTTAATCTAGAAGATTACATCGAACAGCGCATATAATTATCCAAACAATGCAAAATAGTG
 TGAAGAAAGGATGAATTTTATAACAGCAGGAAACAATAAGTTTCCCCATGGTTTAAACTTTT
 ATGGTGTATAACAATGTTATTGAAGAGGAAATAATGGTGACTCGTCTAATGTAAATCGAC
 CGCAACACATCAACCTTCAGCATGAGTTTATTCCAGGAAGATAACGAAGGTGATGAAACAG
 ATTTTCACTCCATGTTTATTATTAATCATAGAAGACGATTAGAAACAAACCGCTAATATT
 CCGATTATGGTGAAGATGAAGACGTAGATGATTATGATCGCCCAAAATGCTACTTTCAACA
 GTTACTATGGCTCAGCATCCAACACGCAAGAACTTCCATTACATGGAAGGATGCCTTCAA
 GATCAAAATATGATTACTACGATTTTATGGTTGGCAACAATACTGGCAATTAACAACCAAT
 TGAATGTATATATATCCCTTAAAGAAATGAACGTGGTCAAGACACCTATCAAGAACAAACA
 ATAGCATAAATGAATGGTAGCATCCATGAATGGTGAACGATGACGTTACCCATTTCCATA
 TCAAAATAACGATATTGTTGGTTTACTCACCGCACAACTTTTACTCAAGGAAGTCCCAAT
 TTGTTGAAGATGAAGAAATTTTCTTTATCTTCGATTTGTTATATCATCACTATTGATGACAG
 GATTCATCTTGGGATTTTATTGGCCACTAATAAAGAACTACAAGATGTAGACGTGGTAG
 TGATCGATAATGTGATTTCAAGTCTCGGACGAGTGTATCTTCGACATCAACAGATAGTGCTT
 TTAATCCAGGATTTCTCAGTATAAGCGTTTCCCAAGTCGATTTGGACATTTTTCGAAAAA
 GTTCTTACCTGAAGTGGATTTCTAATGCTGACTGTACAGTAAATGGAACAGGAACCGAAAA
 TTTTACAAATAACGACAAATCTTTCGTAGTTGAAGAGAGTGCTAATAATGATATATTAGT
 GTGGGAACATAGAGACGGTATTACTAGGAACCGCTAAAAAATAGAGACACCTAATAAGT
 TCCAGGCGCGCGCATTAAATAGGAACATACGATGTGTGAGTCTCGAGTGTCAAGCTTTTAA
 GTCTTGGGTCTCGTGAAGCCAAAGCACGAAAAACGACGATGATGACGATGTATGGCGACG
 ATGGTGACGATGAAAAACAATACTAATGAAAGACAATAACAAAGCAACCAATGTAGTACGAG
 ATGACAAAGAAGATGATACTAAAAAATGGAAGCTACTAATCAAGCATGATTACGATATGA
 TAGTCCGTGGAACATGAAGTATGAGTGCCTTTTTCAAATACGCAAAAAATCTACGGCTA
 TTTCAAAAGGATTCATGGTCCATCTCGTGAAGAGTGA

YNL054W, 1165 aa (SEQ ID NO 228)

MTEEDRKLTVETETVEAPVANNLLSNNSNVVAPNPSIPSASTSTSPHLREIVDDSVATA
 NTTSNVVQHNLPTIDNNLMDSDATSHNQDHWHSIDINRAGTSMSTSDIPTDLHLEHIGSVS
 TNNNSNNALINHNPLSSHLNPNPSSSLRNKKSSLLVASNPAPASDVELSKKPKAVI SNMN
 PTSNIALYQARSANIHGPSSTSSAKAFKASAFSNNTAPSTSNIGSNTPPAPLLPLPS
 LSQONKPKPIERPMTHTVNSREILLENLLDDTKAKNAPANSTTHDNGPVANDGLRI PNH
 SNADDNENNNMKKNKNIINSQKNERNDTTSKICTTSTKTAPSTAPLGSNTDNTQALTAASVS
 SSNADNHNHNKKKTSNNNGNNSNSASNKTNADIKNSNADLSASTSNNNAINDDSHESNS
 EKPTKADFFAARLATAVGENEISDSEETFVYESAANSTKNLIFPDSSSQQQQQQQPPKQ
 QQQQQNHGITSKISAPLLNNNNKLLSRLKNSRHI STGAILNNTIATISTPNPLNSNVMQN
 NNNLMSGHNLDELSSIKQEPHQLQQQPPMDVQSDVSYTSDNPDSNVIAKSPDKRSSL
 YLSKVSPHLLSSTSSNGNTISCPNVATNSQELPEPNNDISTKKSLSNSTLRHSSANRNSN
 VGNKNRPLRTTVTSKIFDSNPNGAPLRRYSGVPDHNLEDYIEOPHNYPTMONSVKKDEFY
 NSRNNKRFPHGLNFGYDNNVIEEENNGDSSNVNRPHQTNLQHEFIPEDNESDENDIHSMFY
 YHKNLDLETPLKPLSDYGEDEDVDDYDRPNATFNSYVGSANTHELPLHGMRPSRNSNDY
 DFMVGNNTGNNSNQLNEYTPLMRKRGRLSRTNNSIMNGSIHMNGNDNDVTHSNINNDIV
 GYSPHNFYSRKNSSPFVKVKNFLYLAFVSSLLMTGLFLFLLATNKLQDQDVVVVMDNVS
 SSDELIPDITVSAFNPGFSSISVSQVDLDIFAKSSYLKCDNSGNDCTVMEQERKILQITTN
 LSLVEESANNIDISGGNIETVLLGTAKKLEPLKFKQGAFFNRNYDVSVSKLSPGSRSE
 KHENDDDDDDDGDDGDDDENNTNERQYKSKPNARDDKEDDTKKWLLIKHXYELIVRGSKM
 YEVPFFNTQKSTAIQKDSMVHFGKK

YNL067W, 1076 bp, CDS: 501-1076 (SEQ ID NO 229)

GACGACTATTGATGCCAGGCAAAATTTGGATTCTACTGCTCTCTTTTAAAGAAGACAAGTG
 TGTGATATCTGAGCGTAGGAACCAATTTTGAACATGATTACTTACAGCCAAGAAAAATC

FIG. 1 - 79

TAITTTTCATGTTTAGCATTTGCCATTTCTTCTGTGTACACAGTGTGTGCTTGCCAGGAAC
TAGGAGAGCATGTATACAAGCATCAATGTTACGAATGTACGATCCCGTTTGATCTGTAGT
GTAAACTCATGTGGTGGCACTGGTGTGTTTCCAGAGTGCACATTAACCTGGGAATTTT
TTTTTCTCTTAGTGAAATTTTTTTTTAAAGCGACGCACAGGAAAAGTGAAAATATTATTAA
ACGGACCGCAACATGAAAAAATAATACCAACCATATTCTATTCTCTTCCCTTCCCTTAC
CTATTCTCTTTTGAATAGTTTCTTTCTCTCTGAAACGACAAATAAACCAAACTCTA
GCCCTCAATAGTCTAAAGATGAAGTACATTCAAACCGAACAAATAATGAAATCCCGAG
AAGGTTGTACTGTACGATTAAGTCCAGAATCGTCAAGGTTGTCCGGTCCAAGAGGTACT
TGACCAAGCACTTGAAGCATATTGATGTTTACCTTCCCAAGGTCAACAACTTGAATCA
ACGTTGTCTGTTCACAAACGGTGACAGAAGCACCTTCCCGCTTTGAGAACCGTTAAATCTT
TCGTTGACACATGATCACTGGTGTACCAAGGGTTACAGTACAGATGAGATACGCTGT
ACGCGCATTTCCCAATCAACGTCACATGTTGAAAAGGATGGTGTCTAAATTCATTGAAG
TCGAAAACTTTTGGGTGACAAGAGATCAGAAACGTCCTCAGTTAGAGATGGTGTACTTA
TCGAATCTCTACTAACGTAAAGGACGAAATCGTCTTATCTGGTAACTCTGTTGAAGACG
TTTCCCAAAATGCCGCTGACTTGCACAAATCTGTCTGTGTTAGAAACAGGATATGCCGTA
AGTTTTCGATGCTATCTACGTTTCCCAAGGGTTTCAATGTGCAAGACATGTAA

YNL067W, 191 aa (SEQ ID NO 230)

MKYIQTEQQIEIPGVTVISKSRIVKVGPRGTLTKNLKHIDVTFKVNQLIKVAHVHNG
DRKHVAALRTVKSLVDNMITGVTKGYKMYKRVYVYAHFPINVINVEKDGAKFIEVRNLFGD
KIRNVFVRDGVTTIEFTSNVKEIVLSGNSVEDVSQNAADLQICRVNRKDIRKPLDGIY
VSHKGFIVEDM

YNL075W, 1373 bp, CDS: 501-1373 (SEQ ID NO 231)

TCGATGGATATCCCATCCAAGAACAGGAATACCTGGGTTTTTGAAGACCAGAATGGAGATC
TCTGAGGAAGAAAAGATGGTACGTACAATATCACCGCTTGACAAATACGAGTATTGCAAC
AGTAATGGAATGGTAAATGATGACACCTCTAATCAGAGAACGGAAGCACTGGGCGCTAAG
ACGAGTAATGGAGGGCGAATATGATTACTAAGTTAAATAAATCAGATACAGATATTAAAG
TCTTTTCAAAAAAAGATAATGTCTATATTTTACTATCTACGCACTGAAAGAGATCTCTTC
TAATGACACACTATTCTACTCGGTAACGGATATTGTGTACTGAAAAATATAAAAAATTT
TATCCCGGAAATGCGATGAGATGAAATGCATGAAGTAGCGTATATATTGATTGTCATGAG
GTTTGACTTGAAGGGCATATATCTCGGTTTTTATCATTGATTCAAGTGTCCCAATAAT
AATAAAACAGTTAAATCGAAATGCTAAGAAGACAAGCCGCTGAAAGGAGAGAATATCTAT
ACAGAAAGCGCAAGAATTACAAGATTCTCAACTGCAACAAAAACGTCAAATAATTAAC
AAGCGCTAGCTCAGGGGAAGCCATTGCCAAAGGAACATGACAGAAGATGAGAGTTTACAAA
AGGATTTTCAGATATGACCAAGTTTAAAGGAGAGCGAAGAAGCAGATGATCTACAGGTTG
ATGATGAATATGCTGCCCAAGTGGTATAATGGATCCAAGAAATCATGCTCAACAATCTC
GTGACCCAAGCACTCGTCTCTCGCAATTTGCCAAAGAAATTAACCTGCTATTTCCTCAATG
CTGTGAGCTGAACAGAGTAAATATGTGTATGCCAAATCTAGTGGATCTGTGTAATAAAT
CCGCTACTACAGATTGGTGGTATTACATGAACATAGAGGTGTTCCAACTTCTTTGACCA
TATCACATTTCCCATGGAACCCACTGCACAGTTAGTTTACACATGTTGTTATGAGAC
ATGATATTTATAAATGCTGGTAAACCAAGCGAAGTGAATCCACTATATATTGATAACT
TTACTACCGCTTTTAGGGAAGAAGTAGTCTGTATTTTAAAGCACTTGTTCATGCGGGGG
CCAAAAAGATTTCCGAAGAGTAACTCACTTTTTCGAATAGGGGTGATTTCATTAGCGTTA
GACAGCATGATATGTGAGAACAGAGAGGGAGTAGAGATTGCCGAAGTGGTCTAGAT
TGTAGATGAGGTTGTTTGAACCTGAGTTGGGAACCTTAGAAAAAAGAGATGATGTTG
AGTGGCAGTTGAGAAGATTCTAAGGACTGCCAATAAAAAAGACTATTGTGA

YNL075W, 290 aa (SEQ ID NO 232)

MLRRQARERREYLYRKAQELQDSQLQKQRIKQALAQGKPLPKELAEDESLQKDFRYDQ
SLKSESEADLDQVDEYAATSGIMDPRIIVTTSRDPSTRLSQFAKEIKLLFPNAVRLNRG
NYVMPNLVDACKKSGTLDVLVLEHHRGVPSTLSIHFPHGPTAQFSLHNVVMRHDINAG
NQSEVNPHLIFDNFTALGRKVVCLIKHLFNAAGPKKDSERVITFANRGDFISVRQHVYVR
TREGVEIAEVGPRFEMRLFELRLGTLENKDADVEVQLRRFIRNTANKKDYL

YNL096C, 1418 bp, exon1: 501-644, intron1: 645-989, exon2:
990-1418 (SEQ ID NO 233)

AAACACCTACTTTATAGACACGACCAAACTTTCCACAACCTTTCATCAGAGAGAAATGTTG

FIG. 1 - 80

ATCAAGTTGAATGCGTGAAGTAGCAATTTCGAAACAACAACCTACCTGTCATTCTGCATAG
 TACTAGTTTACGAAAGGCACAGAAAATAACAAAAAAGTCAATTTTCTACGGT
 CTCCTACCGTACCTCTTTAAATCGGTACATATTATGTTTGTCTTAATTTCAATATTTTCGGA
 AAAAGCGAGCGCCCTGGTAAAATGTGGTTCAAGCGCTCGGAGCCTTTGCTGTGTAACAC
 CAAATGCAATTTCAGTACAGTTCCACACAGTTTGGGTTTCCAGCCTGGCTTTAGGGAAGAA
 TGGGCTCCTACCTAGCGGTTTCATAATACGCGGAGGGGAAATACCAAAATGCTATTGATTAATGG
 TTAATAATGTTGTTTATTGACTTTGTATATACAAAAGAGAGAAACCAACACACTAAAG
 ACTAGACACATAACTGACCAATGTCTCTGTCCAAATCCAAAGATCTTATCCCAAGCTTCCAA
 GTGAGTTGGAATTACAAGTCGCAAGACCTTTCATCGATCTAGAAAGCTCTCTCCAGAAC
 TAAAGGCTGACTTGAGACCAATGCAAAATCAAATCTATCAGAGAAATGTTTAAAGTTAT
 ATAATTTGGAAGCAGCAACATTGTGATTTCTTCAAAGGGGTTCTTTCGAGTAATTTT
 CAAAAAGAGTGATTTTGTAGCAGTATCTGTATGAAATTTTTCATGTGTTTCGAGAAAAATAG
 TAATTCGAGAGCTGTCAATACCATGAACGTTGCGATGAGCCTTTGAACTATAAAGGCCCT
 CCTTGGTCAGTACCAATATCGATGAATAAATAGAAGCAGCGGAAAAAGACCTTACCCCA
 AGGAGAAGAATCAACAACCCCTTTTGTGTTATGAATGAACCAATTTCAGTTACTAATTTTAT
 TTCAACGCTGTGTTGATTTCTTATTGTTTATGATTGATTCACCGGTGGTAAGAAAGCACTAG
 TCCTTTTGTCTCCAGTTCCAGCTTTGTCTGCATACCATAAGGTCCAAACCAATGACCC
 GTGAATTTGGAAGAAGAAATTCCTGACCGTCATGTTATTTCTTGGCTGAAAGAGAAATG
 TGCCAAAACCTCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCTCAGAATTTGA
 CTGCTTTTTCAGCACAAGGTTTGGGAAGACATGTTTTCCCAACCTGAAATGTGCGGTAA
 AAGTTAGATATTTGTTTGGTGGTAACAAGATCCAAAAGGTTTGTGACCTCAAGATG
 TTCAACAATCGACTACAAGTTGGAATCTTTCCAAGCTGTCTACAACAAGTTGACTGGCA
 AACAAATGTTTTTGAAATTCGAAGCCAGACCAACTAA

YNL096C, 190 aa (SEQ ID NO 234)
 MSSVQSKLSQAPSELELQVAKTFIDLESSSPELKADLRPLQIKSIREIDVTGGKKALVL
 FVPVPALSAHYHKVQTKLTRELEKFPDRHVIFLAERRILPKPSRTSRQVQKRPRSRSLTA
 VHDKVLDEMVPFPEIVGKRVRVYLVGGNKIQKVLDSKDVQQIDYKLESPQAVYNKLTGKQ
 IVFEIPSQTN

YNL162W, 1333 bp, exon1: 501-504, intron1: 505-986, exon2:
 987-1333 (SEQ ID NO 235)

TTTCATCACCAATATAGACTAATGCGTTTGGAAAGCGCAAACCGCAGTGACAAATAGCAAA
 TATGTAGCTGTGCATATCGGCATATAATAACAGTTTCTACCAAAATGCTGTCCATACATCA
 GAGATCTTACATCCTTACATCTAAAGTAAACCTAGACATTTACTTCGAGTTTACTTTTT
 TTTTTATTATCTATTTTTTCTCTGCGGACATTTAACACCTGAATTCGCCCTAACGCCA
 GGACTGATCTCTGCCAGGGAAGGGAGCTTTGTCTAGTGCCAAATAGGCCGACAGTAGGAA
 GGTTCACAGCAGCTGGCCCGCAGAGTGTATGGGTCAAGGAAATAGCCGCAACCTTCTCTTT
 TGCCCGGGAAGGCGGTTCAATCTACCTTCGAAGGGCTAGTACATGAGCGCGAAGGAGGC
 AGATAATAGCAACCAATTAAGTGGTCCAAATGCATCTTGAAATCTAATCCTTAATAGAGGAA
 AACACAATATTACGTAAAAATGGGTATGTTATAAACCAATATCTCTAATGGTGAATAAAA
 TCAGGACCAATAAAGAAAAAGCTAATTTGATTTTATTTGTCAATGAAATTTTCATAATCGTC
 ATGAATGCATAAACGACACACCTAGCAACTGTATAATCTCGCCCTAAAAAGGCGGTATA
 CACAAAATCAAAACGATGCGCAATAAAAGTTTCAGCAGTCAGCAATGAACACGAGATATGCA
 GCAACAGAGATCATATGATGAGGAGTCTTTCTGTTTTCGTGATAATATGCTCTGAAA
 AAGCTCCAAACAGCAGCAGTAGCCTATTGTGGAAGCTCAAAAAGGCTTCTATTTCCTCG
 CTATCTTCAGATTGTGCAAGTATATTCTTTGAGGAAGGAAACGTAAGGGGGATTAAGTTGG
 ATAACTGTATTCTTTTCAATATGCTAGATTGTGCTTACACCTTACTGATTTTTCCTTA
 CTAATTAACAACTTTTTACTAACATTAGTACGATGTCTCATCTATTCTCTATTAGTTTAA
 CGTTCCAAAGACGCAAGAACCTACTGTAAGGGTAAGACCTGTGTAAGACACACTACA
 CAAAGGTTACTCAATACAAAGCTGGTAAGGCTCTCTTGTGTGCCAAGGTAAAGAGAGCTTA
 TGACCGTAACAACTCTGGTTTCGGTGGTCAAAACAAGCTGTGTTCCACAAGAAAGACTAA
 GACTACCAAGAAGGTTGTTTTCGATTGGAAATGTGTCAAATGTAGACCCAGAGCCCAATT
 GACCTTGAAGAGATGCAAGCAGCTTCGAATTTGGGTGGTGAAGAAGACAAAGGGTCAAGC
 TTTGCAATCTGTA

FIG. 1 - 81

YNL162W, 116 aa (SEQ ID NO 236)
 MVRCLLYFFYLNVFTRKTYCKGKTCRKHTQHKVTOYKAGKASLFAQGGKRRYDRKQSGF
 GGQTKPVFHHKAKNTTKKVLRLCEVCCKTRAQLTLKRCKHFELGGSEKKQKQALQF

YNL178W, 1223 bp, CDS: 501-1223 (SEQ ID NO 237)
 GGCTCCACGTCAGTTCCACACAATAACATTACGTAGTGTTCACGGGAAGCAGTTACATCT
 CAACTAACATCAATTGCTGGTGAGCCTACACACTGCATGCGTAAACGCTCAACGGGATTC
 GTTAGTATTTTTTGGCGCGCGGTAATTCCTCTGTTTCTTTCTTGAATTCACATCTCTTT
 CATGTTCCCTTTGGAAATAATCTAATTCCTCATGATTAAATGAGACGTGTTTTGTTGTTCCGT
 AACATCCATACCTTTCTCTGTATAATATTCCTGCTGTAAAGTTGTTTTTTATGAAAAA
 AACATTTCTTTCTTTGAGATGAGGCGCGCGAGCCTTCTCCCATGGGCACTGGTAAAT
 TTTCCAAATCAATCGAGCTCTTTGAAATACACAGCATTTTTCATACATTTTAAGCAATT
 TCTAGTTTGTAGATATTGTTAGATTAGTTTGTGAACATGTTTTGATACACTGAAAAATAAA
 ACAGCAACAACTACAAAAATGGTGCCTTTAATCTTAAGAAAAAGAAAGCTAGTCGCTG
 ACGGTGCTCTTCAAGCTGAATTGAACGAATTCCTCACCAGAGAATTAGCTGAAGAAAGTT
 ACTCGGTGTTGAAAGTCCGTGTCACCTCAACCAAGACCGAAGTTATCATCAGAGCTACCA
 GAACTCAAGATGTTTTGGGTGAAAAACGGTAGAAGAATCAACGAATTAACTTGTTGTTGTT
 AAAAGAGATTCAGTACGCTCCAGGTACTATTGTTTATATGCTGAAAGAGTTCAAGACC
 GTGTTTGTTCGCGTGTGCTCAAGCTGAATCTATGAAATTCAAATTTGTTGAACCGGTTTGG
 CTATCAGAAGAGCTGCTTACGCGTGTGCTCAGATACGTTATGGAATCTGGTGTCAAGGTT
 GTGAAGTTGTTGTTTTCGCGTAACTAAGAGCTGCCAGAGCTAAGGCTATGAAATTTGCTG
 ACGGTTTCTTGATTCACTCTGGTCAACCAAGTCAACGACTTCATTGACACTGCTACTAGAC
 ACGTCTTGATGAGACAAGGTGTTTTGGGTATCAAGGTTAAGATTATGAGAGACCCAGTA
 AGAGCAGAAGCTGGTCAAGGCTTTGCCAGATGCTCACCATCATTTGAACCAAAAGAG
 AAGAACCAATTCCTTGCTCCATCTGTCAAGACTACAGACCAGCTGAAGAACTGAAGCTC
 AAGCTGAACCAAGTTGAAGCTTAG

YNL178W, 240 aa (SEQ ID NO 238)
 MVALISKRKRLVADGVFYAELNEFFTRELAEEGYSVGEVVRVPTKTEVIIRATRTRQDVLG
 ENRRINELTLLVQRKFYAPGTVILYAERVQDRGLSVAQAESMKPKLLNGLAIRRAAY
 GVRYVMESGAKGCEVVVSGKLRAARAKAMKPADGFLIHSGQPVNDFIDTRATRVLMRQG
 VLGKVKIMRDPAKSRTPGKALPDVATIIPEKEEPI LAPSVKYRPAEETEQAEPVEA

YNL182C, 2168 bp, CDS: 501-2168 (SEQ ID NO 239)
 CTTTGATAAAATTAATACGGTAAGATACCGTGTGAACATTTATAATAACTGCCACGCTTAT
 AGCATGTACGCTATACATTTACGTGCTGAGCTCCTAGGAAAGCTCATGAGCAGCCACTGT
 ATCGTGGAGCATAACTACAACAAAGAATACACAGCGTCACATAGAGCGTTTGTGAGAGGA
 GAAGTTGAAATAGGACTTGATCTTGGGGGAGAGGGGATTTGAAAGCACCCATTCAAGGAT
 ATGTGCTGTAAATGAAGTGTAGCGCGCGATTCACTGTAATAAGAGTGATGATTTGAT
 AGGCCATTTACATCATATGGCAAAATGTTGAAAACTGTACGCGCGAACTAAAAATTTT
 TTTTACATCCCCTAAATGAAATTTTAAATCGATGCCCATTTCAAATATGCTTTATTTCGA
 AGGACGGCTCTGACAAGGCAATATGCGTTAAGATTGATTGTTCAATATTCTATAAAACAGG
 ATCTTTCAAGGGAGATAAAATGGAATGAGCAAGTTATTTTACAACAAATACCTCAGGAA
 CAATAGCTTCTGTACACTCATTTGAACAGATATAAATTTGAGGCAATGCTCCACTCAATCAA
 GAAATAGCTGTGTTCAAGTAGGAAATAAATACCTTTTATTGCTCAAGCAAAAAGCAT
 TAAATCAATGTCTCAATCTGTCAAGTTCTTTCAAAGAGAAATCTGTTGAACAGCGCTTAC
 CATTAACCTGAAATCCTAAAAATGCTCGAAGTAGTTGAAAAATGATGGTGTGATGATGATA
 GAATTCAGAGTGTCATCATATAATTTACAGACTTCAATCTTCCGTACCTTTTACTTGGCT
 CCACGATAGCTCGGGTAAATTTGATCATATGGGAGTTAAATTCAGGGATTTTATTGAACGCTGA
 AGCCTATGGCTCATATCCAAAGTATCACAAGATTAAGTCCATTTTAAACGGGAGCAAGTATA
 TTATTACTTCTGGTACAGATTGAGAGTTATTTATATGGCAAACTGTTGACTTGTATATCAG
 CGTCTCAAGATGATCTCAAGCCTTTATGTATTCCTTCAAGCATCACTCTACCCGCTGACAG
 CATTTCAAGTTTCTTCTAGTCAAGGAAATTTTATCATGTACTGATACGAAACTCTTCA
 AGGTTCTCAAGATGCTACCATATGATGCTATGATTTGAGTTTAAATAGGAGCAAAAAGA
 AGCAGAAGGCAAAACGAAATGACGTTAGTATTGGTAAGACCCAGTATGCTTGGCAGAT
 TTACAACCTCTTATTCTATCAAAATCATTGATGGATCTGCTGACAGAGCATGCTATATA
 TTGGTACTGCGGAAGGTGTTTTTTCATTGAATTTATTTTATAAACTAAAGGGTAAATGCTA
 TCGTTAATCTGCTACAGTCCGCGGAGTAAACACAGTTCAAAAAGGTAGGGTTTTTCC

FIG. 1 - 82

TAGTGCACGTAACCTACTAAGTGGCGGCGAAAAATGAAGATTTGGATGCACATATATGCAA
 TGGGCGCAACTTGTCTGTGAGAAATGTCTCTAAATTCAAATGTGTCAATGCTAGAAAATATCAA
 TGGATGGTACATTATTATTGTATCGGTGATACGAGGGGGAAGTTTCTATTGCGGAAAAATTT
 ACTCAAAACAAATATTAGAACTATCCAACTTTAACTACATCACAGGATTCAGTTGGAG
 AAGTGACCAATCTCTTAAACCAACCTTACAGAGCTCGAACGTGGAAATTTACTTTTGAAG
 GAGAAATCCAAAGGCAACACCTTAGTAAATGAATATGGTCAACAATTTTATGAAGATACCAA
 ACTTTACAAAGAGTTTATCTTTTGTGGTAAAAACAAGGCCATTACACGATATTTTGGTATC
 AGATAGGAGAAACGAGAAGCAGAGACAGATCCCTAAAGCTCGCATTAACACTTAAACGACTTTA
 ATGCTTATTGGGAGAGTCAAACGCAAGAAATCGATATTTTCACATATCCGTAAGAGGTG
 CAAGCAATGTAAAGTGATTGACAAATAAATCGACGCCACTTCATCTTTAGACACGAATG
 CCGCTAAAGATGAGGAATACAGAACTTAAAGACCAATAGAAGCAATTAAGTCAATGCGCT
 ACAAGGAGTTACGTGACATGCACGAAAAGCTGTACGAGGAACACCAACAGATGCTTTGACA
 AGCAATAA

YNL182C, 555 aa (SEQ ID NO 240)

MDEQVIFTNTSGTIAVSHFSEQINLRQCSTQSRNSCVQVGNKYLFIAQAQKALINVYNL
 SSGFSKRESVEQRLPLPEILKCLEVVENDGVQYDRIQGVNHNLPDFNLPYLLLGSTPESGKL
 IYNELNSGILLNVKEMAHYQSITKIKSILNGKYIITSGNDSRVIIWQTVDLVSASNDPPK
 PLCILHDHLLPVTDFVQSSSQGKFLSCTDTKLFVTSQDATIRCYDLSLIGSKKKQKANEV
 DVSIGKTPVLLATFTTTPYSIKSVLDPADRACVYTAEGCFSLNLFYKLGKNAIVNLQS
 AGVNTVQKGRVSLVQRNSLTGGENEDLALYMGQVLCENVLNSNVSCLEISMDGTLILL
 IGDTEGKVSIAEISYKQIIIRTIQTLLTSQDSVGEVTNLLNTPYRLERGNLLPEGSKGQ
 PSNNNGHNFPMKIPNLRQVIFDGNKNGHLHDIWYQIPEPEAETDPNLALPLNDFNAYLEQV
 KTQESIFSHIGKVSSNVKVIDNKIDATSSLSNAKDEEITELKTNI EALTHAYKELRDM
 HEKLYEEHQMLDQ

YNL190W, 1115 bp, CDS: 501-1115 (SEQ ID NO 241)

AATGCGCTCCGTCAGTCAGTGGCTGTGTGCTGAAACGAGACAATTTCTCAATTCTGTTGT
 TTGTGTACTGTATTTGTATCTTTACTATATATATGTGTGTAAGTTTCTTTTACCAATTA
 GTGCTCACTTCTCGTCTTTTATTAGGTGTGTGTGTGTGCGTAATTTTCGTTTCCGCTG
 ATTACTTTATATAGTGTAGTTTGTCTTGAATGTAATAAAGACTTCTGTTTTATTTTGT
 TTGTTATTTAGAAACAGTCTATCTGGTTAACTTAAACGAGTGAGCTTAAGATAATCTGA
 CTACAAGAAAACCAAGCTTCTATTACTTTGTTCCTTTCTCTTTTCTTTTGAATAAA
 GAATTTTCTCTTAAAGGAGTAACTTAAGCATTTAGCTGCACATTAACACTTTTTTTTTTA
 CTCTTAACACACACTTTTGGAAAGACATTTATTTTTTCGACCTTCTTTCCCAAATAC
 CAGCGCTTTATAATTGAAATATGAAGTTCTCTTCTGTACTGCTATTACTCTAGCCACCG
 TTGCGACCGGTGCTCACTGCTAAGAAGGGTGAACATGATTTCACTACCACTTTAACTTTGT
 CATCGGAGCGTAGTTTAACTACTACCACTTACTCATACCACTCAAGATAGTGAAGT
 TCACAAGACTTCCAAGTCCAAGACCCCAACCACTGGTACTCAAGTACGCTAAGT
 TCACAAGACCTCCAAGTCCAAGACCCCAACCACTACCGGTACTCAAGTACGCTAAGT
 TCACAAGACCTCCAAGTCCAAGACCCCAACCACTACCGGTACTCAAGTACGCTAAGT
 TCACAAGACCTCCAAGTCCAAGACCCCAACCACTACCGGTACTCAAGTATGTTAAGT
 TCACAAGACCTCCAAGTCCAAGACCCCAACCACTACCGGTACTCAAGTATGTTAAGT
 ATGCCGCCCTGGTCCATCTAATTTCACTCCATAAAATTTGTTTGGTGTATACCGCTGGTA
 GTGCTGCGGTAGCCGGTGCTTATTACTATTATAA

YNL190W, 204 aa (SEQ ID NO 242)

MKFSVTAITLATVATVATAKKGEHDFTTLLTSSDGLSTTTTSTHTTHYKGFKNRKS
 KTFNHTGTHYKGFKNRKSSTKTFNHTGTHYKGFKNRKSSTKTFNHTGTHYKGFKNRKS
 KTFNHTGTHYKGFKNRKSSTKTFNHTGTHYKGFKNRKSSTKTFNHTGTHYKGFKNRKS
 NFNSIKLFGVTAGSAAVAGALLL

YNL208W, 1115 bp, CDS: 501-1115 (SEQ ID NO 243)

GGTTATACACATATATATATTTTTCATTTTAAAGTCTTAGCTTTGTATCTTAGATGAA
 GTTTTGTGTTCTGTATATACAGTCAAGATATCATACAATCATAAATTCATTTCTCT
 GTTPTCCCTCTTGAGGCATCAAAACGAGTGTGTTGACTGATACACCAACATCAAGCA
 ACTTTTCTGGCTGCCAAAGCTGTGGCAGTATGAAACTGCTTTTTCGGCTGCATAAAACA

FIG. 1 - 83

ACCATGTGGAGTTTITACTGTATTTCGCATTTCCGCCCGCTAGCATTTCTCGTTCATGCTA
 AAAATGAGCGGTGGGCTAAATTATTCAGTATTAAATAATTCGGGCACCCGACAGCCCATACC
 GGAAGAGGGGCTGGCTGTTGGGCTTGGCAAACCACTCAATCTGAGCAGTCAATTTATAAAG
 AAAGACTTTAATTTGTCTTGTCTAAACACTTTGTAAGCCTTCCAAAATATAGATCACCTTAAAG
 CAATCTAACAAAGTGTCCAAAATGTCTGCAACGAATTTCTACTCAAGTGGCCCAACAAAGGTG
 AATATAACCAAGCAAAACCAACGAAGAAGAACTGGTGTCTCCAAACCAACGGTCAATTAAGGTG
 CCGACAATGGTTAACCCCAACGCGTGAACGTGGTTTATTTTCCACTATTGTAGGTGGCAGTG
 CCGGTGCGTACGCTGGATCTAAGGTGTGGAACAACCACTTCTAAGTTAGTGGTGTGGTCTGG
 GCGCATAGGTGTGGTTCATTCCTTCCCAACAAGATATCTGATGAGCGCTAAGACAGCATAAAC
 AACAGAGCAATACGGCAACTCAAACTTCGGAGGTCTCTCTCAAGGTGGACACAACAACC
 ATCACCGTCAGACAATAACAACAATAACGGTGGATTGGCGGTCCAGCGCGCCCTGGCGG
 TCAAGGTTTCCGAAGACAAGGCCCAAGGATTGGAGTCTTGGTCCCAAGAGTTTGG
 TGGTCCAGGTGGCCCAAGGATTGGTGGTCCAAATCTCAAGAATTCGGCGGCCAGGTGGC
 CAAGGATTTCGGTGGTCCAAACCTCAGGAATTCGGGGGCCAAGGTTCGTCAGGATTCAAT
 GCGGTTACAGTTGGTGGAATGGCTCAACAGAGTGA

YNL208W, 204 aa (SEQ ID NO 244)

MSANEFYSSGQGGYQNNQERTGAPNNGQYADNGNPNGERGLFSTIVGGSAGAYAGS
 KVSNNHKLGGVLGAIGGAFLANKISDERKEHKQEQYGNISNFGGAPGGGHHNHROTIT
 TITVDLAVQAALAVKVSSEDKAHLKLEVLVHKSLLVQVAKDSVVQILKNSAARWPRIRWSK
 PSGIRGPRSSRIQWRFTLVNGSTE

YNL210W, 1313 bp, CDS: 501-1313 (SEQ ID NO 245)

TCATAACGGGTTCTTTTCAAAAACCGTAAGAAATTTGAGGTACACCACTAAATACAAA
 TTGTTTCATACCGGTGACTATATCAAGAACTTCGTAAGGAACATTTAGAAAACCTCAATA
 TAGTAAAGTTTTCATCAGCAATCTTATCTGAGTAATATTATCTACGATCTAAATATAGGAT
 GATCTGCCGATTTAGGAATCGTACTGTAGATTGCTCTTGGCGACAGATATAGTGAATATC
 CTTTTCACAAAGTGGATACAGGTGGCTATCACTACCGCCATTTCACTAGGCAAGTAGAGTA
 TTGAGAAAACCGGTAAACTTTGAAAGTTGCAGATGCGAATATATATCTGGCTTTTGTAGTT
 CTATCCGCTAAACGGGACGATCGCATTTTAGCCGCCGACAGTGTAAATATAAGTAAATGAA
 CTTGGGTTAATTTGATTACGCGTACAGCTACTAATAAAATAAGACCGAGAGTTTAAATC
 AGCTAGTGCATACCAAAAACATGAGTAACCAACACAGCCCTCAGCCATTTTGTGTTGACA
 CCAAAATTGGTGAAACTATTAGAAGAGCTCCAGGAGGGAAGCAATTCACCAATAAAAACA
 TATTCCCGGAAAAGCATTATATTTGAAGCTCGCTCTTGATTATCTTTCTTCAGAAAGA
 ATTTACTAGAGTTTTCGCTCCACCTTGACAAGATAAAAGGAGTCATTAGACCAAACTATG
 AACTATATATATTTTGTGCCCTGTTGGAGGTGGATCTCTCAATCTGGTATTTTACCAGCA
 ATATATTTGGAATATGTTGCCAGGTTTGTTCAGGGGAGGACTTGGAGGTTTAAATA
 ATACTTTTACACATATCACGATAACCGCCTACGTATTCTCCAAGAAGACTTTTCTCAAT
 TGTTCAAAAAACTCAAACTAAGGCTTCTGTACTATGTTTACAGTGGAGGAATTTTTC
 TGACAACCAAGAAATTTTACCTCAAACTCAACAGTGGCAGAATCTGCAAAAGAGCACTA
 ATAAAGTACAGCAAAATGGGCGGCAACCGCAGATTTTCATAGTCACCTAGAAATAAAAC
 TGAACAAAACACAAATCACTTTCTCATTTGGAGCTAAAGGAACGAGAATTTGAAAGCTTGA
 GGAAGAAATCAGGCGCCAGCATAAAAAATAATACCTATTAGTGATAAAATGACTGCACATG
 AAAGSAACCACTTGAATCTGTTTCAACAAACATACTAATTTCCGGGTGACTTATACTCAA
 TTGCATTAGCCGTCACCGATATAGAGTCTGCATTAATTACTTTGGATTATATAG

YNL210W, 270 aa (SEQ ID NO 246)

MSNQHSPPQFCLDTKLVLKLEELQEGKQFNKNKIFPEKALYLKLALDYSPFRKNLLEFCV
 HLDKI KGVIRPNYDTIYLCLLEVDLLNLVFTDNLILEICLPRFVSREDLRFVNNTFTYTH
 DNRRLILQEDFSLFKIKTKASVLCFTVEEIFLTNQEILPNSTVAELQKSTNKNVQTYNG
 PQRHDFIVTLEIKLNTQITFLIGAKGTRIESLREKSGASIKIIPISDKMTAHERNHPS
 VQQTILISGDLYSIALAVTISIESALITLTL

YOL031C, 1766 bp, CDS: 501-1766 (SEQ ID NO 247)

AGTTTTTTTTTCTCGAGAAATTTGTAACAAAAGAAGCAAGACACAGAAGATGATAAGAG
 AGAGAAACCAAGAAAGAAACCAAACTGTTGGGTTCCACCGAGAGATATTGACATATT
 GACCTTAGAAAAAGGCATTACTGAGGCTACTGACTAAAGCGCGTTACATAAATGCATAGTA
 TATTTCTTGTGTATACGAGCGGCCAACTAGTGGCAGCAAGATGTAATGAACGATTCA

FIG. 1 - 84

TCTCGAGGTTTGGAGGCCCACTAGATCAAAACGTAATAGCGGGTGAAGTGTCTTGGA
CGTTAGAAAGTAACTCCGAGATCGAAGCTAAACAGAGATTAGATTTCGGGTAAACGGAA
TTGTGATAATTAAAGAAAGCCAGACTATGTGAAAAGGCCACGTAAATGATAGAGACACATA
TTAGCAACTATAATAGACTAGTTTTCGCATCGCTGGAAGTTCTCGATTATGAATATCACT
TCCAAGAACGCCAAACTTAGAATGGTCCGGATTCTTCCCATAAATTTGAGCGCCCTATCTT
CGAATTAGTGGCGAGTACAAATATTGCATTTCATCCATACACTCAGTGCCATCTGGAGGCG
AAATCATATCTGCAGAAGATCTTAAAGAACTTGAAATTTTCAGGGAAATTCGATCTCGGTTG
ATAATCGTTGCTATCTTAAGATATTGAAACCAAGACAGGATTGGCAGCCCATCTAGCCAG
CTCAAGAACTCCCGGTGGTTTGGACATTAGAATAAACATGGACACAGGTTTAAAGAGG
CAAACTAAATGATGAGAAGATGTCGGTGATAATGGTAGCCATGAGTTAATTGTATCTT
CAGAAGACATGAAAGCATCGCTGGTGACTATGAATTTTCCAGTGATTTCAAAAGAAATGA
GAAACATCATAGATTCTAACCCGACTTTATCTTTCACAGGACATTGCCAGATTGGAGGATA
GTTTGTATAGATAATGGAATTTGCGCATGATATPACAGCACGGCTACAAAATTTATATCCC
ATGAAATTCGCCCTCTTGGCCAACCTTAGTCTCAATGAAATTTTCCCGTTTAACTATGAGAG
AGCTCAGTACTAGAGTCAATTACCAGCTCTTGGAGAACAACTCCCTGTAGTCGAGTTCA
TTAATGAAAGTTTTCAAAATTTTAAAGCAAAATCATGGCCGCTCTGTCAAATTTTGAATG
ATTCTTAAACACAGATCCTCTAATATCTTAATAAAAGATACCTGTGCTCAATTTTAAACGAAT
TACCTGTGCACATCCGAAGATCTTCTATATACTCTACGGTGTGTTTACAAAAATGATATG
AAGAGAACCAACAGGACAAACAGTTACAAATAAAAGTCTCGAGTTGTATCAGCAAAAATTT
TGAAGGCCCATGATGACAAAATGACGATACAAATCTAATTTTGTCCAAAAGAAATGCTG
AGAATTTGGTCTGCAAACTGCAAGAGTGGGCAACGAGTTCCAAGAGATGGTCCAGAACA
AAGATGAGTGAACTACATACAAGAACGTTTGTGACACCTTTTACAACCTTGAAGAAATA
TTTTCAAAGTGACATCAGATCAACAAGGGTGTGTAATTTGGTTAGGCCAACACATGTA
AAGCCAGGCAATCTAATCTGGACAAATGGGCTCCAGAGAGAGATPACTGAAACAGACTCAT
TTGATAAGAAACTTATCGACAGCAGCACTTGATCTTTGGCAACCCATGGCTCATAGAA
TAAAAAATTTCAAGAGTGAACCTGCA

YOL031C, 421 aa (SEQ ID NO 248)

MVRILPIILSALSLSKLVASTILHSHSVSPSGEIIISAEDLKELEISGNSICVDNRCYPK
IFEPHRDWPQILPGQELPGGLDIRINMDTGLKEAKLNDEKNVGDNGSHELISSSEDMKAS
PGDVEFSSDFKEMRNIDISNPTLSSQDIARLEDSFRIMEFAHDYKHGYKIITHEFALLA
NLSLINELPLTLRELSTRVITSLRNNP PVVEFINESFPNFKSKIMAALSNLNDNSNRSS
NILIKRYLSILNELPVTSEDLPIYSTVVLQNVYERNKDKQLQIKVLELISKILKMDMYE
NDDTINLILFKRNAENWSSNLQEWANEFQEMVQNKSIDELHTRTFDFTLNLYLKKIFKSDIT
INKGLNLWLAQQCKARQSNLNDNGLQERDTEQDSFDKLLIDSRHLIFGNPMHRIKNFRDE
L

YOL048C, 821 bp, CDS: 501-821 (SEQ ID NO 249)

TAACTACATGATTTTGTGTTGCATTGATGACTGTGTTTATGACTAACATATTTAAATTT
TTATTTGTTAACCGTAGGGGTTTATGAAGTGCTGACGAATCCTGTTTATTTGGAAGCATA
TTTACTGTTTGGCGGTTTGCTATGCCCTGATTTTGTCACTATTGCTGGTCTCTTTATG
TCACACTGTATCCGCTTTTAGTGACATGGGCCATCTGTTATTAGGGCCTCTTGGTGTA
TACTGGTTCAATATTCAATGGATTTTACAAACGAATCTCTGACTGCGCTTTGTTTGTAGAA
CACTGGTCTTGACCCCATATTACGAATCAGATATTGTATATATCTTTGGTGTGCAAGACC
AAGATGAATTTTCAAACGAGGTGAAGGATTTCGCTTAAACCACAAAGGCCACATAGAAAA
TCGATGAACCTGATGCGGTGAGAAATTTCAACACAATAAAGGGAAGTCGGATTTTAAAGA
TTCCCGCATATTACTATTGAGAAATGTTTPTTAAAGTCTCCAATTTTACTTCACTAACATTTAC
GTGCTGATTAATCTTATGTAGGACCAATCTTGCAAACTCACTAATGGCCCCAAAAGAA
CCTTTACCTATTTCGACAGGTACTTTTACTAAAGGATTCAGTAAGAAACAGGCCAAAG
ATTTTCAGTACGACATTACGCAAGTTTCATATGTTTCGGTATGTCTGCGCGTCTACTAG
AGTTAATACCTCTTTCACAAATAGTCCACATATCTAGCAACACTGTTGGTGAGCTAAT
GGTGACTTCGCTACTAAAGGTTGAAAGAAAGAGGAATGA

YOL048C, 106 aa (SEQ ID NO 250)

MFVKVSNFTSLTLLSLIPVGFILANQLMKPRFTYTLQRYFLKGFSKQAKDFQYEHY
ASFICFGMSAGLLELIPFTIVTISSTNVGAARKWCTSLLKGERKKE

FIG. 1 - 85

YOR010C, 1256 bp, CDS: 501-1256 (SEQ ID NO 251)
 ACATTTCACAAAAAAGACATTTCCTGCCAAAAGTAGAAGGCAAGAAAACCCCTGGAGGAAT
 CATAGGCAAGAAAAGAAAAGAAAGAGTTTCATCTTTAAAACTACCTTTCAAGGCTTTATTC
 GTTCCCTCGTAAAGGACACACGAAAAAAATAACAGTACCTTCGACAGAGGAGTCGACAGATT
 AGGTCGCAAGGGAATCCTTGAAAGCCAAAGAGTTTTCCTCGTAATGATCTCCCAAGCAAA
 CCATCAACATTGTGGGTCAAAGTTTAGTGTAAAGTGTCTACTGAACATCTCTTAATAGCT
 GAGCATCTGTGAGTAAACGAGTAAGCAGAAAAACAAGTAAGTTTCAACTTTTCGTA
 ACTACGAAAAATAATATATAAGTAGTTAACGAAAAATCGAACAATGAGAGCTCTCACATAT
 CATCTCTCTTTTCCAGTTTAGCCATTATCAGCACAAATAACAAAAACACATCGTACATC
 GCTTCAACTTAACAAAAAATGGCTTACATCAAGATCGCTTTATTAGCTGCTATCGCTG
 CTTTGGCTTTCGCCCAAACCTCAGGAAGAAATGTACGAAATGGAAGCTTATTTTGAATGAGC
 TTAAGTCCCAACTTGCAAGAATATATTAGTTTGGCTGAAGATTCTTCATCTGGATTTCCT
 TAAGCAGTCTGCCATCTGGTGTGTTTAGACATCGGTTTAGCTTTGGCTTCGCCCACTGATG
 ACTCTCACTACTCTTGTACTCTGAGGTTGACTTTGCTGCTGTTAGCAAGATGTTGACCA
 TGGTTCCATGGTATTTCTTCAGGCTTCTACCAGAAATGGAATCCTTGTAGGAACCTTCA
 CCACCGCTGCCCTCTTCTACTGAAGCTTCTTCTGCTGCTACTTCTTCGCTGTTGCTTCCT
 CCAGTGAACACTACTTCTTCTGCCGTCGCTTCTCCAGTGAAGCTACTTCTTCTGCCGTG
 CTTCTTCCAGTGAAGCTTCTTCTTCTGCTGCTACTTCTTCTGCTGCTGCTTCTTCCAGT
 AGGCTACCTCTTCCACCGTCGCTTCTCTACCAAGGCTGCTCTTCCACTAAGGCTTCTTCT
 CCTGCTGTTTCTTTCAGCTGTGCTTCTTCCACCAAGGCTCGCGCACTTCTTCAAAATCA
 GTGATGGTCAAGTTCAAGCCACTAGCAGCTGTTTCCGAACAACTGAAAACGGTGCTGCCA
 AGGCTGTCATCGGTATGGTGCTGGTGTCTAGCGCCGTCGCCCATGTTATTATAA

YOR010C, 251 aa (SEQ ID NO 252)
 MAYIKIALAAIAALASAQTEIDELNVILNDVKSNLQEYISLAEDSSSGFSLSSLPSSG
 VLDIGLALASATDSDSYTTLSEVDFAAVSKMLTMVFWYSRLLPELESLLGSTTAASST
 ESSAASSTSAVASSSETTSSAVASSEATSSAVASSEATSSAVASSEATSSAVASSEATSSV
 ASSTKAASSTKASSAVSSAVASSTKASAIQISDGQVQATSTVSEQTENGAAKAVIGMG
 AGVMAAAMLL

YOR019W, 2693 bp, CDS: 501-2693 (SEQ ID NO 253)
 CATTGATCTCGAGCACAGCTGCTCTTTCTCTCAATGAATTACGTTATATGTTAATCACA
 CAAGCATCAGTTTTCATCGCAAAAAGAAAATATTAGAGTTCTTGCAATTCAGATGTACC
 TCAATTATAAATCAATCACTCCCTATGTTCTTGTCTGGTAGTACTGCTTTTGTCTTAATT
 ACTGCTGAATCAGCCTTCTAGAAGACCGTTCTGTTTCAGCCGCTTCGCCCTTTTCAAAGC
 TTGCGCGGCTGAGTTTATGAGGGGCGGCTTTTGTGAAATGGCAATCTACCAATTATTAG
 TAGCAATATGATTGTCAGATAGATACATATATCTCTTCTGGGTTCTATGTTCTGTTACCA
 TCCACACTAATGCTAGGACAGAAAGAAAGGACATCGAATCCAACAATGATTAATAAATAA
 GGACTCTCATTAATAAAGGCTTTAATATCAACTTGTCTATAGATCAGCAGCCCTTTTGG
 CAAGTCAACCTTAATATATATGATTCTGTTTTCGCCCAAAATGACTTGCAAAATGCT
 ACAGAAGCCTCAATTGATGTTTCAGGACACAAATTCGAAGAGAGAAATGAACAAACCC
 TTAATAAAGCGGCGCAAAAAGAAAGGAGGAGTTTCCAAACCATGTTGCTCTTGACACAGCTG
 CTTCCACCGCTGTTTATTTCTTCTATAGACGACAGCAGGGAAGGATTCAAAGGTGTATCTG
 TTCCCACTATTACAGATGGAAGAGTGCTATGACGATGAACAGACTCTTTTCTGCCCAA
 ATTTGCAATATTATTGAGAGATACATTCCAATCATCACTTTTCTGAAATCTAGAAAAG
 AGAACAAATCTGAATCCAGTAGTTTTCATGAGATCTCCTCAAAGTTGTTGGAAGAAATTC
 TCGACATCAAAAATATTCTTCTGATCAGAAATGGAAGAAATAGTGGAGGAGACATTC
 CAAGCAGCGCAGTAATTTGCAACGAAACGTTGATGATAAACAGGTTTGAAGAAAGCTGGA
 TAAAGTTATGGCGCAAAAGAAATCAACAATAAATGAAAGGCTGAATGACAAAAAATAAT
 GGTTTTACTTACCAGAACTTATCTTCTCTGAAGAGCGTATTAACCGTTATATATAGAGGAG
 ATGATAGTGACCATGTACAAAGAACAAAAAGAAAGCATTAATACTTCAACAAAAGG
 TCGGATATCCCAATAACCTTAAGACAATGTTTGTACATTAACCGGAAAAAACATACGTT
 GGGTTGCCCTAGACTGGACAGTCTACAAGTTTGCACGAAATCTTGATCACATTGTTGTCTA
 TAACATCACTGCCAAAAATGATTTCTAACAGGAAAAAACTGCAAAAAGATGATACAGAAAT
 GGGCAGCGGATATCAAAAAGAGTAATAGATCAAAAATTAACAGCATTTTGTGATTATA
 TTTACAGCTAGTAAAGAGTGGTCAAAAATACCGTCAAAATTACTTTAGAAATAATGTAGT
 GCAAAAATAAAAAAGTCTGGTAGATGTCATTAATGTCCTACTCCAGATTCTTAGTTC
 TTGCTACTTTAAAGCAGGAGCAAAATGAGAACTTATTACATATAAATCAAAAAGCTGA

FIG. 1 - 86

CAGATGTCCTTCTCTGTTAGTTATCCGATTCCCACATTTGTTGTTCCCTCGAAACGAATGT
ATTTCGTTCGAACTGAATCTACAAAGAGAAGTAAATGAACATTATGCTCTCAAAAAATCATAT
TGAAGCAGCAACACACTGACGTTGAGAGCATGAGCAGTTCAATGTTCAAAAAAATACAA
TATCAGATATTTCTTCACATATTTCCGTAGATTTCGTACGCCGAAGATTTCAAAAGGCAAG
GCTCATCAAAAAGCAGTTCAACACCTCTAATGATTCCATTCCAAGAAAAATTGACCGGTC
TCGCCAGCATTTCAAGAAGGAAGATCACGGGTGATATAGAAAAATTACAAGACGATGAGA
AAGATAGAGAATGTACTAAGGAAAAAATTTTGTGAAGAAAAATTGATATCATATATAGAG
AGTCATTGGAAGCTCTTTTAGCGATAGAGACGTTGCTTGGTAAAAATGATCGCATGCCA
GTCACGGTGCACAAATTTCCAGCTTTAAGAATGCTTTGATAGGCCAATGGGTGCAAAAAACA
CAAAGTTTAGAAAAATCTTTAATACCATAATTCTCTCAGAGGAACAAAAATACCAACAACA
CTATTAAACTCAGTAGCTCGCTACGCTCCCAATCAAGTTTGCAACCTCTGTATAAACACA
AAGATGGGAAGACGCCCTTGGCAAGCGCAAGAAATCTGCCTGATATAAGCAGCAGTATTT
CCTTCGCAAGAAAAATTTCTTTGATCCATCTGATAAAAGCAGTAGTGTGTGATAATAGCA
TTCTTTTGAGGAAAGTTTAAAGTGCCTGCGTCTAAGAAAAAGTCAAAACTAATGACTCTCT
CAAGTAGTGACAGGTCAAAAGAAAAAGCTCGTCTAGTTTGTAGTACTGTGAACACCTTGAC
TGGGGTGAAGTTGGGATTTTAAAGTGTGTTAAAGTGGAAAGTTCTCTGGAATAAATCAT
CCAGTAGGAAGTAATAGTAGCAGTGGCGATGTTTTTGAAAGTGATGATCGTAAGCACAAGA
AAAAAGAGAAGAAAAAAGAAGAAATCATTTGTTCTTATTCGGCAAAATATGA

YOR019W, 730 aa (SEQ ID NO 254)

MISVCPQNDLQKCYRSLTFDVPQGFEEERNEQNLKRAKKKGSFQPSVAFDVPSTAGYS
SIDDSREGFKGVPPVNNYYTMEECYDDETFDSFSPNLQYLLRDTFQSSPFLNTRKENKSESS
SFPMRSSKLLLEKNSIDIKYFLVSKNGKILVRDYPSTPVI VNETLMINRFEKNWIKLWRQR
KLTVINERLNDEKWKFTYPELIFSEERIKPLYRGDDAPCTKEQKRKKHKLQKQVGYFPNNP
KTQCHIRINGKKHTWVALDWTIVYKFAARNLDHIVITTLPKMISNRKKTADDTWAPGYQK
EVIDQKLNDFIDYILQLVKVVKISVKITLEIIVGKIKKSLVDVINVHTVPDFVLVATLKHE
RNEILNDIKLTDVFPVSYPIPTFVVPKRMYSFELNLRQVNEHVHVSNNMKHEHTD
VESMSSSMFKNPTISDISSHISVDSYAEDEFKRGYIKKQFNSTNDSIPRKLTLGLAQHSRR
KITGDIERLQDEKDRCTKEKLLLLKKIDIIRESLKKSLAIETLPGKNVSQSHGDQIS
SFKNALINGKSSKNYKFRKSLPIPYSSSEQNVTITIKLSSSPTSQIKFATSVKHKDGRAAL
GKARNLPDIRHSISFDKENSFPDPSDKSSSDVNSIPLRKVKSAALRKVKTNMDSSSSAGSK
KSSSSFTVNTFTGGGVGIFKVKFSGSSSGNKSSRRNSSSGDVFEESDRNDKKKKKKKK
KSLFLPFGKI

YOR027W, 2270 bp, CDS: 501-2270 (SEQ ID NO 255)

AATTTTCCCCCGCTCATAGTTCCATACACGGCTGGCTCTGATGGCATAATTTTCATGCT
GGAACTTACAAACCCGCAAGAAAAATAAAATTTCCGCAAAATTTAACGAAGACAGCGTGG
TTAAAAATTGCTTGTTCGGACAATATTTCTATGCTGGCAACTTCTGATGACTTTTCAAGA
CAAAACGCCGCAATTTGACCAAACTATTGAACATAAACGCAAGTTCAATATACATAATATTG
ACTATGAGAACTGATATCTTCGTGAAGATTTCGTGTAGTATGATAGAACAATTCAGAAAAA
AAATTCAGATTTCATCGCTCTCTCTCGCTTCTCTCTCTTTAAGGAATAAAGAAAAATCA
CATACATAGATTAAAGTAAATAGGATCTGCTAGAAAAATTATATATAGATTCAATCTCTTA
TTAAGGTATCTTGTTTAAGCCCAAAAGTCTGCTCCCAATTTCTCTCACTGTAGCTACTTAA
ACAACTTATACGCAAGAAAGATGTCTATTGACAGCCGATGAATACAAACAACCAAGTTAACG
CTGCATTACCGCTAAGGATTACGATAAAGCGATAGAGCTCTTCACTAAAGCTATTGAG
TTCTGAAAATCTCAAAACCATGTTTATATTCTAACAGGTCGCGCTGTTTATCTCTTTAA
AGAAATTAGTGACGCGATTGAATGATGCTAATGAATGTGTCAAAATCAATCCATCTTGTT
CTAAGGGTTTATAATAGACTCGGTGCGCCCATTTAGGTTCTGGCGATCTCGACGAAGCTG
AAAGCAACTACAAAAAGCCTTGGAGTTGGATGCCAGTAAACAGGCGGCCAAAGAGGAT
TGGATTGAGGTTCAATCGTACCCAAACAGGCAAGACAGGCACAGCTGATTAGGGTTGACG
AGTTGTTCTGACCCAAATTTAATTGAAAATTTAAAGAAAGAACCAAAAAATAGCGGAA
TGATGAAGGACCTCAATTAGTGCGCTAAACTGATTGGGTACAAACAATAATCCGCAAGCTA
TTGGCCAAAGATCTGTTTACTGATCCAAGATTAAATGACCATCATGCTACATTGATGGGG
TTGATTATAACATCGATGATATAAACCAATCAAACTCCATGCCAAAGACCGGAACCA
GTAAAGCACTGAACAAAAGAAAGTGTCTGAACCAAAAGCGGATTTCCACTACGAGCAAG
AAAAATCTCTCTAAGCACCACAGAAAGAAAGAAATGAAGAAATCCGAGCAATGGAAGTCT
ATGAAGATGACTCTAAAATTGAGGCCACAGAGAAAGGCCGAAGGTAAACAGTTTAC
AGGCACGTCATTCGATGAAGCTATAGAGCACTACAACAGGCGTGGGAACCTGCATAAG

FIG. 1 - 87

ATATTACCTATTTAAACAACCGTGTCTGTCTGAATACGAAAAAGGCGAATACGAGACAG
 CTATTTCTTACCTTGAATGATGCTGTTGAGCAAGGTAGAGAAATGAGACGGATTTACAAGG
 TCATTTTCCAAATCATTTTGGCGGTATTGGTAATGCCTATCACAATTTGGGTGACTTTGAAGA
 AAACATATAGAATCTACCAAAAATCATTGACCGAACATCGTACTGCTGACATTTTGACCA
 AGTTAAGAAAGTCTGAAAAAGAAATTTGAAGAAAGCTGAGCGGAGGCGTATGTTTAAACCTG
 AAAAGGCGGAGGAAGCCGCTTCTGAAGGTAAAGGAATATTTTACCAAGAGTGATTTGGCCGA
 ATGCTGTTTAAAGGCTTACACTGAAATGATCAAAAGGGCACCTGAAGATGCTACTAGAGGATTT
 CTAATAGAGCTGTGCTGACTAGCGAAGTTAATGTCTTTCCTTGAAGCTATCGCAGATTTGTA
 ACAAGACCTLTGAAAAAGATCCAAAATTTCTGTGAGAGCTTATATCAGAAAGGCCACCGCACA
 AAATTTGCTGTTTAAAGAATATGCTTCCGCTTTGGAAACACTAGATGCGGCGCAGAACCAAG
 ATGCTGAAGTGAAATTAATGGTTCTAGTGCAGGGAATATGATCAACTGCTACTACAAGGCAA
 GCCAACAAAGATTTCCAACTTGGTACCAGTAACGAAACCCGAGAAGAACCTATCAAAGGG
 CCATGAAAGACTCTGAAGTGGCTGCGATCATGCAAGATCCGTTATGCAAGATTTTTCG
 AGCAGGCCCAACAGAAATCCCGCTGCTTTACAAGAACACATGAAAAATCCAGAAGTATTC
 AAAAGATTACAGCGTTGATCGCTGCTGGTATCATCCGACTGGCCGCTAA

YOR027W, 589 aa (SEQ ID NO 256)

MSLTADAEYKQGNAAFTAKDYDKAIELFTKAEVSETPNHVLYSNRSACYTSLKKFSDAL
 NDANECVKINPWSKGYNRLGAAHLGLDLDEAESNYKKALELDASNKAKNEGLDQVHRT
 QQARQAQPDLLGLTLQFLADPNLILENLKKNPKTSEMMKDPQLVAKLIGYKQNFQAGDLFT
 DPLRLTMTATLMGVLDLNMDDINQSNMPKPEPTSKSTEQKKDAEPQSDSTTSKENSAP
 QREESKESEPMEVEDDEDKIEADKEKAEGNKFKYKARQFDEAIEHYNKAWELHKDITYLNN
 RAAAEYKEGEYETAISTLNDAVEQGREMRADYKVISKSFARIGNAYHKLGLDKKTIYYQ
 KSLTEHRTADILLTKLRNAEKELKAAEAYVNPKEAEARLEGKEYPTKSDWPNVAKYT
 EMIKRAPEDARGYSNRAAALAKLMSFPEAIADCNKAIIEKDPNFVRAIRYKATQAIIVKEV
 ASALETLDAARTKDAEAVNNGSSAREIDQLYYKASQORFPGTSPNETPEETYQRAMKDPV
 AAIMQDPVMSILQQAQONPAALQEHMKNPEVFKKIQTLLIAGIIRTGR

YOR31W, 710 bp, CDS: 501-710 (SEQ ID NO 257)

CTGCAGAAAGTACAGCTGCCTTTTATTTCTTGTGGTCATTTATTTTTCAGTCA
 GATATACACAGAAATCAAATCCCATCGTCAACGTCACGTATAAACGATTAATTTACAGTA
 ATACCATACTCTACCAACATTTATTTAGTCCGACGTTTCAGTCTCTGATGGTGTTCCAAATC
 CTTCTGGCATGTGACTTCTGTGCAGAAACCTTCAAAATGAGTTCCACTTTACGTCAGATC
 GCATAACAAACCGGTCAATATTTTTCCTTTTGTCTAAACCCCTACTGCAAGGCACTTTTA
 AGAAAAAGAACAAATAAATGCGTCTTTATTTGCTGTGTGGAAGTGATTTTGTCTTTCGGAG
 AAAAAAGGATAGGGAATGCGAGAGGGCTGTGAAGTAGTGATCAAGCGGGGCTATATAAG
 AAGGGCGCACATCGTCCCCCTAAGAAATAGCGAAGCGATATTACACTGAACACTACAATG
 TCAATATGATCTCAATAAATATGACTGTAAAAATATGTGACTGTGAAGCGGAATGTGTGA
 AGGACTTTGCTGCACTTGCCATGAGCACTGCCTTCCAAGCTGTCTTGGCGGTGAAAAAGTGCA
 AATGTGATCAGCAGCGGAAGCCCTCAATGTAAGAGTTGTGGTGAAAAATGCAAAATGCG
 AAACACGCTGCATTTGTGAAAGAGTAAATGCAATTTGTGAAAAATGTTAG

YOR031W, 69 aa (SEQ ID NO 258)

MTVKICDCEGECKKDSCHGSGTCLPSCSGGEKCKDHSPTGSPQCKSGEKKCKETTCTCE
 KSKCNCEK

YOR096W, 1474 bp, exon1: 501-644, intron1: 645-1045, exon2:
 1046-1474 (SEQ ID NO 259)

AAACCCATACACAATGAACCTTATCACACCCAAACATATGATATGGTATTTAAAAAATGAA
 AAAAATCTATTATCTTTAGCGTAATTTATTTGAAGAAAAAAGCAGTGCAGCGGTAATTTT
 TGTCACCTCAGTAAGTACAGAGAGAGCGGAATGTACTCCCGCGGCTAGCTGGAGACCATGGC
 TCTGCGCTAGGATTTCTCTATGCTTTCTTTACCAATCACTTTGTTCCGGCGGAGGCGCG
 CGAAGCTCGCTTTCTTTCAGCTAGCAATCATGTTCTTGCAGCGCTCGTAGACTCATGTA
 TGGCAGTTGCTGCACTTGCCATGAATAATCCCTAGTGAAGCCTCTATGCAATTAATCCAGTTA
 CTGCGTTAGAAATCTGGTAAAATGTCTAATCTTATTACATTACAGCAACGATATAGATT
 TGATTGAAAAATTAGCTCTGCGACTTGGTATATATCTTATTTTGAAGAAAGCTGAAAGGAA
 GAAAGATCATCAGAACCAACATGTCTGCTCCACAGCCAAGATTTGTCTCAAGCTCCAA
 CTGAATTGGAATTACAAGTTGCTCAAGCTTTCGTTGAATTGGAATAATCTTCTCCAGAAT

FIG. 1 - 88

TGAAAGCTGAGTTGAGACCTTTTGCAATTCAAGTCCATCAGAGAAGTATGTTTATTAATTG
 AATCTAAACTTTAAGAATAATGGAGAGTAACAAGGAAAAAAGTGTGAACGGGACGATACC
 AGAATGCTTTCAATCTAGAAAAAGTATAAAAGATAAGGACTAGGACTCAAATGTTATTTGGCT
 GACTATGCTGCTGAACCTTGATGCTAAGCAAAATACATCATCTTCAAGAAAAAGGCTCATCC
 AGTGTTTAAGAAGAAGGGAACGATTACTAGATCATGCTATACGCAGTAAGGTTTTCGATA
 GTTAATTACAATCGGTCCAAGTCTTAAGCGGTGTGCTCCATGCATATATCTTACAAGT
 TACTGGCGCTCAACTCTTCAAATATTCAAATATCACCTAATCAAACCTTACTAACATTTTC
 CTTTTTTGTGTTTCTCTCTTTATAGATCGAGCTGTGCTGGTGGTAAGAAGGCTTTGGCCAT
 TTTTGTTCAGTCCCATCTTTGGCTGGTTTCCACAAGGTTCAAACAAAGTTGACCCGCTGA
 ATTGGAAAAGAAAAATCCAAGACCGCTCATGTCTCTTCTTGGCTGAAAGAAGAACTCTGGCC
 AAAGCCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACCTTGACTGT
 TGTTCATGACAAAGATCTTGAAGACTTAGTCTTCCCACTGAAATCGTTGGTTAAGAGAT
 TAGATATTGTTTGGTGGTAAACAAGATCCAAAAGGTTTGTGACTCAAAGAGATGTCCA
 ACAAAATCGACTACAAATTGAATCTTTCGAAGCTGTTTACAACAAATGACTGGTAAGCA
 AATTGTTTTCGAAATCCAAGTGAAACTCATTAG

YOR096W, 190 aa (SEQ ID NO 260)
 MSAPQAKILSQAPTELELQVAQAFVLELNSPELKAELRPLQFKSIREIDVAGGKKALAI
 FVPVPSLAGFHKVQTKLTRELEKFKQDRHVIFLAERRILPKPSRTSRQVQKRPRTSLTA
 VHDKILELDLVPFTEIVGKRVRVLVGGNKIQVLLDSKDVQQIDYKLESPQAVYNKLTGKQ
 IVFEIPSETH

YOR248W, 803 bp, CDS: 501-803 (SEQ ID NO 261)
 ACCCAATTTTACAAATTTTTTTTTCCTATTGAGCCATAGTACCATTAAATAGGCTCTCGTCC
 ATTCCCTTGTTTTTTTTTATGTTTCAATTACATPACATAAATTAATAATACATACACT
 TCACCTCTCACTCTAGTCTAGTCTCTTTATCAACCAAAAAATAAAAAATGCTTCAATCCGTTGT
 CTTTTCGCTCTTTTAACTCTCGCAAGTCTGTGTGTCAGCGATTATTAACAACAATACCT
 TCTCAACAATACCACTTTAGCGCCAGCTACTCTCTGTGGTCCCAAGAGACTACCATATC
 GTACGCCGACGACACCACTACTCTTTTTGTCACTCAACGGTCTACTTCCAGGAGCTGGT
 CACCTCAACTCTCAGCCACCATTACCAGTGGCGCTCTCTCTTGTCCACCTCTCTCGGC
 CTCTGGATCTGTAAACCCAGAATCCACCAATGAAATTTACCTCCACCTCGACTATCACGTC
 CACTTTGTGCTCAACCTTCAATGACTCCACTACTTTGTCTCCATCATCTACTGACGCAAG
 TGTCAGTGACGAAGATTCAACAACAAGATGCAAAAGGTCAAGTCCCTTTGAACAGGCTTC
 AACTTCCAATGGTTGGTCCCAATCAAAAAGTTTGTCACTGTCAACCAATGAGCCCGTTAC
 CCGATACGTTACAGTCAACCCAAATACGACTACACAATACGTTACTGTCAACGGTGCACC
 TTCTGTACCACTACTCTCCAGGTAAAGTACATAGGTACAAACCACTTCAGATTACTAA
 TTCGACCAAGTTGGTGAATATGA

YOR248W, 100 aa (SEQ ID NO 262)
 MTPLLCLHHLQVSVTKIQTTKMQRSSPLNRLQLPMVASQSLSLSPMSPLPSTLQSP
 QRLNHTLLSPVHLLFLPLQVTVNGTTPRLRLIRPVGEL

YOR293W, 1255 bp, exon1: 501-552, intron1: 553-989, exon2:
 990-1255 (SEQ ID NO 263)
 AACTTTCGAAATATATACTCTGAGTCTTGCTCCCGGTTTTGTACGATGTTCTTAATGCA
 AACACACGTCCTTTAAAGATCCCTGTAGGTTTCATTAAAGGCAACTTCCATACACGTT
 GAAGTGCCAATTTTTTCCCTACATCCAAGCATCTCGGTTGTATGGGTGTATACCCGGT
 TTTTCTTTTTTATTTCCAGAGAAGTACAATTTAGGCGGGTTTCAAATTTCCCTCTGTGTG
 CGAGAAGACGCTCCGGTAGCCTAGGCTCACTCCGGTCTCTTCCCAATTTCTATACGCGC
 GATAGGCATCTGTGGAGAGCGGCACTAGGGAGACCGGTGGGAAGCACCGGTATCTAGTA
 ACGACGCTCTTTTGCAAAAATATCCATTAAATGCAATGTAACCTAGATTAACTAGGTAT
 TAAGATTTCGCAATTTTGGCTGGATTATTAAGTTCGAGTAGCAAAAGTTTAGCAAGAATA
 GTACGAATCAAGTAGCAAGATGTTGATGCCAAAGGAAGACAGAAACAAGTACCCCAAT
 ACTTATTCCAAGTATGTTTATAGAATAACTTTCAAGAACATGAAGATACACGGAAGTC
 AAGCGAGGGAAGTTATCCGTATACACAGTAGCGGTAGTGTGCAATTCATATACAGATGTT
 TCAAAACACAGATGGATACCATGATATGAGGTTAAAGGATTTCTATGAATATATTAG
 TGGATTACATAGAAGAAATACAAGGAACCGGTGACGACATTTTCGAAAGGACAGCACA
 AGGCCATCGACCTTGGAGAGCTATGAAATATGGTATACGTCTATATTTGGGCAAGAAAA

FIG. 1 - 89

CGGTAACAACTGTTTTACGCGGAGATCCAACCTTTTGATCCTTACCAGTAGTACCACGAATCAT
 CTATATGATCTCTTTTACTAATCTATCTTCAATTTTCAACGGAGAGATGTAAACATCATCTCT
 CTCCTATGATAATTTTCTTTTTTTATACAGAAGGTGTGTGTGCGCAAGAAGGATTTTCAA
 CCAAGCCGAAGCACGAAGAAATTTGACACCAAGAAGCTTGTATGTCATTAAAGGCTTTTACAATC
 CTGACCTCTTCAAGGTTTACGCTCAAGACTCAATCTCATGGCAATACTACTACTACACCTT
 GACTGAAGAAGGTGTGTAATACTTGAGAGAATACTTGAACCTGCGCAGAACACATTTGTTCC
 AGGTACCTACATTTCAAGAAGAAACCCAACTCAAGACCAACAAAGAATATTTAA

YOR293W, 105 aa (SEQ ID NO 264)

MLMPKEDRNKIHQVLFQEGVVVAKDFNQAKHEEIDTKNLYVIKALQSLTSKGVVKTFQS
 WQYYYTTLTEEGVEYLREYLNLPHEHIVPGTYIQERNPTQRPQRRY

YOR312C, 1432 bp, exon1: 501-507, intron1: 508-914, exon2:
 915-1432 (SEQ ID NO 265)

TATTTACAAGCTAGATAAAAAAAAAAATCAAAATAGCAAGCTATTCTGTCATATCTTAAGGT
 GCTGATTTGTTGTAGGCACGAAGTAAACAAGCTCTTCCCCAAAAACAATAATACGGTTTTC
 CGGGACTGTTCACCCGTACATTTTACGTTTCCGACGCGCGATGCTATCTTTGAAATTTT
 ATCTCTTTTCAAGTAACCCATGACCAAGTAGGGCGGCTTACTACCGAAGAGAAAAATGTCC
 CGGGCTTAGACAGTTACTTCCAGGGCCAGGGCCAGGCCACACGGACAGAGGCAGATTTCCA
 AGTTGTTTCCGATAGCTGTCTAGCTCTTTCTCAATTTTCCGCCAGATTCTGTCTAATTT
 CTTTCCGCTCGAGTTGGCAACAGTACGAAGAAGTAATCTAATAGATAGATATAACCGTT
 TTTGAGGGCATTAATTTTGCAGAAGATAATAGAAGAAACCGTAACAAGGAATCAAGCA
 AAGAAAAAGTATGTAATAGAATGTATTGTATGCTTGTGGAATGAATGTCAATGTAGCTAT
 TTTATATGCTGAGCTCAAAATGAAATGAACATATCGTGGAAATTTAAATACTGAAGAATA
 CCAATAAGTCAATGCAACCTGTGAATGTTTTCCTGAAATACGCCAATACTGAATACG
 AITATTAACCTAAATTTGCTTCTAGAAGGAAGCGGCTACCAATTTAAATCTGATGATATG
 GTTAATATCAATTTGAGAAGTCTTCAATGAGGACTATAGAATACCATTCCAGGAATATATA
 GAGGAATTAACCTGAATCAGAGATCTATTTTGAACATTCATTTACATGTAAATGTCTGC
 AATAAAGCAATATTTTGAATATGCAAGTTTACTAACAAGAAATAAATCTCTTTTGGATT
 TTTATCTTTTAACAGTGGCTCATTTCAAAGAAATACCAAGTCATTTGGTCGTCGTTTACCAAC
 CGAATCCGTTCCAGAACCAAGTTGTTCAGAATGAGAATTTTGTCTGCAAAATGAAGTCAT
 CGCCAAAGTCTCGTTACTGGTATTTCTTGCAAAAATTTGCCAAGGTTAAGAAGGCTTCTCG
 TGAAATTTGTTTCCATCAACCAAAATCAACGAAGCTCACCCAAACCAAGGTCAAGAACTTCGG
 TGTTTGGGTATAGATACGATTCCAGATCTGGTACTCACAAACATGTACAAGGAATACAGAGA
 CGTATCCAGATGCTGCGCTCGAAACCTTATACCAAGACATGGCTGCTACACAGCAGC
 TAGATTTAGATCTTATTCACATCTTTGAAGGTTGCTGAAATTTGAAAGACATGCTGATGTCAA
 GAGACAAATACGCTCAAGCAATTTCTTGACCAAGGATTTAAATTCCTCAATCTACAGAGT
 CCAAAAAATCTACCAAGACTTCTCTTACAAGAGACCATCAACCTTCTACTAA

YOR312C, 174 aa (SEQ ID NO 266)

MYLAHFKEYQVIGRRLPTESVPEPKLFRMRIFASNEVIAKSRVWYFLQKLHKVKKASGEI
 VSIQINEAHPKVKNFVWVVRYSRSGTHNMVKEIRDVSRVAAVETLYQDMAARHRRF
 RSIHLKVAIEKTAADVQRQYVKQFLTKDLKFLPHRVQSKSTKTFYKYRPSSTFY

YOR369C, 932 bp, CDS: 501-932 (SEQ ID NO 267)

CTTCTTACAAGTTAATGAAATAGTATATATATGTAATAAAAAAATCTGCTTCATGTATATA
 CGCACTCGTTATTGAGGTATTGCGAATGTAGCAGTTGAAATAGCAAGACGAGGTTTGT
 ACATCTTGGCATATTAATAGTTATTTCGGGGTTTGTTCGGCTCAACGGTGTATATAAAA
 AGAAATCCAGTACTGTTTACCATTTGTGCATCCGTACATTTGATTGTTTACAACATCTTC
 ACATTTCCATTTGTGGAATCATTTTATTTTTCAGAATACCTTACCCGCAAGCAAACTTT
 CAAGCAAACTTACAATTTGCAAAAATTTTATCGAATTTCTCCGACAGACATATTTATAAAGT
 TATGTCATCTCTTATACCAACAGGCTCTATAAGTGTTCCTTGTTCATTTGTTTCCCAAT
 TCAAAACTCTTCCAGGAGCAGTTTAAATATCTTACTGTGCAAGAAGTCAAAAATAGACT
 ATATATATTGAGAAGAAAAATGTCTGACGTTGAAGAAGCTGTTGAAGTTCAAGAAGAAA
 CTGTTGTTGAACAAACTGCCGAAGTTACTATCGAAGATGCTTTGAAGTTGTTTGTGAGAA
 CCGCTTTGGTTTACGATGGCTAGCTAGAGTTTGAAGAATCTACCAAGGCTTTTACCA
 GAGGTGAAGCTTTATGGTTGTTTGGTCAGCTCTGTTACTGAAGTCAACATTTATCAAGT
 TGGTTGAAGGTTTGGCTAACGACCCAGAAAAACAGGTTCCATTGATCAAGGTTGCTGATG

FIG. 1 - 90

CTAAGCAATTAGGTGAATGGGCTGGTTTGGGTAAGATCGACCGTGAAGGTAACGCCAGAA
 AGGTTCTCGGTGCCTCCGTTGTGTGTGCAAGAACTGGGGTGCAGAACTGATGAATTGT
 CCATGATCATGGAACACTTCTCCCAACAATAA

YOR369C, 143 aa (SEQ ID NO 268)

MSDVVEVVEVQEEVTVEQTAETVIEDALKVVLRTALVHDGLARGLRESTKALTRGEALLV
 VLVSSTVEANIILKVEGLANDPENKVPLIKVADAKQLGEWAGLGKIDREGNARKVVGASV
 VVVKNWGAETDELSMIMEHFSQ

YPL047W, 800 bp, CDS: 501-800 (SEQ ID NO 269)

GGTTAGGGGCCAAGATTACGTTCCAGCTTTCGATGTGCGACACAGATTGGGAATCTTACGA
 CTATGCAAAAGTTGGATCCCAACTAACGACGACGACAAAGAAATTCATCAATAACATGTGGGC
 CTGGGATAAGCCAGTTTCCGTCAATGGCGAACCAAGGAAATTTGTGACGGTAAGGTCTT
 AAAATAATCTCTTCGTACTATCCTTCATGTGCGCTTTTATTATAAAGTATGCTAGGTAGT
 TTTATCTATATCTTATTTATGACGCAATATAGGGTAACAGAGTTTTCGTGCTCGAAATG
 TCCGCAGAAAAAAATCAAGTTTTCCTTTTCGTATCTTGGATTATGTTATATAATAGAT
 GCATGTATTATATATAGCAGTGAATTGCTTATTTCTTGATTCTGAGGAATCGAAGAA
 GTAACCTTAGGCTTTCCTCGGTGAGCAGAGCAGTATAATACTCTCAAATCTTTAGGT
 TACGGGTTTTCCTGTTGCGATGACCGAAGAACTATTACTATAGATTTCTTTTCAAATG
 GGATACCTGAATACCTGTTTAACCACATGTATCCAGGACATTTGAGCTCGGGAAACCACTC
 AACACAAATTGCTGAAGACAAGATATCCGGATCTTCGAGTTATTAATTCGACCGAAG
 GATCTCTCGATATTATGAGCTACAGAAGCAACAAGAGTCTCTCAGTATATTCACTGTG
 AGAATTGTGGCAGGATGTGTCGCAACAGACTAGCAGCTCATTTACAGAGATGTTTGA
 GTAGGGGTGCTAGACGTTGA

YPL047W, 99 aa (SEQ ID NO 270)

MTEETITIDISINGILNLLTTLIQDIVARETTQQLLKTRYPDLSYYFDPNGSLDING
 LQKQESSYQHICENCGRDVSANRLAHLQRCLSRGARR

YPL090C, 1605 bp, exon1: 501-506, intron1: 507-900, exon2:
 901-1605 (SEQ ID NO 271)

GTAAGCAGAAGCCGGAAGAAGACAAGAGGTTTCATTGAGAGAAAACATCCGTACATTCGAG
 TTCTCATTTGAACCCATACATTTCAACTATTTTACATAGTTCGTTTTCATGTGTAAAAT
 TGTCTACGACGCGCGGAGCATCGGAAAGTTGGAACGTGCGCGATTGACCAAAATCCCCT
 GGGGCGGTGCATTCGTAGGCGAGGAAGCCACTGGACACTCTGCCCGTTCCCACTTTGGAAG
 ATTGGCGTAATTCACGCTCCTCTATCGATTCTAGCGGGAAGTTATCTCTCTGTGAAG
 CGTTGGAGGAATGCCGCTACCTAGGTAAGTCTACTGGGTGGGAATTCAGTACCGACGTC
 TAGGAACATCATGATGCTGCAGTTTCTTTGAAATTTTCATATACAGTGTACCAAGGATAA
 AGTGGTTAATGCTTATTCGTCATTGAATTTTATATTTTGCTTAAGAGAAGTGACAAAAAGA
 GTGAAGACAGACTATACATCATGAAGGTATGATTTATGATACTATTATTGAGGGGCAACA
 GAGAACTTTATATGTGGAAGAAATGGCATGAAAGTTTGAAGTGAGAAAGAACTAAACAGA
 ACCAGACGTCGTAAAGATTTTAGAAAATTTTATGGAAAGAGCAGGAAGACTACCATAT
 ACTAATTTGATGCGGTTTGTGGCGTTATTTTAAACAAACAGAGCGGGTTTACATATACTGT
 TACTACAAACCGTGAAATTTGAAGCAGTTTCATATACTTGGAGTATAGTCAATAAAAGACA
 GCTTTTTCATCTTCCACTTAATAATTTCTCTAGAGTAATAAACTTCACCCATTCAAACA
 TTAATTTTGAATAGTATATACTAACAAATTTTCTTAATAACCTGTGAAAATTTAAAAATAG
 TGAACATTTTCTTACCAGTTAAACGGGTCTCAAAAGACCTTCGAAATTTGATGATGAACAC
 CGTATTCGTGTTTTCCTCGACAAGAGAACTCGTCAAGAGTCGATGGTGGAAGCCGTTGGT
 GACGAATTTCAAGGGTTACGTCCTCAAGATCTCTGGTGGTAACGACAAACAAGGTTTCCCA
 ATGAAGCAAGGTTGTTTGTGCAACTAGAACTCAAGTTGTTGTTGACCAAGAACGTTTCTT
 TGTCTACAGACCAAGACGTGATGGTGAAGAAAGAGAAAGTCCGTCAGAGGTGCCATTGTT
 GGTCACAGATTTGGCTGTCTTGGCTTTGGTCATTGTCAAGAAAGGTGAGCAAGAAATGGAA
 GGTCCTAAGTACACTACTGTTCCAAAGAGATTTGGGTCCAAAGAGAGCTAACACATCAGA
 AAGTCTTCGCTTTGTGTCGAAGAGATGACGTTCTGTGATTTCGTCACTACAGAGAAGTCT
 ACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAAAGATTTGGTTACTCCTCAA
 AGATTGCAAGAAAGAGACACCAAGAGCTTTGAAGGTCAAGAACGCTCAAGCTCAAGTCAA
 GAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTGCTGAAAGAAAGGCTGAG
 AAGGCTGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCTTAA

FIG. 1 - 91

YPL090C, 236 aa (SEQ ID NO 272)
MKLNISYPVNGSKTFEIDDEHRIRVFFDKRIGQEVDEGAVGDEFKGYVFKISGGNDKQG
FMKQGVLLPPIKLLKLLTKNVSCYRPRRDGERKRKSVRGAI VGPDLAVLALVI VKKGQEE
LEGLDITTTVPKRIGPKRANNIRKF FGLSKEDDVDFVIRREVTKGEKTYTKAPKTRQLVLT
PQRLQRKRHRQALVKRNAQAQREAAAEYAQLLAKRLSERKAEKAEIRKRRASSLKA

YPL137C, 4331 bp, CDS: 501-4331 (SEQ ID NO 273)
GTCTCAGTGATGCAATCATCATGGCAGGGGCATTAAATTAAGGTTAAGGAACCACTTCTCT
AGCCCATCTCCAAACAATAACAATATTAGACCTAGCCCAATTGATACCCATGAGCGTGCA
GTCAITGGCATTGGATTATTCATCTCTTTTCGCTGTCTCTTTCTTTTCAAGTTTGTGCATC
ATCATCGCTTCACTTTTTCGCTTTTCCATCTTTCTTTTGTCTGCAAAATTAAGGGAAGAGGG
GTAAAAACCGCAAGGAAGAACAAAGAAAGAGGGTAGTGCAAGAAAAAGAAAGAGAAAA
AAAAAAAAGTAATCTTGATACCGTGAGCAATAAGCTAACGGAAAGCGTTAAGAAAGAA
GAGCGTGTTTTGGGAAAAATAACCAACCAACGATTAAGCTAAAATTTCAGTTTATATTAATCTAT
AGTAGTCTCTATAGAAAATTGGCAATAACGGAAACAATAGTCCACCAAGCAAGCATAGGGA
TGGGAGATAGCATCTAGGTTATGATAACTAACACCGAGTTCGATGTGCCCGTAGATTGGT
TGATATAAGGTTAAGTAGAGTAGCGGAAGACAAATACGAAGCCATCGAGGCGTTCTCATGCTCGC
CAGCCTCTCTCTCATCTACGTCTCTCTTCGAAAAACGGAGACAAATAGCACGAGTGTGATA
GGTCTAGCAAAATGATAAGCCTCGTGGCAGGTCGTCACTCTGATTCGAATGCAGCATCTTTGTA
ATACTGAGAAACAGGATTGGAAGAGGAACGATGGTAATACCTCTGCATCAGACACTGATA
ACATACCGCTACTTACTCTTATTAATAGCGGTAAACGGAGCGATTCCGCTGACATTTGATA
ATCCGGCTACGCTAGACGCCATAGACCTTATAGATAATGATGACAAACGGCTTCAAGTACTC
AATTTGTAAGGAAAAACGTTCCACTTCTATATCCAAATGCTGTGGTCTCTGTCCTCAAAACCAA
GACTGGCCAGTCTTGCCATAAACGCCACCGCATCTTCTTCTGTGTGGCAAGGAAAGCAAC
CGCCAAATTTCTTACCATTCTAATGCTACTCTCAAGAGAAGCAACTCGACTAGTGGAGAAA
AGACTAAAAGGTTCGATTTTTGGATCTTTGTGTTTGAACCAACGGTCTACTCTTCTTCAGTCT
CCACTGCCAAGAAACCATTAACCTGTGTGTTAATACTAGCACTGAGAATGAGTCTGGTG
CGATTAAAGCAGTTTGGCAGTCTCTGATCCAGCGGTGAAGGAGATATCATCACCATTAGAG
GAGTGGCACCACAGCTAGCAAGCCACAGACACTTATCTCCCTCCCTCGCACTTGGCAG
TAAAGACCTATCTACAGTTTCATTGAAAAGGGTCTCGTTTGGCGTTCGATAAATTCGAAAT
CGATCTCTCCCCAACCACTTCTTCAAGAACCCCAAAAAAGGGAACATCTTATCCCTCGT
ATGACATGATAAGCGAGGTTCTCTTCTATTTCCGTGGGTATTTCCAGTAGCAACCAATCGG
CCAAGTCAACCAATTTCCAACATTAAGGGACCGTGTGACACTAAGAAAGTCTAAAGAAATATA
TACTCGCCCTGGAAAAATCAAAAGTTGGCTTTAAGGGAGGCTGCTAAGCATCAGCAAGAAG
CTCATTTTGTCTGCTAATAGAAATAGCCTTTGAAGTAGCCAATTTAAGACTGCTTCGGATG
CAGGCGGTAAAGCTTACTGAAAAATGTCATCAGAAGGCACCAATTACGAAGCAAGAAAGAGG
TGTCACCTTCAAAATGTTGAAGCTGATCGGGAGCTTGAGAATAATAAACTTGACAGAAACCT
TCTCAAAAGCCGGCATGTATAAGCCCAATTCATATGCATGAGCACTATTTCGAAGAAAGCTG
ATCAAGATAAGTACCAAGACGGTCATTCTATTGAAAATAACGAAGTTACGCTGGATGTGTA
TTTACACAAGATGCTGCCATTTAAGGGAATTTTACCATTCCGCTTACCTTAAGACAAG
TAAAGGACAAGACAGCTCCCTTGCAAAATATGAAAGTTTGAACCCCTAAGCTCACTTTGA
TCGATATTCTTTCTCTTTTGTGATTTTCATCACCATTTGCTCCCATTCACAGATTGTTTTCG
ACAATGATGCTTTAAACCAGGATATGTTTCAAGATAATATTCTGCTTTTGTGTAAGCTTCA
CAGTTTGGACAAATTGAGTTTAAAGAAATGTACGAATCGACCAAGATGGAATGGAATTTAC
TATGTAAGTTCCCTTTTGTCTAAACAAATCACTGAAACAAGCTCGACATTTCCTCAACAGAAA
TCAAACTTGCTACCTTGCATGAAATCACTATATCGCCATAACATGGAATGGAAGCTTGTATTCTG
ACGTTTGTCTCAGAGATCTCAACAACTTATAGAAGATTTGTTATCAATGGTATTCGAAT
TTAGCAAAATTTCTTACTCATGCTTTGACGCTTTACTGACATCTTTGCTACCTCAACAAAA
ACCTTTTCGAAATCGGGCATCAGGCTTGGTTTACGAGGTGCCACTACTCTCAATATGCTCTC
AGGATTTGCTGAAATTTATCTTCAATTTGATGTCTCAATATAACGCTCAGGCTGTGATG
TAGCGTTTAAATGATCTGTCCATATGATTAAAGCCAATGGTTGGTAAACATATCTGCTCTAT
CATATGATAAATTTAAGATATTTTCATTTGAACAGCACTAATATTTCACACTCTTATGATTT
TAGCTTTTGTCTTGAATATCTTTCTAAGTTGCCTAACTTGATTTTGTGATTTGATGTA
ATTTGTGCAATGCTTTCTGACATTTTACCTACATGTACAAGTATTTCACAAAGATTTC
CGAACCTGAAGAGGATACATTTGGATAGCAATAATTGACATTTAAAGGAACACTGCTGTG
TTTGTAATATTTTGTATTAAGTGCAAACTGCTGTCGATGTGTCAATGACATTAACCAAG
TTGAAACTTCTATCTAATGAACGGCAGCATTTCTCCGTTTCAACAACTTAACACAGCG
CGACTTGGATAGTTTCGAGCATTGGACGTTTAAAGGCCAATTTGCTAAAAATAGTTTTT

FIG. 1 - 92

CATCCACACTTTACGCATTTGCTAGAGACTCTCCAACTTGATTGGTTTGTAGATTTTGACT
 ATGATTTGATATCAAGAAGATTCAATCAAGAATAGCAGTGTGCTTGATGAGAAATATGA
 AACGGACCATTGGATTTCGACTTTCCAGTTAGATGAATTTGGATTTCGCAAGATGATTTCGTAT
 TCGATTGGCTCTTTAGTAACTATGACCCGCTGAAAGTGTTTAGAAAAACTGAACCTGTTAA
 GCGATAGAGATTACAAAGGTCAAAAAAGACACCCAGAGAGATATTTGCTGAAAAAATATA
 TGTGAAAGATTCCATATCTTGCACCAATATGTTTCAGCATACATAGATACTATGTTGCGAAA
 AAGGAAATCAGGTGAATTGCCATTGCAAGAAAAAAGAAACCTGTGAAGATTACTCTCTTT
 TGGAAACAAAACCTTATGCAATATACTAGAATTTGTTTTCGCATATATCCGAATCTGAATGATG
 TCCTTGGATTCCAGCAGGATGATTTCGAAGGAAAGTGTGTGACTCCAGCGAAGATTCAAAAT
 TACCAGCATTTGAAGCAGCTTGAATCCGGATACCATGTTCCCGAAGAAAAAATACACCTG
 AGAATGATGTAATACAGCAAGAACCACTTTAATGGCCACGATTCTCGGTAAACATTTATTG
 ACCTTTTACAGGCAAAACCATTTGGTGTTCAGCAATACATCATCTAGTACTTCTGTAGGTT
 GTAAAAAGCAGGAAGAAGAAGGTTGAACATACATAAATGGGGTTTCTTCGTTTCAAGCAGC
 AGAGGTCCTTTATACCTTGAAATTAATCAACAAGGCAGACACCTTTGCGATCAGGTGATA
 CGCCTATCAACACAGAAACAGCTGGTAAGTCAACTTCACTTCTCCTCAGTTTCAACTTCTA
 ACAATGAAACTGCTACCACTAGTTTATTATGAGCCAGCTAATCCTAAGATTTTACCAAAAA
 TCCATCTGGCTGCTGCTTTAAGATCGGCAATCATGAAGGCTAAAGGTTAGTATTGATCTG
 ATGATTTGATTGATCAGAACGTTTAACCTCAACAACATAGAAATTTGAGAACATTTATGTTGGTAA
 CCATTGAGAAATACGCTTCGACATTTACACCAAGCGTGGATTCTGATGATCTGTCGCGCCA
 ATACCGATAAAGGATCCGTAGAAAATTTGCCCTGCGACTTCAACTGACGACCCAAATTTGTG
 AAGTCAAAGTCACTGCTACCTATGACAAAATTTAAATAATTTTGTGATGGAGAGGTCAA
 TCAGACTTTGA

YPL137C, 1276 aa (SEQ ID NO 274)

MITNTEFDPVVDWLYKGKSRKNTWTKPSRPSTSPASSSTSSSKNGDNSTSGNRSSNDKP
 RARSSSVSNAALCNTEKPLDKRNDGNTSASDTNIPLLTFINSNGNRSDADINDPATVDA
 IDLINDNDNGSSTQFVKRRSTSI SNAVVSXKPLASSAINATASSVVGKGFHPTSSPS
 NATLKRKSTSGEKTKRISIFGSLFKRSTSSSASTAKKPLPVNVTSTENESGKIKAVAT
 PDRVKEITSSPMRGVAPTASKPQTPIPLSPALAVKDLSTVSLKRVSFVADKPFESDPFQOL
 PSRTPKKGNILIPDDMISEVPSISVGISSSNSQSAKSTNSNIKGPLYTKKSEYILALENQ
 KLALREAAKHQOEAFANRIAFEVANFKTASDAGGKLTEKSSSEGTITKQREEVSPPNVE
 ADRELENNKLAEENLSKAGIDKPIHMHYFKEPDQDKYQDGHSENNNEVTLVDVIYTRCCH
 LREILPPISTLRQVKDKTAPLQILKFLNPKPTLIDLSPFCDFITIAPIHTIVFDVNALNQ
 DMFRITISALVNSTVLKLSLRNVRIDQDGWKLCKFLLNKSLNKLDISQTKIKSDLAE
 SLYRHNMDWNLFDTVLQSRSKHPIEELLFNGIQFSKIPYSCFARLLTSFATQKNFPESGI
 RLGLGATTTSNISQDCLKFIFNWMQYVNVQVDLAPNDLSTMIKPMVKGKLSALSYDNLRY
 FILNSTNISTSYDLALLKLYLSKLPNLIFLDLSNLSQCFDILPYMYKYLPRFPNLKRTH
 LDSNNLTLEKLAUVCNILIKKSLSHVSMTNQNVENFYLMNGTDSVPVQNTDGDLDSSS
 TLDVKGQFAKNSFSSTLYAFARDSPNLIGLDFDYDLISEEQSRIALCLMRNMKRTMDST
 FQLEDLDQDLDLFDGLSVMTAESVLEKLNLLSDKSTVKVKDITTKRYLLKKYIEKFHLL
 HNNVQHTIDTFEKKRSGELPLQEKENLVRLLLEQNLNILELFSHNPNLNDVLGSSRD
 DSKESVDSSEDSKLPALKHVESGYHVPKEKIQPENDVITARPHLMATDSGKTIDVFTGKP
 LVFKHTSSSSTSVGCKQEEEEGLHKWGFVQQQSRSLYPENESTRQTFPAGSDTPINTE
 AGKSTSSPSVSTSNNETATTSLSFPANPKILPKIPSGAVLRSALIMKAGKIDISDILLQNV
 NSNIELENIYGESISASSTFTPGVDSVAPNTDKGSVETLPAVSTDDPNCVEKVTAT
 YDKLLNNLSMERSIRL

YPL159C, 1262 bp, CDS: 501-1262 (SEQ ID NO 275)

AAACAAGCGGATTTGAGTATTACGTTAAGATCTCCATTGTGCTATGCTAAATCCTGCCTAC
 TCAACACAGCATTTATTCGCTACCAACAGGTGTGGTCAAGAGGTCATTGACTCTTCCTGTC
 GGTATGAAAAATTTAAAAATATAATAACATAAGTTTGCATTCAATTAATATTAATATAAA
 TCAACGATATCAACCATAGAACCATAATCAATAAATTTGTTACCTTAAATGGGATCATCG
 CCTTTTATCACCATCGACGATAACAACGCCATTTCTGTCTACCGTTCTTTTCTTCGCT
 CGCAATATCAGAATCGTTTATCCCAAGGGTAGTTATAGCAACTATTAAATAACTTAGA
 TGTTCCTTAACTATTTCGCTCATACGTACACAAACACCCGCTAGATATACGACTCTCTG
 CTGTGCAACATTTAAAGGTGCTTTTAAAACTACTAATCGTATTTTACGACGGTCAGAAC
 GCAAAGTCGGACGATAAACTATGTTGAAGCTAGCTCGTCAATTTATTCGCGCTTTACAA
 GGAAACAATGCCATTTCTTCAGGAATAGTCTCACTTCTAGAAGATTTCAGTCTTCCTTTA

FIG. 1 - 93

CGTCTTAAAGTAACCAAGTCTTTACTATCTAAAAATCAAATGAAATCCAAAAGAAAAAGG
 GCAGTAAAAAGCGCAGCTACCATCGTCAACCCCGGAAACAGCAATCTGACCACTTAA
 TAAAGCAAAAACAGACAATCACAAGAAAGAACATAGCGATGTGAGAGGTTCTCATTTAA
 AAAAGAAAAGAAAGCGATTTTTCGTGGCTACCAAGAGTACCATCCACCTCACATTTAAAGC
 AGAGTGCATGACCAACAAATGTACTCTATTCTGGATATAGACCCCTTATTCATCAATCCCA
 ATGACCCGAAAGCTAAAGGAAGACACCGGAAGTACGTTATACGAATTTGCGATGAAGCTG
 AAGATTTAAATGAACCTCTATCACCATTGGATTTCCTCTGCCACTGGACCTGAATCTCTTT
 CAGAGTGGGGAATATACCTAGTGAACCTTGAAAAATTTGAAGCCTTTTCATCCACCTA
 AGGAAAAATCAATGAACACAAATGAGCTTATTCAATGTAAGTGCTAAGAGAAATACATTAG
 TTGACAAATAAACAAAGTGAGACGCTTCAGCGGAAATGGAATGAAATTTTCAAAGAGAAG
 GAAAGGGGAGAAAAAGTCAGTAGTGACGTTGCTCCAAATGAAGAAAAAATCTGAGGGAT
 GA

YPL159C, 253 aa (SEQ ID NO 276)
 MLKLARPFIPPLSRNNALSSGIVLTSSRFQSSFTFLSNQSLLSKNQMSKRKKGSKKAAY
 HRQPPEHEHTAFLIKQNTITKKEHSDVRGSHLKKKRSDFSWLPRVPSTSHLKQSDMTTN
 VLYSGYRPLFINPNDPKLKEDTGSTLYEFAMKLEDLNEFLSPWISSATGLEPFWSEWENIP
 SELLKNLKFPHFPPEKSMNTNELIHVSARKNVLVDNKTSETLQRKMDSEFSKRGRGKRKS
 VVTLLQMKKKLEGG

YPL175W, 1940 bp, exon1: 501-514, intron1: 515-568, exon2:
 569-1940 (SEQ ID NO 277)

ACGTTATTTTCAAAAACACATACGAAATCGCTGGACTTTCTCACTAAAGGCTTCCGGAGCC
 TCGCGTCTCTCCATCCCATCTCTTCCACATATACCGGGGTTCTGATGGCATTCCTATA
 GCTTGCTCAAAGTCTCTCGAGTTTAGCTCATCTCTGTGAGTTATTGCTGGTTCTTCAACA
 TCTCGGAAGAGTAGTGTAGCCCTTAGTATTCCACATATCCTTTGTATCTCATATGCGAAC
 TTGCTTAATACAATGTATACAAAAATAACAGCTTGAAAAAATCTCAGGGTCTTTTCAT
 TGAATTAATCTCATCTCTGCTATTTTAAGTTTTCGTTTGCAACCCGAGACTGTGCGAGCTAG
 AAAATTTCAATGATACGATTAAAAATAATCGATGCCAGTAATAGCTCCAAAAAATTAAT
 GCAAAAAATACGAGATACATATAAACTACAGCTTAGCTAACTTAACTATTATATAAAAA
 AATGGGCTTCAATATAGCGTATGTCTAGCTACAGCATGTGTCCAAATACATTAAGAA
 TGCTCTCTTTTGTGTGTATCTAACCCAGTAAAGTTGAGAGTTATAACAAATGAAATAGGA
 TGCTGTGCGACTTTTTTTATCCACAGTTAGGTGGAGTCGAATTCATATATATCATTTAT
 CGCAGAAACTAATCGATTGTGGGCCATTCTGTGCTCATTTAACTACAGCTTACAAAGATC
 GAGTCGCGCTACACATCTTACCACCGGTCTAAAGGCTTATCAGTACCATTTTGTGA
 TTTTCAGAGAAACCACTTTCCCACTGTTTTTTCAACATTTCCAATATAAGGAATATTCT
 TTCTCAGAGAACGAGATCCAAATGTTCATTTCTCATGTAGCGCTTCCACGTTCCGCTCAG
 AGGGAATTTCTCATGCTAACTACTATGGGATTGAGAACTGTGTTCCAGGCACCATTCATCT
 ACGGTTTAAATAAATTAACGTCGATTGGGTGAATAAGTTGCTAACATTTACCTTGACAA
 ACATAGATCGGGTTATATGTGTTTCTTAATACATGCAAGAAAAATGATTTGTAGAACAG
 AATTAAAGTCTGATATAATCTCAGTAATTTCCCAACGCGAGTGGTGAGCGAAGATTCAAAC
 CAAGGGATCTACTGTTGGCACCAAGAGAAAAACAAGTAGGGGATAAGATAGTGTATCGTGG
 TCATCGGAAGGCTCTTTCCAAACAAAGGGTCCGATTCTACTTACTCGCATATTTCCGAAG
 TTTGTTCTCTCAGTGAAGATGTGCAATTTATAGTAGCGGGCGATGGTCCAAAGTCTCATAG
 ATTTTCAACAAATGATTGAAGTCATAGACTACAAAAACGTTGCAACTCTTAGGCTCTGT
 TTCCACATGAGAAAGTCAGGAGTGTATTATGTCAAGGTGACATATATTACACGCTAGTT
 TAACAGAAGCATTTGGTACAATTCTAGTTAGGGCCGCACTCTGTAAATTGCTAATTGTAA
 GCACACAGTCCGAGGAATTCGCGAAGTGTACCAATGAGATGACTGTTTATGTCAGAAAC
 AGACATCCGTTTCTGACCTTGTTCAGCAACAAATAAAGCTATCAATATCATATAAGAAAT
 AAGCTTTGGACACTTCTCTTTTCATGATAGCGTGTCTAAATGTACGACTGGATGGAGC
 TAGCCAAAGGACAGTAGAGATATATCTAATATATCTTCTTCTTCTCCGCTGATGATA
 AAGATTGGATGAAATGGTAGCAAACTTTTCAAAAGAGATGGAATCTGGGCTAAACATC
 TTTATCTGTTATGTGGAATGTAGAGTACATGCTTTTTCCTCTTAGAGTGCTATACC
 CAGGGATGAAATCGATCTAGCTCCAAATGCCCCAAGAAAAAGTGTCTAACGAGACGA
 AGGAAGCAAGAGAACTTAA

YPL175W, 461 aa (SEQ ID NO 278)
 MSSHKVESYNNENRMLCDFPQLGGVEFHIIHLSQKLIDLGHSSVVIITHAYKDRVGRV

FIG. 1 - 94

HLTNGLKVYHVPFFVIFRETTTFVFSTFPIIRNILLREQIQIVSHSGSASTFAHEGILH
 ANTMGLRVTFFDHSLYGFNNLTSIWVNKLLFTFLTNIDRIVCSNTCKENMIVRTLESFD
 IISVIFPNVAVSDEPKPRDPTGGTKRKQSRDKIVIVVIGRLFPNKGSDLLTRIIPKVCSSH
 EDVEFIVAGDGPFIIDFQPMIESHRLQKRVQLGSGVPEHKVRVDLQCQGDLYLHASITEAF
 GTLLVEAASCNLLIVTTQVGGIEPEVLPNEMTVYAEQTSVSDLVQATNKAINIIRSKALOT
 SSPHDSVSKMYDMDVAKRTVEIYTNISSTSSADDKDMKVMANLYKRDGIWAKHLYLLC
 GIVEYMLFFLEWLYPRDEIDLAPKWPKKTVSNETKEARET

YPL180W, 2900 bp, CDS: 501-2900 (SEQ ID NO 279)

CTCAATGGAATTTGAGTGAAGATCAGTCTGATCGAGGGAATTTGTACGATTCGTGGAAA
 ACCAGCATTTTCGTAGAAAAAGTTGATACGATTTACAACGGTTATAATGAAAGTCTATCAA
 TGATGGACGACCTGACTAGAGAGTTACTACTATGGGAGAAAAAATATTCAAATAACACATA
 ATGCCATTCAATAAACGCAAAACACTGCAATATATTCTCAACCAAGATTAACCTGTAAT
 GAGGCGAACAACACATCTATACATATATATACATCTATATGGATATAAAAAACGACTAAT
 TCAACGTTGTTTTTATCAACCGAGCTTACTCTGTACGGGTAAACGCAAGGATAGCTAGT
 TCGCGATGGTATAGCGATTTCGGTGGCAGCATGATTAAAGGAATCCAAACATCTAATGGAC
 TAGCACATTTATCGATTACGGGTACGGTAAACATAGATATTGGGATATATCATATCATCT
 CTCTAGTAGTAACATAAATTATGGTTCTCGAGGAGGAGCTTTGAAGTCAGACACGTAGTG
 TAACATCTCTTAATGCGTCAACAGTATCACACCAAGCAATTTGAGACAGCTTTTCGA
 CTAGGTCGAGAGCAAGAGTAAACGCAAGCTTCAAAGGTTTCGGTAGAGTTTAAACACATG
 ATGCGACCCCTGGATAATGATTATTTTAATAAGCACACGTTTTCGAAATGCAAGAGATT
 CTGATGCACTTTTCGAAAGCGCAAGCATAGTGGGTGAATATGACAGCTTTTAAACAAGAG
 TAAAGTCCAATCAAGGAAAAAGATCAGCATCTTTCTATAGTCGGGTGCAATAACGCTGC
 TCAGTCCAAAGAACAGCAGCTCAATCTTAATACTGGAAGCTGCTGGTTTCGGCTGAAACAC
 GAAGAGTAAGAGTACCAATCTGTTCTGAGTCTTCGAGATGCGCAAGAACTCAAAAAAGA
 GTGAATCTACTACTGACGAGGAGGTGGAATGCTTTTTCGGAAGACAACATTTGAAGTGGAA
 AGGTGAATTAATGATAAAGTAATAGCCGAGCATGTTATGCTCGAAGAAAAAAGAAATGTCG
 AGCAATTAATACAGAAATGAATACAAATCCCGGATTAATAGATGAACAAGAGACAGATA
 AATCAGGTACTGATGGAAGGAAAAATCATAGAGCTGTATCTTACCAATTACCTCATTTAT
 CTTCCAATAACTATTTTCGGAGAATCAAGCCATCTATAGAACATCAGAAAGTGGAGAAA
 CATCTCCAAGCTCAATTTGAAACAAAACTGAATGCAACAAGTGAATCAAATGGAAGGGGCG
 AATCAAAGGTGCAAGGAAGCTGATATGATGACTTGTTCAGCCATTCTCAAAAATTTGA
 GGGCTCATTTGGTTAAAGCGGGCGATAATATATCAGAAGCACCATATGATAAAGAAAAA
 AAATCTTATGTTGGTAATACCTTAGCTGCACATAAAAGTAATCAAAAACCAAGTCAATT
 CAGATGAACAGTTTGATCAGGAAGATCACATTTGATGCCCTTAGGAGTAATTTCAATCAAGAA
 AAAGCGCATCGAGCTTTATGCTCTTTAGGAGACAAAGTTCTAAACAACACAAATTTATTA
 ACGAAGAAGAAGATCTAATCAAGCCTGATGATATTTCTTCGCTGGTACCAAGGATATTG
 AAGGCGATAGCTTACTGGAATAATATGCGCCTAATATGATTCTTCCAGTCGACTGGAG
 TTGAACGTAGATTGAAAAATTCATCATCCATCCAAAATTCGCTTGGGAATGAAATTCATG
 ACTCGGTTGAGCATATGGCTTCAGGTGATCTTTTAATGAACCTGGATGATGGCAAAATTCG
 GCAAGAGCAGAAAAATGTTGGAAGATCTCAACTTGGCCAAAATATACCGAACTCTCAGT
 CTACTTTTCCCGACCATTGCTAACATCGGTAGTAAAGATAATAATGTACCAAGCACAACCT
 TTTCGACCTCCATATCGAGTTTAAACCAATAAATTTGAGGAGAGCTGCTCCTGAAAGCTTCC
 ATGGTTCAAGAAATGAATAATAATTTTTCACAAGAAAGGTAATCAGAATCTACTTCTGAGAT
 CCAACGATCTCAACAAAAATTTCTGAGCCCCGGCTCTCCATTGTCCAACGAACATATTA
 CATCTAGTACGAACCTCCGGTAGCGATGCAACAGCAAACTCCAAGTCCGAGTCAAAATTTA
 ATAGCTTCGCCAGATTCTTAAATCAGATGGGATTTGATCGAGAATCAAGAACACAAGAA
 AATTATGGTTTCGAGAGGAGAAATCTTAATTTGACTTAAGTTTCAACAAATGACGGTATGTG
 ACTCTACTTTATGGCAGGAAACATTTGATGCGAAAAAGGGAGTTTGAAGAAATTTCCAGTCA
 AATACTCTTAATGTAAAAAGATTTTTACAACCCATTAGATGAAGCATTTGTGTAGAGTACAAC
 CTATTAATACCGGGAATGCAAAATATATCAGGAAAAAAGCCATAACGATGCTCTAGCTCAA
 TCGCAATCTTAGCTAGTGTATACAGATCATAGGATGAGGAGATTTCGCTCTTACTACTCT
 ATGACAAAAAATTTGATGATCTTTATCCACATCTTGAAGTCAAAGATTTACGCGAGTGT
 TGTCCGGTATATGGAAGGCGAAAGTTACTTATTTAAACAGGATGTTAATCCAACTACAACA
 AGAATAGGACACAAGAGTACAACCAACGAGCTTGGCCACATCTGCTTCACAGAAATGCACGTA
 ACTTGTCTGAGGGGCCGATGGGTTCCAGCAGCAGTTTTCACACCAACCGCTCATTAATCT
 CTCTGCAGCCGATACGAGGGCAGTGAATCGCAGGATGGAAATGTGGGCTACATGCATA
 CACAGCCACAACAAGGTGA

FIG. 1 - 95

YPL180W, 799 aa (SEQ ID NO 280)
 MVHRGRTLKSDTDVTSNLNAVSHQSKPFRQFSTRSRAKSNASFKGLRRVLTHDGTLDND
 YFNKNHVQCKKSSDALFRKRTISGLNMTALTRVKSNOGKRSASFHSPVHNTLLSPKNSS
 HSNTGTAGTGLKPRRSKSTQSVLSLRDAQESKKSESTTDEEVECFSEDNIEDGKVNNDKV
 IAEHVMPEKKNVQQLNQNELQSPDSIDEQEEEDKSGTDGKENHRAVSLPLHLSNNYFG
 ESSHSIEHQKDGSETSPSSIETKLNATSVINEEQGSKVTKEADIDDLSSHSQNLRLASLVKA
 GDNISEAPYDKKKILLDVGNTLAHKSNQKPSHSDEQFDQEDHIDAFRNSNSRKSDDSSFM
 SLRRQSSQKHLLNEEEDLIKPDIDISSAGTKDIEGHSLENYAFNMILSQSTGVERRFEN
 SSSIQNSLGNIEHDSGEHMASGDTFNELDDGKLKRSKKNNGRSQGLQNI PNSSQSTFTPIA
 NIGSKDNVFPQHNFTSTISSLTNNLRRAAPESFPHGRSMNNI FHKKGNNLLLRSDNKN
 SAAPASPLSNEHITSSITNSGSDANRQNSGAKFNSFAQLKSDGIDAESRTQRKLWLQRE
 NSIMDLSSQNGSDSIFMAGNIDAKREFERISHEYSNVKRFYNPLDEALLRQVPIITGNA
 NNIRKSHNDQASTAHSSSDTHKDEDDLFTNYDKKFDL YPHLASAKIQAVLSGIWKS
 ESYLFNKDVNPINKNRTTSTNHSVGHASQNAARNLLRGPMGSSSTTLHQVRVINSLQPTTR
 AVNRMRNVGMHTPQQQR

YPL218W, 1212 bp, exon1: 501-528, intron1: 529-667, exon2:
 668-1212 (SEQ ID NO 281)

TGATACAAGCAGGCATAGGAAACACATGAGTTTGCATATGTATTATGCAGGTTTCATT
 TGTTCCTTCCCTTATTTCCTTTTCATAGTATTTATTTTATTTATTTATTTTATTTT
 GGATTTTATTTTATTTCTTTTTTAAAGCTAAGAAAGTAATTCGCGCATAAATAAGCGTGTG
 CTGGCCCTCGATAGGTACCTATAGTATACAGAAGCTTACGAAAGCTCCTCGCAGGATGGCA
 CTCTCAAAATTTTCGCGCTCAACATGGCGTATTGTACATTATATCGTTTCTATCATTTATATC
 GTATACGCCCGCAATATCCCGACAACCTCGCTGCAACGCGTTGACCGAAGAACTCGAACA
 AGAGATCGCATAAATAACAAAGGAAACGAATTACTGTCAAAATAGTTATTGTAAATGGA
 TCCTCTAGAAAGGCAACAGTAGATTATTTCTCTCTTTCTAGAAACATCATTTATAACT
 AACAAATATATAATTGGAATAATGGCTGGTGGGATATTTTGGTGGTGGTATGTTTATTCAC
 CCGTGTTCACGTTTTCGGATACTTAGTTTATTCATGTGGTAAACATGTAATGTTTTCAC
 GCTTAAGATCTATTTTTCCTAGAAAGAAATGCGTCTTTTACTAAGTTTATTTTAC
 TGTACAGTCAGAGATGTGTTGGCTTCCCTTGGTCTGTGGAACAAACATGGTAAACTACTT
 TCTTGGGTTTGGATAATGCCGCTAAGACCACTTGTCTACATATGTTAAAGAACGATAGA
 TTGGCAACCTTACAAACCAACATGGCATCCAACTTCTGAAGAACTGGCTATTTGGAACAT
 AAGTTTCAACTTTCGATTTGGGTGGTCTATTTCAAGCTCGTCGTTTATGGAAGGATAT
 TTCCCAAGAGTTAATGGTATCGTCTTTTAGTCGATGCTGCGTACCCTGAAGAGATTTCAT
 GAAGCAGGTGTCGSAATAGATGCTTTATTCAACATTCGCCAATTCGAAGGACGTTCCCTTT
 GTAATTTCTTGGTAACAAGATCGATGCTTCAAACGCGCTTCTGAAGCGGAGTACGTTCT
 GCTTTAGGATTTTGAATACCACTGGCTCTCAAAGAATGAAGGTCAAAGACCATGTGAA
 GTTTTCATGTGTTCCGTTGTTATGAGAAATGGTTATTAGAGGCGTTCCAATGGTATATC
 CAATATATTTAA

YPL218W, 190 aa (SEQ ID NO 282)
 MAGNDIFGWFRDVLASLGLWNKHGKLLFLGLDNAGKTTLLHMLKNDRLATLQPTWHPTSE
 ELAIGNIKFTTFDLGGHIQARRLWKDYFPEVNGITVFLVDAADPERFDEARVELDALFNIA
 ELKDVFPVILGNKIDAPNAVSEALRSALGLNTTGSQRIEGQREVEVFMCSVVMRNGYL
 EAFQWLSQYI

YPR102C, 1025 bp, CDS: 501-1025 (SEQ ID NO 283)
 TCTCTTACAATTCACTTGCATTAATGAAGGAGTGCTATTCCTTCGTTTGGCCACCCCTTTT
 GCTGCTTTTCCCTCATATCACATAATACCGGAGAGGCTCTTCTCGGACGAGCGCAACAT
 CCAACCATCTTAAGGATATGGGTGTACTGACGATGCGATTATTTCAATTAAGTTCTGTCTT
 TTTTGTATAAATGAAAAAGAACGGTGAAATCCATAGAAATACAGAGAGCGGACGCAAAACA
 CGCGCAGACTCTACGGGTAAATAGACTCACATCCACGCTGACCACTTTCATTCGAACCTTT
 TTCACTTTGAGGGAATTTATGTTTCACTAGCAAAGGTAGCCCACTTACCACCTGACGCTAT
 GCGAAGGTTTCACTGTTTGTATACATCTTGATAGTAACCGCAGGCTCTTCTTCTAGTTCAT
 ATTTTATTTGATTTTCAACTAATATTTATTTTTCAGTGGAAGGGAAGGTGAACCAAGA
 ACATACAACCAATAGCCAAAGATGCTCGCCAAAGCTCAAAACCCCTATGCGGTGATTGGA
 TCGAAAAGTTGGCTTTAAACATTTCTGTTGGTGAATCTGGTGACAGATGACACAGACGCT
 CCAAGGTTTATGAGCAATATCTGGTCAAACCTCCAGTTTCAATCCAAGGCCAGATACACTG

FIG. 1 - 96

TCAGAACTTTCGGTATCAGAAGAAACGAAAAAATTGCTGTTACCGTCAGAGGTC
CAAAGGCTGAAGAAATTTTGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA
GAAACTTCTCTGCTACCGGTAACCTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTTCATATGTCGTCATGAACAGAC
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACCGTTGGTAACTCCACAAGA
CAACTAAGGAAGACACCGTCTCTTGGTTCAGCAAAAGTACGATGCTGATGTTTGGACA
AATAA

YPR102C, 174 aa (SEQ ID NO 284)

MSAKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIR
RNEKIAVHVTVRGPKAEIILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI
GIFGMDFYVVMNRPGARVTRRKRCGTGNSHKTTKEDTVSWFKQYDADVLDK

FIG. 1 - 97

YBL051C_homolog_1 1229bp PathoSeq: 1..1229; CDS: <1..>1229 (SEQ ID NO 285)
AGAGAACGTATTGAAGAGGAGAAAAAGGAGAAAAAGAGGTCATTGGAAGAACACATCGTTCTGCA
TCAAATGCCTTCTATGGCTCTCTTATTGTGAGCTGCTTCAACTACAGCAGCACTAAAAATTGAGT
GTGGCTGGCACAATCTCTTCATACCAGTGAAGAAATGTTTAAATTTACCTTTTAACTAATTC
CTGTTTCAATGCCCCAGCAGTAGAAATTAATTTTAAATGATCTTGAAGTTTGGAAATTGTACACTCAA
TTAGTATTATACCGAGATGATATTACCAATCTACTTTTGAATTAGCTTATATCACCAGCAATTTG
AATATTCTCTAACGGAAAAATCATATCAATTTTATGTAATTTTGAATTTATTAGAATTGTTTGTAT
AATGGGTTGATAAATTAATTAGAAGAAAAACAGGATACATGTCTCACTGTTATATCTCAACATCTATT
ATTCTTAATTTCTCAACAGGTGTCTGGGCCAATCTACCCGCAACACATCAACAGAAATCAACAGAAATCA
CAACAGCAACAGCAACACATCAACATCAACATCTCTCATCTCATCATCGATGATGAACCTTCAT
CAATTGGGTGGTACATTAGCTGTCCAGCGCACCTGAATTATTAAAGATCCCAATCGCAATCAGCA
TTACCGTGTGCCAAGATTGAGACAGCAAACTCTACACCAATTTCAACAAAAATCAACAAAGTTTCAGCAC
CAAAATCAACCCACACAAACAAACAGCAACAGCATGTTCAACCAACATAAATATTATCAATCAG
CAATCTATTTCAAAGCCAAACACATCTCGGAGACCTTATTCTCAATCATATAAATATTATCAACAA
CAACAGCAACAGCAGCAACAAACAGCTCAACAAACAGCTCAACAAACAAACAAACAAATATCA
TATCAACAGGACACACAGTCAACAGTTTCAACACCTACATTGAATTTCTTCTAGTGTCTGTCATTA
CTTAGATCAAGTAGGATGATCAATTTGTGTGATGTGAGATCCACACTCCCAACAGTAGTTTGTCT
CAACAGCAACAAACAAACAAACAAACAGCAACAGCGCCCACTAACTTCATCAATCCATGATTCT
CCAACACCATCATCATTTTACCACCTTCAACAGCAGCCACCAACCAACCAATCATACCTATCCAAT
TACCATCAGGGGTTGTGATCTCAACAAAAACTCCATTGGC

YBL051C_homolog_1 409aa (SEQ ID NO 286)
RERIEEKKRKGLEQPHRSASNASMASLLSAASTTAATKNLSVAGTNPSHTTERMFLNLPFNNS
SFNAPPEVINFNDLEVLLEYTQLVLYRDDITKSTFELAI SPANLNI SQRK IISILCNLYLNLELFD
NGLII IRRKPGYIAQCTIQQSIIPNSQQVSGPETHPQQHQQQNLQQQQQQHQHQHPHSSSMNLH
QLGGTLAVPAHPPELLRSQSALPLPRLRQSTSP IQNQVQVQHQNP PQQQQQHQVQPPNYNYNQ
QSIQSPHSARPSQSYNYIQQQQQQQQQQQAQQQQQQQQQLOQYQDGHQSVQSTPQLNSSSAAAL
LRSSSSRSFVDRSTPTPTSSFAQQQQQQQQQQQPPLLSSTHDPSPTPHHLLPPTPPPNHYLSN
YHQGVGSQPKTPL

YBL051C_homolog_2 2153bp public: 1..2153; CDS: 501..2150 (SEQ ID NO 287)
ATAACAAAAAAGAGCAGAACTGTGGGCAACAAACAAACAAACAAACAAAAAATTT
CTGGAATAATCAAATTTGAATCTCAACCCAGCAGCGCGCGCGGACAGAAAAATATATTACAGAAT
ACTTTTGTGATTCAACTCTCTAACTCTTCTATTTTTCTTTTCTCTATATACACTGTATAATC
AATCAACAAATAGCAGGATATCCATTATATACAAATAGATAAACTGTTTAAATTAATTAACTG
ATTGATTGTTGGGAAAAAACAATTTTATATTGGAGAATTGAAATTTCAATCATTTTAAACAAATTCA
AAGCTTTAATTCCACCTATCAAATTTTCAATTATTATTGTTTTCATTATTTTCTTTTCTCTCTT
TTCTCTTCTTCTTCTTTTGGAAACAAAGTAATAGCCGATAAAATTAATTAATTCATACAGCCCA
ATTCATTATTACATTGACTTTTGACAAGAGGTATATATAATGGATTATAGAAATTTTCACTACTAC
CGAATCAATGGGCATGTAATGCAACGTCGTCCTCTCTATCATCATATTATCGTACGCTCGGGCT
ATTCCTCTTCCAATTATGTGTGGAATCTTACACCAATCCCAACAAATCCAATTAACCAATTA
GTAGTGGCAATAGTAATAACAACACTCTAGGCAATAACACTCCCAAAATTAACCAATTAAGATGA
CAATAATAGGAATTTTACAATCTCTGTGGATAAACCAACCATCTATTGCTCTCTTAACTGTTGCTC
CTTGGGTGGAACAGCAACACAAACAAACAAACCTTGATCTGTTGGAATAATAATCAATAACAGACTCCA
GTAATGATGCTCTCTGCTACTAATAATAATATGTTAATGTTAATGTTAATGCCAATGCCAATGTTA
ATGCCAATGCCAATATCCATGCCCAACCCATGTCAACACAAATGTCAACACAAATAATAACAACAGCA
CTAGTATTAAATGCTTCCACGATTTTAAATACTACACCAAGTATTAAATGACACTAAATGATAATGCCA
AAAAAATTAATGTTTCCCATGATTAGTAATAACAATAACAAAGTAACAAATAATAACAACAAACA
CTAACAAATAGTAGTACAGGAAGTCTAACAATGCAAAACATGCTTCTCTGTTTCTAATGCAACGA
CAATGAATAACAGTAATAGTATCAATAGCACCACAAACAACTACTACAATTAACGAAGCTGATGATG
ACGAGTTAATTTCTACTCGGATGTGATTAATAATAATTCATTGTGCCATTAAAAAGGAACAATTTG
TAGATGTGATGACAAATTAACCTGCCATTACCATATGCCTTTAATTATCATTTTGTATATGGTG

FIG. 2 - 1

TGTTTCCTGGGATAGCATTGCGCAATTTACATCTACAGATGAGACATCAGCAGTAGTAAACCAAT
 TGAATGGAAAGAGAAATAGGTGGAAAGAAATTCGTGTTGAATACAAAAATGCTTCGCCACAGA
 AAGAGAAACGTATTGAAAGAGAGAAAGGGAGAAAGGTCATTTGGAAGAACACATCGTTCTG
 CATCAAAATGCTTCTTTGGCTCTCTTATTTGTCAGCTGCTTCAACTACAGCAGCAACTAAAAATTTGA
 GTGGGCTGGCACAAAATCTCTCATACCACTGAAAGAAATGTTTAAATTTTACCTTTTAAACAAT
 CCGCTGTTCAATGCCCAACAGTAGAAATTAATTTTAATGATCTTGAAGTTTGGAAATGTACACCTC
 AATTAGTATTATACCGAGATGATATTACCAAACTCTACTTTTGAATTAGCTATATCACCAGCATAT
 TTGAATATTCTCAACGGAATCATATCAATTTATGTAATTTATTGAATTTATTAGAATTTGTTG
 ATAAATGGGTGCTACTAAATTAGAAAAAACAGGATCCATGCTCAGTGATAACTCAAAAACTTA
 TTATTCCTAATTCTCAACAGGTGCTGGGCCAACTCACCAGCACCACCATCAAAAGAACTCAACTTC
 ACCACAGCAACAGCAACACATCAACATCAACATCAACATCTTAAACATTTCATCATCGATGATGAACCTT
 CATCAATTGGGTGGTACATTAGCTGTTCACAGCCACCATGA

YBL051C_homolog_2 550aa (SEQ ID NO 288)
 MDRFRLSTTPNQMTVMQRRPSLSLSASGYSSSNYGGNPTPNPNNSNTNNSSGNSNNTHGNN
 TPKLSTQRLTNNRNLSQWLNQPSIAPSNVVPVWEQQQQOQLDLENNNTKTDSSNDASATNNNNVN
 VNVNANANVNANANITHAQTHVNTVNANTTATSLNASTILNTTPSINTDNDNAKKINVSMI SNNNN
 NNSNNNNNNNNNSSTGSSSIAMMLPSVSNATMMNSNSINSTWNNTTINEADDELIPTAIVIKNI
 PPAKKEQLLDVMTKLNLPYAFNYHFDNGVFRGLAFANFTSDSTSAVNVNQLNGREGGRKLRV
 EYKKMLPAQERERIEREKREKRGLEEQHRSASNASLASLSAASATTKNLVSAGTNPSPHTFR
 MFLNLPNNSSSFNAPVEINFNDLEVLLEYTLQVLVYRDDITKSTFELAI SPSIFEFYSTEHNILNC
 NYLNLLEFDNGLLLLRKPKGSIACITQKSIIPNSQVSGPTHPHHHKQNLHQOQOQHTSTSTS
 LTFIIDEPPSSI GWYISCSAP

YBL066C_homolog 3254bp PathoSeq: 1..94/2146..3254, public:
 95..2145; CDS: 501..3251 (SEQ ID NO 289)
 ATAAAAAAGAAATACAATAAAAAAATTTCTCTCTGTGAAAAGGCAATTCGGGTCTAGTAGTA
 AACAAAGCTTAATAATTTCTCCCATTCAAATTTACAAAGGACGATGCAGAAAGTAGTTTTCAAATT
 CAGTTCTCTTTCTTTTATATATTTTCTCTACTTTCTCTCTCTCTCTCTGACAGTATATTAATA
 AATATTCTTTTAACTTATTTTCAATCAAGAAGGTACTGAAGATATCAATTTAACTCTCAGTTAAA
 TCCATATTACCAAGTTGTGGAATAATCAGAAGAAAAAAGAGAGAAAAATCAGCGGAATTAC
 GTTCTCAACAGAAAAAACAATAATTTTATTTATTCATCCAAAGGTATAACAAGAACGTTAGGAA
 TAAATATAAAATTAACCAAGCTGCCATCAACGCTGTGCGACAACCAATCGACTCCTCCCTTAAAC
 TAGAACCATAGAACCTCAACATTTGTTTCTATAGAAAAATGAAGTTTGAAGAAAGGTAAAGTGAGAA
 TTTTGCCATAAACCATCCCCTACCAACCAACCCACAAACCCCATTGCCATTACTTCCAGCTCAAA
 CTAACCTGTAAACTCAAAAGAAAAATCAGCAGCCAGTACACCTGGAAATGAATCAAGAAATCAA
 GAAATCAAATCTTACAGCTTCAACACCCACAGTGCTACACCAACATCAGTCGGAACACCTCCAC
 AGAAACTTCCAACCAACAGGTATAGGCCAGTGACTTCATGTACTTTTGTGCTCAACATAAAA
 TCAAAATGTAATGCTTCAGATAATATCAACACCATGTGAAAGATGTAAAAAATGGGTTTGAAT
 GTGAAATTTGACCCGGAATTAGACCTCGCAAGGGTCACAAAATCCAATCTTGAATCGGAATGTTG
 ATGAATTTGAAGGCCAAGATTTGAATGTGTACTAAAAATGAATCTTTGTCTCACACAAGCTTTGAATC
 AACAAATTTGAACACCGCTTGCAACAGCAACACTGTCTGGATCGCAATCTCAACAAACAATC
 CTCCAAATCCACAGCGTGCATTGTCTATACGTCTGCAAACTCATCACCAGAATGTGCAATTTAGCA
 ATGCTACGCCAAATTCCTCTGTGCAAGTATTCAACAAATGCACCGCTGACTCAGCAAAATTCG
 ACAATCTCCATACGCTTTAAATACACCAGAAAAACATGAAGAATTACAACCAATCTCAGAATTTA
 TTTGGGTGACGTTACTTTGCCATTAAACAGGGCCAAATCAGTTACACGACAGTTTATGACACAC
 ATTTACCATTTTGGCAATAATAATATCTCGATCTGCCACCGAATGTATCATTAATCTCAATTCG
 TTTCTGGGCCGATGATTCTTACCAGCAAGCTTATCAGAACCGAACCCAACTTTATATGTCGTGGG
 CACTCTTTAAATGAACATTTAGCAATTTGAAACATGTTGGATTAAAAACACCAAGATCACTCAATGTA
 TCCAGGCTTGATCATACTTCAATATGGCCGTTTACCTAATGAAAAAATTTTGGATGATTCGCTCT
 ATAGATTTTGTGGATTGCAAGAAGAACTGTGCTATTACAATTAGGCTACATCGTGGTGGAGAAATCA
 TTCAGAAATTTAGTCGGAATCAAGTAAGTCTAGGACCTGATGCAAGAAAGGTGGAGGACCTGCTTCAT
 GGTTCAGAGTTTCTTTGTGAAACAGTTTGGCTCATCATTTGTGGGGTGGCCACTTCAATTAACA
 CTACTGATTTATTTAGAGAATGCTCGTGTGATAAATCGTGCCTAAAAAATTTCCGTTGTTTGA

FIG. 2 - 2

TTTCGCTATCTATTTTCCAATGCAAAATTAGTTAATATTATGGGTATTAGCGTTACTAGACCAGACG
 GTTATTGGAGCCTCTGAATCGTGCTGGTTCACCTTAGTTTATTGGATAGAGAAATGGAAAGATTAA
 GATTTAAACTTCAATTTTGAAGAAGGGGGCCAAATGGAAGTATATTATTGTATATTAATTTAGTGA
 TCTGCTGCTTTGCCTTTACCAGGTACACCTATCGAGGATCAAGTCAAGTATGTTCAGTTTGTGAT
 ATTTATCAGCAACAAGAAATCGTGACAATCGTTTCTAAAATGGTGAATGACATTTCATCTGTGTAAT
 TGCCAAATATATATCAGACAAGCAGTGACATATAGTGTTCATGTTGTTCAAATACATTGTGCAA
 GATATTGTGATTGACAAGTATGTGATAGTGTGCTAGACAGCTGATTGTTACTGTGATCGTTTATTTA
 GAAACACGTTGAGTTCTCGGAAAGATTGCAAAACGATATTCTCGAACAGCAAAGTTCTAGAAA
 ATTTGAACATGGTGTGTATATAATTATCCTGAAATATTTTAAATGATCTGGAAATAGGAGATTCAA
 GTATTATCACCAGAAATGAGGTCAATTGTGACAGCATCTTATCTATGATTGGTTTGGTGTGTGATC
 ATGAGGCAAGAAGACGATCAGTACTTGATAAGGGGAAAAGACAGGCTCAGGCTAACAGAAAAATCT
 TCGCCCTTGCCATTTTTACAACCAAATCCTAAGGATGATTCAAGACAATTACCAGACATCACCTA
 ATGGAACACTACTATTACTACATTAAGTCCCAACTGATCAAGCTATGAATCAAGCAAACTGAAATCTT
 TTGATTCCAGCAAAACCACTTGAATAAAATGGTATTCCTTACCTATGCTTGAAGCTACTGGTTCAA
 CAAGAGAAGTTTATGATTCTTTACCTCGCAATCTTTACCATCACAAGCACAACCTCTTCAGCAGT
 ATCCAATGCAGCAAGATCAACAACAGCAAGAACCATCACAACAACAACAAGACACCTGCGAGC
 AACTGCAGCAATACCAACAACAGCAGCAATCGAATCAACAGCAACCACTCTTCAACATCAAGAC
 AGTTTCAACAATCACCACCAACCGCAATTTCAATGATTCTTCAACGCGCCGCTTTCAGCAACCAC
 CTTTATTATTGGCAAACTACCCGTACCACAACTTATTTCGCAAAAGATTGATGAAATGAATATGT
 CACCAGAAGTAAACAAGAAACCTCTGTTCTCCATTTGCAATCTCAAACTACCAAACTTTTGTGATC
 AACAAACAAGTGGATGGTTTAATAATGATAACCAAGATGACGACTTTTGGGTGGTTGATGTGA
 ATATGATGCAAGAGAAATAA

YBL066C_homolog 917aa (SEQ ID NO 290)

MKFEKGKVRILPKPSPTTNPQTPLPLPAQTTPVNSKRKSAASTPGNESKSRKSNSTASTPNSA
 TPTSVGTPPQKTSKPTGHRPVTSTCTCRQHKIKCNASDNYPNPCRCKMKGLKCEIDPEFRPRKGS
 QIQSLKSDVDLAKIEMLTKNESLITQALNQHNLNHASQQQSSGSGSQSQQHPPNFORALSYTSA
 NSSPQVAFSNASPIPSVTSTIQONAPLTHENSNDSPYALNTPENIEELQPISEFILGVDVTLPLNRA
 ELHDKFMTHTLPLPFIISRSATELYHKSQLLFWAVILTASLSEPEPKLYMSLASLIKQIAETCW
 IKTPRSTHVIQALILSIWPLPNEKVLDDCSYRFVGLAKNLSLQGLHHRGGEFIOEFSRNQVSLGP
 DAERWRTRSWLAVFFCEQFWSSLLGLPPSINTDYLLLENARVDKSLPKNFCLISLSIFQCKLVNI
 MGISVTRPDGLLEPSNRAGSLSLLDRELERLRFKLQFEEGGPIEVYLYIKLIMCCFAIPGPTIE
 DQVKYVSFAYL SATRIVTIVSKMVDISLIELPIYIRQAVTVSVFMLFKLHLSRYLIDKYVDSARQ
 SIVTVHRLFRNTLSSWKDLQNDISRTAKVLENLNMVLYNYPEIFLNDSENESSIIITRMRSHLTAS
 LFYDLVWCHEARRRSVLDDKGRQAQENKKILPLPFYNIQTKDDFTTTTSPNGTITTLTVPTDQ
 AMNQAKSKSFDDSSKPLEINGIPLPML EATGSTRVILDSLPSQSLPSQAFTLQQVYMQDQQQQEPS
 QQQQKHQSQQSQYQQQQQSNQQQPHLQHQRFQQSPFPQFSMISTTTPLPQPPFFILANSFLPQTY
 LPKIDENMNSPEVKQENSVAFFASQITNFFDQQTSGWFNNDNQDDFLGWFDVNMMEK

YBL078C_homolog 908bp public: 1..908; exon 1: 417..449, intron 1:
 450..533, exon 2: 534..908 (SEQ ID NO 291)

TTATTATTACTATGACACACACTTACTCTCTCTATGTCTCCGCTTACATCACACGATACACGTTT
 GAAACACACCCACCCCTTTTCTTATCTACAAAAAAAATAACAAACTACTATACTACTAAAC
 CTTTTTTTTTTATTATTATTATTGTGATTTTGTATATTATTAACAACTATTATCATCTATATATA
 TACATCCCCATCGATTTCATCGACATAAAGTATGTATGATCATACAGAGGAAAAATACCCCTTTT
 TATTATTACCAAGGTCTCAATGATTAGTGTGGCTAGCGTCTGTTACTACTTACCCCGTGTGTAG
 ATAATTGCCACTCAATCTTAAATTGACCATCGACCACAAAAATAATATGGAAATAATACTAACAGA
 ACTTAGAAACATCACTCATATGAGATGACACAATTCAAAGACGAGCATCTTTTGGTATGTATTACA
 TGATTTTTAGTCTCTGAAATCTTCTCCGATCATCATATACATCAACTTTTCGTGGGTGTTATTCTT
 TAAATAGAAAAGAGACAGCCGAGGACGCCAGAATTGCTCAGAGGTCAAGGATAGAGTACCGATCA
 TCTGTGAAAAGTTGAGAAATTCGATATCCCGGAAATTGATAAACGTAAATATTTAGTGGCAGTGG
 ATTTGACTGTTGGTCAATTGTGTTACGTTATTGAAAAAGATCAAGTTACCAAGCGAAAAAGCCA
 TTTTCATCTTTGTCAATGACATATTACCCCAACCGCTGCATTAAATCAGTACAATCTACGAAGAAC

FIG. 2 - 3

ACAAGGACGAAGATGGTTTCTTATACGTTTATACCTCTGGAGAGAATACTTTTGGCGAGAAACTAG
CAATTGACATTTTCATCATTAGATTTCAGTGATATCCCTGATTATGTTTAA

YBL078C_homolog 135aa (SEQ ID NO 292)

MRSQFDEHPFKRQAEARIAQRFKDRVPIKEKVENSDIPEIDKRKYLVPVDLTGVQFVYVIRK
RIKLPSKEAIFIVNDILPTAALISTIVEEHKDEDFLYLVYSGENTFGEKLAIIDISLDFSDIP
DYV

YBR073W_homolog 2891bp PathoSeq: 1..2891; CDS: 501..2888 (SEQ ID NO 293)

GTGGGCACATCCCAGGAAGTAGAGCATGGACAGTTCGTATGTTGTTATGCTGTGCATACGATACAAAAA
AAACAGAGAAACGAGAAAAAATCGATCGTCAACCTTTATCAACTCATCTACAGCAGCAGCAAGTT
CGTCCCTAAATATGAGTCAAGTCCAACAGAAACCCAAATCGTTTGGTAGATTGTATACCATGTACT
ACTTTTCATTTTCCATTGTGTATGCTTACGACAACGTGAACCATGCTACTTCATACGTTTGTATGA
TGTTTGCCTTATGTTTGCCTATGGGATCTACGCTTATTTGCCTTCAAGTATCATGTTTGCATCT
CCAGAGCATACTATTATGTTTGGCATGGATATTAGTACCATCAACGGTTATGCAAGAGTAGCGCT
GTCTACTTAGTTTATAGTTTAAAAATTTGTTAATATAAACCCAAAGTTTCTAACAGGGCTCTGTTT
GCTCGCATAAAAAAGAAATTTTGTCAAACGCGTATCAGAATGTTTACCTTTTTTTTTTTACACAG
ATCAAAATGAAATGTTTCGACCTAATGCTCCGTTTTCGGCTCTTAGACCAATAAAGGGGGGTGTTCGG
TGGTGCAGAAAGTAGTAAACGAAAAATTGCCCACTACCACCAATCCTTAAACCTGCAAAAGATTGTA
CTACCGATCCCAGCTCAACAAAAATACGTGATCCAATGGAGAAAGAAAACTTCAAAGAAAGAACAAAA
CATGGGACGGGTATGGGTATGCGGTGATTAAACAGCTTGAGAAATGGGCGATGCGAGATATCTATCA
AGAACTCTGATGGCAAAACCTATGGGAAAAAGAGTGTCTTACGTGCACACCTAACCTTGACGACGTGA
TTAGTGTGGGACCTATGAATAGAAATAGACGAAAAAGTAGGGTCTAATCACTCACTCCCCAGACAG
TGACACGTGTACCCACCAAGTTCAAAGAGGTGCTCCTCCACAGCTAGTAGTGCAGAAACCGCTTT
ATGACGACTGTGCGCATGCCATCGCTGTGCTCCTCCAAAAGCCAAAGATTATGTCAAAGTAA
ATATCGATCCACATTTGGCAAAAGTGCTTCGTCCGCTACAGGTTGAAGGTGTGAAGTTTATGTATG
AGTGTTTAATGGGGTACCGTGGGTGTGGCGGGCAGCGGTGTTTGTAGCAGATGAAATGGGGTTGG
GGAAAAACGTGTATGACAATCACTACAATCTGGACGTTGCTCAAACAAAACCGCTTTATGGAAAAAG
GTGCAATGGTAAATAAGGTATTGGTGGTGTGTCCTGTACGCTTATTTCCAATTTGGAGACAGGAGT
TTAGGAAATGGTTAGGTGCTAATAAGCTAAACGTTGTGACGCTCAACAAACCAATGTCAAACGAGA
AACAGGATATACTCAATTTTGGAAAGTTGAAATGTGTACCAAGTGTAGTGGTGAATATGAAAAAC
TTGTGGCACATTTTGTATGAATCTCAGCGGTCAAGTTTGAATTTGTTAGTGTGTGACGAGGGCCATC
GTTTGAAGAAATAGTGCATAATAAGTATTGAAATAATCTTATCAAGCTCAATATTCGAAAGAAAAATTG
TTTTGACGGGTACGCGGATCAAACAGAGTTGGTAGAGTTTCAACAGTTGATCTCGTTTCTCAACC
CGGGTCTGCTTCCGAGCTAAAAATTTGTTTCAAGGAACTTTATAACACCTATATCTAGGGCGGAG
ATATCAACTGTTTTCACCTGAAGTGAAGAAACGCGGTGAAGAGATATCGCAGCATGTGATTGAAT
TGACTCAGATTTTATCTTAGACGTACACAAGCATTTTGGCTAATTAATCTGACACAGAAAACTG
ACATTTTGTGTTTGTTCACCTACATCTGTTCAGCTCAAGTTGTTTCGACTATATAACCAACTTGA
AGAAATTTAATCAGTTTGAAGCAATTTACCATGATCAATTTGTTTAAAAAGATTTCGAATTCCTCT
CGTTTGTGGCGGACGACGAGTTTATTTAAAAAGATTGTTGAAGAAAGTTTAAATTTGGGATTTGGCAT
CGGTAAATAAATCAATCTTGTGGCGCTGCTATTTGGAATTTGCTTGTGGGAAAAAGATTGTCT
TAATTTCCAATACACCAAGACTTTTGGACTTGTGGAACAGGTTTTCGCAAGGTCAGCCTTAACAT
TTTTCGAGATTAGTGGGTGCAGCCCCAACATGTGCTGATGCAAGTTGGTTAATCAGTTTAACACGA
ACCCGACATAAACGTAATTTTATGTGCTGAAATCTGGCGGATGGGATCAACTTGGTCCGGG
CTTCGAGGTGATTTTGTGTGACAAATGACTGGAACCCAGCGACCGATTGTGCAATCGATGTCCGGA
TTACAGAGACGACGAATTTGAAACCGGTGTTTCATTTATAGGCTATTCCACCGGGGTGATTGAGC
AGAAAAATCTTTCAGCAGCAGCTCTGTGAAGAACAAATTTGAGTTTCCAAGTTTGGGCAATGACGCCA
CGTCCAAATCTGATGTGTTTGAACATGATGATTGGAAGAAATTTTGAATAGATACATCGATTGAAGACAA
TATCCAATATCTATGATTTATAGAGTGTGTGTGAGGGCGCAGGGTGCATGTTGAGTTCAGCCAA
CCATAGGAAAGCGAACACCCCCAAAAACAAGCATGGGTACTGCACTTAGAGCTTAAGAAGAGAA
TTGACGATTTGTGAGGCGCTTAAAGAGGACGGCTGTAAATTTGGCTTGAACAGTTATCGACACTACA
ATCCAGAGGTGAACCGTAATTTGGATTGATTGATCTGACCGGATACCCGAATTCGAATTCAGGCT
ATGAAAAATGAACAAATTTGCAATTTACATTTTATATGCTGAGAGTAACATTAATTA

FIG. 2 - 4

YBR073W_homolog 796aa (SEQ ID NO 294)
MFTLFFFTTDMQNVNRPAPFRPRPKGGVAVVQKVVRKRLPTTNNPKPAKILTTDPGSKYVIQW
RKTKSKNKNTWDGDGYAVIKQLENGACEISIKNSDGKPMGRVFTATPNLDDVISVGPYELELDEK
VGSNSTPQTVTRVTHQPKVAPPTASSRKPLDYDCADAIALPPPPKADVYKVNIDPHLAKVLRFH
QVEGVKFMVECLMGYRGFGGHCGLLADENGLKTLMTITITWTLKQNPMEKGAIVNPLVVCPV
TLISNWRQEFPRKWLGAANKLNLVTLNPNMSNEQDILLNFGKLVVYQVLVNVNRYKLVHAFDEL SAVKF
DLLVCDGEHRLKNSANKVLNKLNI PKKIVLTGTPTIQNELVEFHLLISFLNPGVLPELKLFORN
FITPTSRARDINCDFPEVKRGEETISQQLIELTQSFILRRTPAILANYLTKQTDILLFVPTSLQL
KLFDYITNLKRFNQFEAFTINLNFKKICNSPSLLADDEL PKKIVVEEFNLMGASGKINILVPLLLE
IASLGEKIVLISNYTKTLDLLEQVLRKVSILTF SRLDGSTPNNVRSKLVNQFNTPNPDINVFLLSKS
GGMGINLVGASRLILFPNDWNPATDLQSMRSIHRDQGLKPCFIYRLFTTGCIDKEIQRQLVKNKL
SSKFLDNDATSKSDVFDNDLKNIFEIDTSTISNTHDLLECVCBGDSMLSQPTIEESEPPPKQAW
VTALCLKKKIDDGALKRTAVKALNDYRHYNPEVNRNLDPSALHRIANNSSYENKQLPTTFIMS
RVTN

YBR086C_homolog 2643bp PathoSeq: 1..2643; CDS: 501..>2643 (SEQ ID NO 295)
AAAGAATTTCAAATTTAGTATTTAGGTGATAAATTATCGTTGCTCCTTTCTCAACCTACCAATTTTGA
CITTTGTGTACTATACAGATGGTGTGTATTAGTTAAAGTTGCTTTGCTTTGCTTTTCAAATTTCAAAT
TCACAATTTGAATTTACGAATAGAAATAGTTTTCACCTTTTCTTCAAACTCGCGTAAGATTTTTTTTCA
TTCTTCTCAATTTAGTATTTACGAATAGAAAGAATAGTTTTCCTTGTGTGCTCATATTTACAATCAAT
TGGTATTGGTGTATTATATTTTTTTTGGTTCCICCTTTTACCCTCCCTTCGCTGTATAGATTA
TGTTTGTGAAATAAATTTATTACTTATCAATATATTTTTTCTTCCTTCTCCTTCAACTCTCTTC
TTTATACATTTCAATCAACCTTCCAACAATCCTATAAATTACTTACTTACCTCTCTCAATTTGGATTA
ATTGGATTGAATTTGTACAATTTGAATACTTCAACGAGATGACTTTACCAATTCAGGATTTAGAAC
CTGATTATTTATATTTCCGTCAATTTATCTTACCACCGATATAGGATACCAACCCCAAGCTGAAA
AATCATTGAAAAACATTAATTGATTATTATACGATAAAGGGTTTCCGCGCCAAATTAGACCTGGTG
ATTTAGACCATTTGTTAGTCTTTGTTAAATGTCTTCAACAAGTTTCTGGAAGAAGCTGAAAAAG
ATTTAAATTAATAAATTTATGAATTTGGGTGTACCGGGTAAAGATGACGTGTTAGCTTCTAAAATTAGAA
TTATTTATCAATACTTAACTTATCCACAATCAGTTGGTGGATGTGGATTACTCTCAATTTCTGGGG
ATTGGAATTTGTACACAGTATTGTCCAATTAATGACCTTTAATGAAACCACTTTAGTTGAAG
ATTTAAAAATTAATGTTACTACCAACCAATTTATCAATTGCCACTATCAAAAAGACATATTGGAGTTG
AAGTTGCTCTTTATTTTGAATATATAAAACATTACACTTTTGGTTATTTATGCTTTCTATTATTG
GTCTTGATCTCATTTTGAAGAAAGATAACGATTCCTGTTTAACTTTTGGCTTTATCAATTTGCTTT
GGGGGGTTTTTATTCCTTGCAATCATGGCATAGAGAAGAGAACAACTTTGGTTAATGTATGGGGTGTTC
AAAAATAGTCATTTAATGAAGAACAATAATCCGAATTTGGCTTAAAGTCAATGAAAGATATGAAGAAA
AATCAACTTATTTCCATGCAAAATAATACCAATGGATTGAGATTTTAAAAACAATTTGGCATTTTATCC
CCATTTGCCCTTGGTGTGTTGTTGGTGTGTTGATTAGTTATCAATTTGAGTTGTTTCCAGTTGAAATCT
TTTTAACCGATATTTATGAGTGGGCCCGGGAATCTTTATGACTTTATTACCAACCGTTTAAATCA
GTTGATTGTTGCCAATTTTGACCATTTGTTTATAATGCTGTGACCGGATTTATTGTTAAATGGGAAA
ATCATGATAACCAATATAGCAAAAAATAATTTCTATTCTGTTAAAAACCTTTTGTGTGAAATTTCTTGA
CTGGTTATGTTTCCATTAATCATCACTTCAATTCATATATTTTACCAATTTGCTCAITTTGGTGCAACCTC
ATTTAGGTGATATTAAAAACCACTATTGCCACATATGCTGGTGAAGAAATAGATTCTACACCAAACTCT
TGTTGAAATTTAAAGAGTCAAGAGAATTTAAAAATCAATCAAGGTAGATTAGATGCTCAATTCCTTT
ATTTCAATTTGTCACAAATCAAGTTTATACATTTGGTATTGAAATATATTTCTCCCAATTTGGGTTTAAAGT
TGATATTTTAAATTTTATGAAACGAAAAATTCAGAAGAAACCTCAATTTACAACTTAAAGATGATAACC
CTGATGAATCTATTGTTGATACATAATGTGAGATTATCGTTGAAACTTCTCGAATATAATGTTGATG
ATGATTATAGAGGATTTAGTTTACAATTTGGATATTTTGATAATGTTTGGTGGCTTTTGCCCAATGG
CACCATTGGTTTGTATTATTTTCAATTTAAATTTTTTCAAGTTGGATAATTTTAAATTTATGCAATG
GTAAATATTTTCAAAACCAAGTTTCCAAGAAGAGTTGATTCTATTCAATCCATGGAATTTAGCCCTTT
TCTTGTAGCATGGAATTTGGAATCAATTTATTTCCCCCGTGGTCAAGGCAATTTACCGTCATGATCTG
CTCCACCAAAATCTATGGGTCATTTTGCCTTGATATAAGAGTGTGTCATGTTTCACTCTCACTGATTT
TCTTGGTTTATTAATGTTTGTGTTTCAAGACATGGAATTTTGTATTGAGTTATCTTTTATTTGAAT
TCTCTTCTTGTTCAGAGTCAAGTTGAAATGGGAAAAATGATTTGTTGATAATGATATTAAATGA

FIG. 2 - 5

GACATGATTATTATCTCGGAAAGTAAACCAACTTATAAAGTCCACTCGGATGAGTTGTGGGAGA
AGTTTACCCCAACATCAACTTTGAATTTCTACTGGTCTTAAACCAACCGCAGAACTGATGATAAAG
TTGAAAAAATGCTTCTACCGAAGATGCTTATCTGACTCTCGAGAAAACTTACTACTACTGCTA
CTT

YBR086C_homolog 714aa (SEQ ID NO 296)

MTLPIDQLEPDYYISVNYPTTNDGSPTPQAEKSLKLTIDLLYDKGFAAQIRPGDLLHLVLFVKLSS
YKFSEAEKDLKINYEFGVTGKDDVLASKRIIYQVLYTPQSVGGCGITPNSGDWKFVTSIVPTIN
AFNETTLVEDLKINVTQPNLSIATIKKTYGVEVALYFEYIKHYTFWLLLSIIIGLVSHFRKDKRFS
LTFAPINLLWGLVFLASVHRRHQHLVNVWGVQNSHLIEHNSLAKVNERYEEKSYTFHANNYTG
RFLKQLAFIPIALVFGVGLISYQLSCFICFIPTLDIYDGPGRKSLTLLPTVLISVFPVLLITIVNA
VTDIIKWNHNDQYSKNNSILVKTFLVNLFTGYVPLIITFSIYLPFAHLVQPHLGDIKTTIATYA
GENRFFYTKYLLKLSQEEFKINQGRDLAQFFYFIVTNQVILQVLVKYLLPLGRFVFNFTIKIQKK
PQLQTKDDNPDESILHNVRLSLKLPYENVDDDFRGLVLQFGYLIMEFGPVWPLAPLVCIIFNLIFF
KLDNFKLLNGKYFKPVPVRRVDSIHPWNALFLAWIGSIIISPVVTAIFYRHGTAPPKSMGQFALDK
ASVHVSSSVFLVLLMFVSEHGFLLSYLLFEFSSLFKQVWENDFVDNDIKLRHDYYSGKVKPTY
KVHSDLEWEKFTPQSTLNFTEGPKPTAETDDKVEKIASTEDAYSTSAEKSTTTAT

YBR093C_homolog_1 1784bp public: 1..607, PathoSeq: 608..1784; CDS:
399..1781 (SEQ ID NO 297)

CGGTAAATATGTGCACAAAAACAAACAATCAACATATTAATCGTTATCCCAACTTTGTGAGTTT
CTAACACCTTTATTTGTGTTATACAAAATGCAACAATTAATTAACCTTTTGTGAAACCGT
GGGCTCTGTTTAGTTTAACTTCTGTAGTTTATTAATCCGATTGGGTTAGCTCAATAACTGCATTT
TCGTACAATAATAGTTTAACTCAATTTCAAAATCCGATTGAACCGAACACACAAAAAATCCAGTTCT
GGAGAGATTTTCAAAACTTCTATTATAAATAGAACCCTATAAGTCCATAATAATTTCAATGGAAGG
ATTATTTTCTTTTCCCTTTTCTGATTACTTCCCAATTTTCTTCTCTCCAAAAAACCCTTCT
TCATGGTTCTGTTTCTAAATTAATCAATAACGGGTGTTTATTAATAGTCAAAGTGTTTCCCAAG
ATGTTGCTACTCCGCAACAAGCTTCTGTGCAACAATACAATATACTCAATTTTCTTGGCGGTAGTG
CCCCCTATATTCAGAAACCGGATATGGGATTTCTACTGATATCCCTGCTGGTGTGAAATTTGCTC
AAATTCAAATGTATTCAAGACATGGTGAAAGATACCCAGTAAAGTAATGGTAAAAGTTTAGAAG
CAATTTATGCTAAATTTGAAAACACAAAGGTACTTTTAAAGGTGATTGTGATCTTAAATGATT
ACACTTATTTGTCAAAGACCAGAGTAACTATGCTAAGGAAACTAGCCCAAAAAATTCGAAGGAA
CCATATGCCGGTACAACCAATGCCCTTGCGTCATGGTGCTGCGTTTAGAGCCAAATATGGATCCTTAT
ACAAGGAAAACTCAACTTTACCAATCTTCACATCCAATTTCAACAGAGTACATGAAACTTCAAAGT
ATTTGCTAGAGGGTTTGTAGTGATGATTATGAAGAAAGTAAACCTGTCAAGTTTAAACATCATCT
CTGAAGATGCTGATCTTGGTGCCAAATAGTTTGACTCTTAGAAGTGCAATTTCCAAGAACAAAGAAC
TGAGCAGATGATCTGCAAAAAAATAACACAACATATTTAAATGCTATTGCTGAAAGATTAGTATG
AACCAAACCCAGGTTTGAATTTGACTACAAGTATGTCAACAATTTATTCAGTTGGTGCTTATG
AAATCAACGTCAGAGGAATTCACCATTTCTGTGATTATTCACCAATGAAGAACTTAAATGAAGACT
CTTATGTTAAGCATCTTTCCAAATAATTTATTCATGGTGCTGTAATAATACACCAACATCTG
GTTCAAGTATTTTGAATTCATCCTTTGGAACCTTTTAGAAGCACTAAGAACCTTAACTCAAGTATG
TATCATTTGCTCATGATATGATTTGAAATTTTCCATTTGCTTGTAGGATTTTGAAGAACAGCTG
AAGATTACCAACATCTTACATCCCATTCCTTAACCCATACGTCATCTTCTATTGTTCCACAAG
GTGCCAGAAATACACAGAAAACTTCAATGTGGAACGATGCTTATGTTAGATACATATCAACG
ATGCTGTCGTCGCAATTTCAAAATGTGCTACTGGTCCAGGGTTCTCTTGTAAACTGTAGTATTTG
AAAATTTTCGTTAAAGAAAGAAATGGAGATGTTGACTTTGTTAAACAAATGTGGTGTCAATAGTACCT
ACCATCTGAGCTTACTTCTACTGGGATTATAAAATGTCACTTACAGTGCTCCTTTAGAAATGTT
AA

YBR093C_homolog_1 461aa (SEQ ID NO 298)

MVSVSKLINNGLLLTSQSVQDVA TPQQAQSVQYINILFLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHGERYPKSNKSLKLEAIYAKFENYKGTGKGLSFLNDKYTFYVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAAPRAKYSLYKENSTLPIFTSNRNVRHETSNDYFARGFLGDYDEEGKTVKFNILS

FIG. 2 - 6

EDADLGANSLTPRSACSKNKESSSSTAKKYNTTYLNAIAERLVKPNPGLNLTTSDVNNLFSWCAYE
 INVRRSSPCLDLFTNEEFIKNSYGNLDSKYYSNAGANNYTRIIGSVLNSLELLKDTKNSNQVWL
 SFAHDTDLIEI FHSALGLLEPAEDLPTSYIPFPNPVHSSI VPOGARLYTEKLQCGNDYAVVRYI IND
 AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFVKQCGVNSTYPSSELTYFYWDYKNVYSAPLEL

YBR093C_homolog_2 1871bp public: 1..1752, PathoSeq: 1753..1871;
 CDS: 501..1868 (SEQ ID NO 299)
 GAGTTTATGGGATTGGGTTTTCATTAAGACTCTTCGTGATAATGCAATACCAAAACCAAAAT
 TTATTTAACGATGCAATTAATTTATTCATATGTGAGCTATCCATGAATCAGTGAGAAATCTTTATTATG
 GAAGAAATTTGGTCAAAATTTGACAAATGTTTAGTAACCTTATATCTTGGTGTGGGATGGTGCCACA
 AATGGAGATTTGTGAGTGATCATGAAAAATACGTAGTTAAATTTTGTCTCTGTTTTTATTATTATTTA
 GCCACTTTTTTATCCGATTCTTCATATCTTACCTTTGGTAAAGTGATAAGATTAAATCATATTAGTA
 AAAACCCCCCAATGATGAATGTTTGTATTTATAGCCAGACTATAAAAATTTACGGGGATTTAATTCG
 CGACTCACCCAGCTTCTCACACAGTATGTGCTTTTTTCATAAGTATGATTTGAAACCCCTAAAAATATC
 AACTTTCATAATAAACATAATTTCTTCCAGACAACTAAATGGTTGGTTTATCACGAGTACTTAATG
 CTGGGTTTATTCTAAGTGGCAATCTGTTTTCAGAGATGTTGTGTCGCCACATCAAGCATCAATTTATG
 AACATATAAATTTGTCAAGTACCTTGGTGGCAGCGGTCATATATTCAAAATTCAGGGTATGGGA
 TTCTTACTGATATACCGAAAAATGCATATTGAACAAAGTTCAAATGATTAGTAGACATGGTGAGC
 GATTTCCTAGTAAAGGAGATGGGAAATACTTTAATTCAGTATGGAAGTTTCAAGAGATATGGTG
 AATTTCATGGAGATTATCTTTTTTAAATGACTATGAGTATTTTCGTACTAATCCAGATATTATATG
 AAAAGGAGACTACTCTTAAAACTCAAAGGTCCATATTTTGAACACTACAAATTTATTACGACATG
 GAGCTTATTTTAGAAAAGATATCAATCACTATTTGACCAAAAGGAGAAAGCTTGTGTGTTTACTA
 GTAATTTCTGGAAGGTGTATTATCAAAGTGGTGTCTATTTTCGCTCGAGGATTTTATGAGATGATTACT
 CAGAAGATACAGTTGAATTTGTGTGTGTGATGAAGCAAAAAATGGGTGGTAATTCATGTACAC
 CAAGATACGCTTGTAAAACCTTGAATCAAGATTTACACAAAGATTTCGTGATACAGTACGATAAGA
 CTTATTTCGACGATATTTATCTAGATGCGTGTAGACAAATCCCTGGATTAGATTTAAGTGCAGATC
 AGGTCTCGCTATTTCTTTGGTGTGCTTTTGAATTAACGTTAGGGGGTATTCTCCATCTTCGCA
 ATCTATTACAAAAGATGAATTTATCAGAAGTGGGTACCGAAACGATGTTGGTAATTACTATCAAA
 CTGGTCCAGGTAATAATGACAAAGGTAATGGCTCACCTATGTTGGAAGCGCTCGTTGAAATATG
 TTCAAGAAGATTCAAAAATTTGCTTGACATTTACCACATGATACGTATTAGATGATTTTGACAT
 CTTTGGGATTGATTTCTCCACAGGGGATTTCGCCGTGATCGAGTACCATTCCCAATCCATATA
 ATGCAGCAGAAATTTTCCCTCAAGGTGCTAGAACTTACACTGAAAAATTTGAAATGTGGTGAAAAAGC
 AATATGTTAGATTTTATGTGAATGATGCAGTTTATCCATATCCGGATTGTAGTGGAGGTCCTGGGT
 TTACTTGTGAATTTAGTGAATGATTTTATCAAAATAGTTTAAAAGTCGTTTACATGATGTGACTATAAGC
 TTCAATGTGAAGTGGACGGACCGGAATTGACATTTTATTTGGGATTATAAAGACAGAAAGTATA
 ATGCGCGCTTAATAGATCAGTAA

YBR093C_homolog_2 456aa (SEQ ID NO 300)
 MVGLSRVLNAGFILSGQSVFQDVAAAPHQASIEQYNIVKYLGGSGPYIYNSGYISTDIPEKCTIEQ
 VQMISRHGERFP SKGDKGYFNSVMEVF KRYGEFHGDL SFLNDYEFVTN PDYIEKETETPFKNSKGPY
 FGTTNLLRHGAYFRKRYQSLFDQKEKLVVFTSNSGRCYQSGVYFARGLGDDYSEDTVEFVVVD
 KRMGNSLTTRYACKTLNQLDKDLVNQYDKTYLDDILSRVLVDNPLGLDLSADQVSSLFWCAFEI
 NVRGYSPFCNLFTKDEFIRSGYRNDVGNYYQTGPGNNMTKIVIGSPMVEASLKMQLQEDSKIWLTFTH
 TDIEMLYTL SLGLVVPGLDLPVDRVFPNPNYNAEEFFPQARTYTEKLKCGEKQYRIVNDVAVYP
 YPDCSGGPGFTCELNDFIKVLKLSRLHDVDYKLQCEVDGPaelTYFYWDYKDRKNAPLIDQ

YBR093C_homolog_3 1888bp PathoSeq: 1..1656, public: 1657..1888;
 CDS: 500..1885 (SEQ ID NO 301)
 TGTAGTATAAATAAGGGTATGAAATACCAACATCCAGAAATCAACGAGATAGAAGAGAGAGGTT
 TCAATATATATCTTGTGAATAAATACTTCGTCTAATTCATATACACATACAGCTGTACACGC
 TCAATCTCAGGTAAAGAAAGTTTATATTCCATCACTATATAACACAACTACGCTTTGCAAAAAA
 CATTTAAAACTAATCTGGTAATATGAAAATATACGCCCTCGTAGTTCTACGCACGTGGCATCTT
 TATCTATTATTCATCTATACCCCTAATTTATGAATTAGCTTAATAAGACAGCAGTCAAAATTAACCGG
 CTCAATTAATAGTACTTAATAATATGAAGCCGATCAATTAAACCGATCCTTTGAATAATTTGAAAT

FIG. 2 - 7

AAAAAAAGTAAATATAAATAGGTATGCATTTTCCCTACATTTATTTCCTTTCTATTTTAAATTG
 TTTTCTTAACACAGCAACCAACAATGAAATTCAAAAATGGTTTCTGTTTCTTAAATATTGGAACAA
 TGATGTGTTATTAGCTGGTCAAAGTGTCTTCCAAGATGTTGCTACTCCACAGCAAGCTTCTGTGCA
 ACAATATAACATCGTCAATTCCTTGGCGGTAGTGCCCTTATATTCAAGAAACGGATATGGGAT
 TTCTACTGATATCCCTGCTGGTGTGAAATTTGCTCAAATTCAAATGTGATTCAAGACATGGTGAAAG
 ATACCCCAAGTAAAGATATGGTAAAGTTTAGAAGCAATTTATGCTAAATTTGAAACACTACAAGG
 TACTTTTAAAGCTGATTTGGCTTTCTTAAATGATTATACTTATTGTTGTTACTGATTAACAAATTA
 CGAAAAGGAACTAGCCCCAAAAATTTCTGAAGGAACCTATGCCGGTACAACCAATGCCCTTCGCTCA
 CGGTGCTGCGTGTTAGAGCCAAATATGGATCCTTATACAGGAAAAATTAACATATTACAGTTTCTTC
 TTCCAAATTCAGGTAGATGTTCACAACTCTCAAGATATTTTGTCTAGAGGATTTTAGGTGTGACTT
 TAAAGAAGTAAAACTGTCAAGTTTAAACATCATTTCTCTGAAGATGCTGATGTTGGTGCCAAATGTTT
 GACTCCAAGAAGTGCATGTTCCAAGAACAAGAAACGGAGCAGTAGTACTGCCAAAAAATATAACAC
 AACATATTTAAATGCTATCAGTAAAGATTAGTTAAACCAACCCAGGTTTGAAATTTGACTACAAG
 TGATGTCAACAAATTTATTCAGTTGGTGTGCTTATGAAATCAACGTCAGAGGAAGTTCCACATTCG
 TGATTTATTCACCAATGAAGAGTTTATCAAAATATCTTATGGTAATGACCTTTCCAACATATTATC
 TAATGGTCTGGTAAACAAATACACCAGAATCATTTGGTTCAGTGATTTTAAATCTCTCTTTAGAACT
 TTTAAAGACGACTAAAACTCTAATCAAGTATGGTTATCATTTGCTCATGATGATGTTTAGAAAT
 TTTCCATTCGCTTTAGGATTTATGGAAACCAAGTGAAGATTACCAACATCTTACATCCCATCCCT
 TAACCCATACGTCCTATCTTCTATTTGTTCCAACAAGTGCCAGAATATACACAGAAAAATCTCAATG
 TGGAACACGATGCTTATGTTAGATACATTTATCAACGATGCTGTGTGCCAATTCCAAATGTGCTAC
 TGGTCCAGGGTTCTCTGTGTAACCTTGATGATTTTGAATATTCGTTAAAGAAAGAAATGGAAGATG
 TGACTTTGTTAAACAAATGGTGTCAATAGTACCTACCACTGAGCTTACTTTCTACTGGGATTA
 TAAAAATGTCATTTACAATGCTCCTTTAGGTGATTTTTAA

YBR093C_homolog_3 462aa (SEQ ID NO 302)

MVSVSKLLNGLLLAGOSVFDVATPQOASVOQYNI VNSLGGSPAPYIQRNGYGI STDIPAGCEIAQ
 IQLYSRHGERYPKSRNGKSL EAIYAKFENYKGTFGKDLAFLNDYTFVVDKNNYEKETS PKNSEGT
 YAGTITLRHGAAFRAKYGSLYKENS LTPVFSNSNGRCYTSRYFARGFLGDDFKEGKTGVFNIIIS
 EDADVAGANSLTPRSACKSKNKERSSTAKKYNTTYLNAITERLVKPNPGLNLTTSDVNNLFSWCAEY
 INVRGSSPFDLPTNEEFIKYSYGNL SNYYSNAGNNYTRIIGSVILNSLELLKDKTKNSNQWL
 SFAHDTDL EIRFHSALGLLEPAEDLPTSYI PFPNPVYHSSIVPQGARIYTEKIQCGNDAYVRYI LND
 AVVPIPKCATGPGFSCKLDDFENFVKERIGDVFVKQGVNSTYPSELTFYWDYKNVTYNALPLGDF

YBR093C_homolog_4 1886bp PathoSeq: 1..102/1038..1062/1078..1886,
 public: 103..1037/1063..1077; CDS: 501..1883 (SEQ ID NO 303)
 ACTACTTAAATTTGGCATATCCAAACAACTTGAAGTAGGAGTTTCTTATTTTATTTGTTGATTATA
 TATATTTGATTGCGGATTAATGTCATAAATTTTAGTTTCGGTAATATGCTCACAAAAACAACATCA
 ACATATTTAAATCGTTATCCCACTTTGTGTCAGTTTACTAAGACCTTTTATTTTGTGTTATACAAAT
 TGCACAATCAATTACTATAACTTTTTTTTGAACCGTGGGCTCTGTTTAGTTTAACTCTCTGTAGTT
 TTTATTTATCCGATTGGGTTAGCTCAATAACTGCTATTCGTACATAATGTTTAAATCAATCTCAAT
 TCCGATGAACCGAAGACACAAAAAACATCCAGTTCTGGAGAGATTTTCAAAGAACTCTTATTTATAAA
 TAGAACCCCTATAAGTCCATAATAATTCAAATGAAGGATTTATTTCTTTCCCTCTTTCTGATTACT
 TCCCAATTTTCTTCTCTCCAAAAAAAACACCTTCTTCATGTTTCTGTTTCTTAAATTAATCAATA
 ACGGGTGTGTTATTAAGTCTGCAAGGTGTTTCCAAGATGTGTGCTACTCCGCAACCAAGCTCTGTGCG
 AACATACAATATGACTCAATTTTCTTGGCGGTAGTGGCCCTTATATTCAAAGAAACGGATATGGGA
 TTTTCTACTGATATACTCCGTGCTGGTTGTGAAATTTGCTCAAATTCATTTGACTCAAGACATGTGTGAA
 GATTCCCAACAGCAAGATAGTGGGAAAGATTATGAGAAATTTATGCTTAAATTTAAACACTACATGAT
 GTACATTCAAAGGTGATTTGTCAATCTTAAATGATTACACTTATTTGTGCAAGACCAAGAGTAACCT
 ATGCTTAAGGAAACTTAGCCCCAAAAATTTCTGAAGGAACCTATGCCGCTACAACCAATGCCCTTGGCT
 ATGGTGTGCTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAACCTCAACTTTTCAACATCTTCA
 CATCCAAATTTTCAACAGATACATGAAACTTCAAAGTATTTGCTGAGAGGTTTATGATGATGATT
 ATGAAGAAGGTAAACCTGCAAGTTTAAACATCATCTCTGAAGATGCTGATCTTTGGTGCCAAATAGTT
 TGACTCTCTGAGAGTGCATGTTCCAAGAACAAAGAACTGAGCAGTAGTACTGCCAAAAAATATACAA
 CAACATATTTAAATGCTATTGCTGAAAGATTAGTTAAACCAAAACCCAGGTTTGAATTTGACTACAA

FIG. 2 - 8

GTGATGTCAACAATTATTTCAGTTGGTGTGCTTATGAAATCAACGTCAGAGGAAGTTCAACATTCT
 GTGATTTATTACCAATGAAGAATTCATTAAAGAACTCTTATGGTAATGATCTTTCCAAATATTATT
 CTAATGGTGTGTTAATAATTACACGAGAATCATTTGGTTCAGTGATTTTGAATTCATCCTTGGAAAC
 TTTTAAAGACACCGAGAACTCTAAATCAAGTATGGTTATCATTTTGCTCATGATCTGATTTAGAAA
 TTTTCCATTCTGCTTTAGGATTTATGGAACAGCTGAAGATTTACCAACATCTTACATCCCATCC
 CTAACCCATACGTCCATTCTTCTATTGTTCCACAAGGTGCCAGAATATACACAGAAAACTTCAAT
 GTGGAACGATGCTTATGTTAGATACATTTATCAACGATGCTGTCTGCCAATTTCCAAAATGTGCTA
 CTGGTCCAGGTTCTCTTTGTAACCTTGATGATTTTGAAAATTTCTGTTTAAAGAAAGAAATGGAAGTG
 TTGACTTTTATTAACAATGTGGTGTCAAATAGTACCTACCCATCTGAGCTTACTTTTCTACTGGGATT
 ATAAAAATGTCACTTACAATGCTCCCTTAGAATTGTAA

YBR093C_homolog_4 461aa (SEQ ID NO 304)
 MVSVSXLINNGLLITSQSVFQDVATPQQAQSVQYNNILNFLGGSAPYIQRNGYGIISTDIPAGCEIAQ
 IQLYSRHGERPFTASSGQVEKIYAKFKNVNGTFKGDLSFLNDVYTFVFKDQSNYAKETSPKMSIEGT
 YAGTTNALRHGAAPRAKYGSLYKENSTLPIFTSNRNVRHETSKYFARGFLGGDYEBGKTVKFNILS
 EDADLGANSLTPRSACKSKNESSSTAKKYNTTYLNATAERLVKPNPGLNLTTSVDNNVLSWCAYE
 INVRGSSPFDLFTNEEFIKNSYGNLDSKYYSNGAGNNYTRIIGSVILNLSLELLKDTENSNQVWL
 SFAHDTLHLEIFHSALGLLEPAEDLPTSYIPFPNPVHSSIVPQGARLYTEKLCQGNDAVYRYIIND
 AVVPIPKCATGPGFSCKLDGFENFVKERIGDVFIKQCVNSTYPSLELTFYWDYKNVYNAFLEL

YBR181C_YPL090C_homolog 1635bp public: 1..938, PathoSeq:
 939..1635; exon 1: 500..505, intron 1: 506..930, exon 2: 931..1632
 (SEQ ID NO 305)

ATATATATATATTTATGTATTTTATTTATGTTGTTTCAGGAATTTTAAACATGTTTCATGAATAATGA
 TAATCTATATGAACAAATTAAGAAGCTCTTTGGTTTCATTGTCACCAATGTCGCTGACTTAGGGCTA
 TAGCCCTACTTTTACTTGTACGATACTGCATATTTTGTGTTGTGCGAATAGTTAGCGTAAATAATC
 TTTTFTTTTGTGTGTGTCGGGTTTACTTACTCTTCTCTCTTCGCACATATTTTATTAGAGCTTAC
 AGTTGTTTGTATAGTGAGAGTTTCACTAACACAAAGCTTCAACAATACTAACAAATTTTCGCACGC
 TGTGGAAGGAGAACTTACACTGTACACTACACTACACTGTACACTATACACCACCAACAGAAAAA
 AAAAATATCAAAATTTTCAACCTTGAGAGAAAAAAAAGTGGAAAAAAACCTTCTTCTTACATTT
 AGTTAATTTTCAAGAGGCACAAAGGAATTAATCACCATGAAGGTATGTGATTGAATTAACCTT
 ATCAGTAGGATATAATTAGAGCTCTTTATTGGAATTTGCAATAATTTGGATTAATAAGAAAGAGCATA
 AGAGTAGGAGTTTAAACAGGATAATTGGATTAATAAGAGGAAAAAATTTTATCGTCTGTGATT
 TAACAAATCAAGAAATTAAGCAATCAAGTGATATAAGCAAAATGAAGGACTAGTTTATTAGCGGT
 GACATTTTACAGTCACTTAAAGTACTTTTCGATTCAAGGAAAAACCAATTTTAGTATCTTATCAACA
 AACTACAATCAATTTAGTTAACTTCAATAATGACCAATTTTAACTACTGAAAAACAAATAACAT
 GCAAAACAGCAAACTAGTCAAGCTTTACGAATCAGTCAATACTAACCAATCTTTTGTGTTTCA
 TTTTGTAGTTAAACATCTCATATCCAGCCAACGGTCAAAAAATCTATGGATATCGATGATGACACA
 AAATTACGTGTTTCTACGGAAGAAAGAAATGGGTCAAGAAAGTTGAAGGTGACTCAGTTGGAGATGAA
 TTCAAAGTTTACATCTTCAAAATCAGTGGTGGTAACGATAAACCAAGGTGTCCCAATGAACCAAGGT
 GTTATGACCCCAACAGAGTTAGATTATTATTATCTAAAGGCTACTCTGTGTTACAGACCAAGAAAGA
 ACTGTTGAAAGAAAGAAAGAAATCCGTTTAGAGGTGTGATTGTTGCTCAAGATTGTCAGTTTGGCT
 TTGCTPATGTGTTAAACAGGTGCAATGAAATGAAGAGTTAACTGACACCACTGTGTTCAAAAAAGA
 TTAGTTCAAAGAGAGCTAACCCATTAAGAAATCTTTGGTTTAACTAAAGAAAGATGATGTGATAGA
 GATTTCGTGTGTTAGAAGAGAGTTTACTAAAGGTGACAAAACTTACACCAAGGCTCAAGAGATTCAA
 AGATTAGTTACTCCACAACTCTTACAAAGAAAGAGAGCTTTGAAGAGCTAAAAAGCTCAAGAATGCT
 CAACACAAAGAGATGCTGCTGCTGAATACGCTCAATTTGTTGGCTAAGAGATTGCATGAAAGAAAA
 GAAGAAAGAGCTGAAATTAAGTAAAGAAAGAGAGCTGAATCTTAAAGAACTAA

YBR181C_YPL090C_homolog 236aa (SEQ ID NO 306)
 MKLINSYFANGTQKSMIDDDTKLRVSTEKRMGQVEGDSVGFDEFGYIKFTIGGNDKQGVPMKQG
 VMHPTVRVLLLSKSHCYRPRRTGERKRKSVRGCIYAQDLVSLVLSVYKQGDNEIEGLTDTTVPRK
 LGPKRANHIRKFFGLTKEDDVDFVVRREVTGKDKTYTKAPKIQRLVTPQTQLRKRALKAKVKNA
 QQQRDAAEYAQLLAKRLHERKEERAEIKKKRAESLN

FIG. 2 - 9

YCL016C_homolog 1520bp public: 1..1079/1081..1520, PathoSeq: 1080;
 CDS 501..1517 (SEQ ID NO 307)
 GTGACGAGAACTCTCTGCATCTCGAGTCTGCCAACTGCCTCTAACAGCAACAACAATAAGAAACAAT
 GATAACGGAGGAGGATATCCCATACAAACAGAAATAGTTGTGGTGTAGTTGTTGGGGTTGGTGGT
 TCTATATTAATTGGTTGTTGGCGGTTTATTTTACTTGAGAAAGAGAAACAACCGTGATATGAA
 GGTGGATGGACTTCTCGGAGAAAGAAATGAGAAATTTGGGAAGTGATGAGTTCTCAATGGTGAATTG
 GGTGTCAGAGACAGAAATATTAATCAAGGATCAAATTTTAAACAAGGCTATTTTGGATGAGGGT
 GGTTTTATTAAGTATTTTGTAGTTGAATTTAAATTTTGTACCTTAAAGTCTTTTAATTTAAT
 TTTAATAAAAAGTTGGTGATTTTGGCAAACCTTCAAGAGTATTTTGGTGAAAAAAAATAAATTTTG
 GAACGTAAACGGCTAAACATCTTTATACCTCTAAGCAAAATGTCAGAGTACTCTGTGTATCAACAGT
 TGAATGAAGATACAAACGCAACTAAATATACTTTATAAATTAACACAGCTACCATCAAGAGATACATA
 ATCAACTTGAATCCAAGTCAACTAACTTGTATATAAATCTGATATCAATCCCTAGCATTTATGCA
 CTGATTTCAGAACTTTCAAGTTACGACAAATGAACCAATCCAATACAGTCTTGCTATTGAACAAAG
 AACCTGACAAACAAGTTAATTTGGGTTTCAGAAAACCAAGTTATGAATATGAGTTGACAGAAATCAAG
 GTTCGATCGATACGTCGGATATCCCTATTTTCAACGGACAAACAGCACAGCAACCTATTGATTGTA
 TAGCATTTGGAAGATAATTTCGATTTGTTTCACATCAAGAGTTTATTCGAATTGGTATGAGTTGGGAG
 GTTGTGAAAATTGATAATGGAGCATATATAATGAGTGCAGATATTTATCTGAACATTTATATCTAT
 TAATCACCAAATTTGATGAGTTTCAAGATGCACGAGTTTCTCCGGAAGATGTTTCATCCATCATCA
 CGCCCTTTAATGACTCAATGGTAACATCAATCATACACAAATTTTGCATATAGAAAGTGAGA
 AATATCAATTTGAATGATTTAAAAATTACACAGTGGTTGGCAATTTGTGAGATGTCAGAAATCAATC
 ATAAAAATGGACCGATTTTTCAGAGTTCTTATTTGAATTTGGAAATAGTTTGGCGCTCATTTCTATAACC
 TCCATTTGGACATCAGTCAATTTGCGAGGCTATTTACTGCTCCCAATCGAAAAACAAAAATTTGTATG
 TCGACCCAGAAATCTTTATCAGAAAAATTGAGTCAACGATTTCAAGAAATTTGTTGAAATTTGGATAAAA
 GTTGGAACTATGATGAGTTTATTCATTTCAATAAAAAGTTTGTCTGCGGTAAGAAAGGTGCACT
 CAATTTATTTAAAGTATGGCAAGAAAGAAAGTTGGTAGAGATAGATTTATAGTCTGTCTCTAGAT
 AA

YCL016C_homolog 339aa (SEQ ID NO 308)
 MSEYSVYQQLNEDTNATKYTKYKLLQLPSKILNQLESKSTNLYIKSDINSLALCDSSETFKLRQMNH
 SNTVLLLNKEPDKNLKIGFKTSYEYELTEIKGSDTSDIPFNGQTAQQPIDLIALEDNDSICSHQE
 PLSNWYELGGCEIDNGKIVMSADIITELLYLLITKLMSLVQVHEFSPEDVSSIITPPYNDMSMVTSTII
 HKFCTIESEKYQLNDLKITQWFGIVEMSKINKHMTDISEFLLNWKTSLPSFYNPPLDISQLAGYYC
 SPIENKILYVDPESLSENLSQRKFELFDKSWNDEFIPFIKKFVPAGKKVDSIILKYGKKKKVG
 RDRFIVCPR

YCR073WA_homolog 710bp PathoSeq: 1..710; CDS: 315..707 (SEQ ID NO 309)
 GGTGGGGTTCCCATTTTAAATTTAAAAAATTTTTTACCATCCAAAGGATTTTATTTTCCCAAAGAC
 CAAAAAATTTATTTTGAATGGGGATTTAAATGGGGATATTTTATTTTGCTTGATGAAAGATTT
 AGTAAACCGTTTGAAGCTCTGATTCAAATTTAGGTCAAGCTAAAAGAGAAATATTTGATTATTA
 CTGGTGATAAAAAACCAAGAAATTTTCCATCTGTGATGAATCATTAATGATGATTTCTCAAGAGCTG
 CTGATGAATATGAAAAACAATGATTAATAATTTTGCTAAAAAAGATTCGGTGAACTTACCTTTAT
 TTGATTTATTTTATTTAGGTTGTGCACCGGATGGTCAATTTGCTCATTTTCTCAATGATGGTG
 AACATTTGAGAGAAAAATAGCTTTGGGTTTACCATGATCAAAATGCTCTCTGCGGACAGAAAAATA
 GAATAACTTTTATCTATCCCAAGTTATATGTCATTCGCAAGAGTGACATTTGTTGTAAGGGTTAA
 CTAAGGCACCAATTTATTAACCAATTTATGGAAGAGCAGAAAAAGGTTTACCAAGTTCAATTTGTTA
 ATGAAGGTGCTGCTGGTAGAGTGAGTTGGTTGTTGATGATGATGATGATGATGATGATTTGTTTGATA
 TAACTAAAAAGAAATACAAATATTTATCTTATACCTGAACCAAGTCATTAA

YCR073WA_homolog 131aa (SEQ ID NO 310)
 VKLPLFDLFLGCPDGHIALSLFNNHGQLEKRLKAWLPVSNAPSGPENRITLSIPVICHARSVTF
 VVEGLTKAPIIKITIMERPEKGLPSSIVNEGAAGRVSWFVDDDALNDLFDITKKYKYLSTPEPSH

FIG. 2 - 10

YDL010W_homolog 1190bp PathoSeq: 1..1190; CDS: 501..1187 (SEQ ID NO 311)
TGTTACAAACATCTCTGTTGGAGAGATAATTGAATTCAAATTAACGTGTTGAATCCAACATTGAA
CAATGAATACACGTCCTCAAGAAAAATTTGACATGATTAGAATTCGCGGTCAATTACATTTCCCGGAACG
TCTTTGGACTACTTGGATACAAACAATGGAATAATGAGGAAAAATGAGGAAAAACGAGGAAA
ACGAGGAAAAATTTTACCAGAGAGTAATTTATATTACAAGCATTTGAAGAGGAGCAAGTGAACGCCCC
AAACAGAAACAATACCGAACATCACAAAAAAGACAACAGCTAAAAATTTTTTGGTCAGAA
CAACACTTTGGAAGAAAGAAAAAACCGAAAAAGAAATTCATCTAAAAACATACACAATATAT
ATATATATATATAAATATATCCATATACATATGCTTTAAATTTAACTTCCCGCCCTTTCTTTCTTC
TTTTTGAATTATATCGATTTTAAAAACTACACTTCATCTGGCTGGAGTTAGACAATTAAAGAATAA
TAGCATTAACGGCCCTTTGTCTTGGTTTAAATTTTACTTTACATAAAGTTGGATCCAACGCTGCAT
CCTTTGGTTCATGCACAAGCATCAGACCAACCAACAAACATAACCAAAAGTACTACATATA
CCGCCACTAATGACGAATCAGTTGCCAATCTCATTTGATTTCAAAAATGATCCTCAAACTGATGACA
AAATAAATCAAAAAATATCACAAAGATCAAGATGAAGCCATCAATGGTAATAAAGACACTAATAAG
ACACCACCAAAAGTCAAACAGATAATGGTGAATATGATCCAATATCTGATTTGATAAAAATTAGAT
CATTTACCCAATGACAATTTTCAGTAAATCATATTTGTCATATTCAAAAAAGATTAAACAAATGT
TATTAGAAAAATATGATATAACACCAGCACCAAAATGTTGTTGAATTAGATCGATGAAATATGGAG
CTGAATTACAAAGTTATTTTACAGAGAAAGAGTGGGAGAGAAGTTCACCAAAAGTATGGTTGGT
AATCATTTGAAAGTAGGGGTGGTTGATGAATTTGAAAACTTCATAAAGATAATGATTGATTA
AATTGTTAGTTGAATGGGGTCTGGTCGTTTACAAGTTGCAAGAAGAATACCCCATCAATGCCT
AA

YDL010W_homolog 229aa (SEQ ID NO 312)
MAGVRLRIIALTAFVLGLFTLHKVGSNAASLVHAQASDQPNKHNKSTTYTATNDESVANLID
SKNFDPTDDKINQKISQDQDEAINGNKDKNKDTTKVDPNGEYDPISDLKIRSLSPMTIFSKSYC
PYSKKIKQLLEKYDITPAFNVVELDRYEAGELQSYLTEKSGRRTPVNVLVGKSFESRGGCDEFE
KLHKNDLKLLEWVGSGRLQVAKNTPSNA

YDL083C_YMR143W_homolog 1256bp PathoSeq: 1..1256; exon 1:
501..521, intron 1: 522..848, exon 2: 849..1253 (SEQ ID NO 313)
AGTGGTTGTTCAATAATGGTAAAGTTCTTGGAAATAGCCATTGTTGCTTCTGGTGGTTAGACTTGT
AGGAAGTAGAACTGTTTCCAATGAAAGTAGTTTAAATAGAAAAATTTTCAAAAGTGCCTGAAGC
CCAGTCTGAATGTGCGAGGAAGCCCAAGTCAGTTAGTAGTGTCTTCCCTCCACTGTCTGTAATACA
AAATTTCCCTTAGTGAATAATGCGAAATATATCTGTACTGGGAACCCCGGAAAAAAGAAACCTA
TGCTCAAAACTATATGTACTGTACACAATCTAGGGCTATAGCCCTAATATTTGACAGGAAGAACTT
TAACATTTGGTGCAGAGAGCGTTTCCAATTTTCTTTTTCAGGTGTAGTCTGTTCTATGGCAATAC
TGTTGTTAGTAGAGAGTGTCTCGCACTAACAGAACATTTTTCAGAACAGGAAAAATTTTGAAT
CTAACATCTTTTACTGAAAGCCCAAGCATCAACACAATTAATGTCAACCCAATCTGTTCAAGTATGTA
AACGAATTGAATAAAGAGATAGAGAGATGTTTATTAATCAAAATACGAAAGGAAAGGCAATTA
AAAGGAAATCAAAAGTCCCAACCTTGCAGTAGAAGAAATGAGGTATATGAAATTTGATAGATAGCC
AGAACGGTGTACATAAATGGGATATAGAACAAACTATACGAGGAGTTTGTTCACACGATCATTC
AATAACCCAGAAACGATAAATTTTAGCGACCATTAATGACACTTGAAGGCTACACTGGGCCAATA
GAATATCTCCATATACACTTTTGAACATTTTACTTAACAATTTACTTTTCTAGACTTTTGGTA
AAAAGAAAGACTGCCACTGCGGTGTGCTATGTTAAAGCCGGTAAAGTTTAAATTAATAATGACGGTT
CCCCATCACTTGGTCAACACGAAATCTTAAGTTTCAAGTTTACGAAACCATTCAGTTCTGGTTG
GTTTACATAAATTTCAAGGTATCGACATCAGAGTTAAAGTCACTGGTGGTGGTCACTGTTCTCAAG
TCTACGCCATCAGACAAGCTATGTCTAAAGGTTTGGTTGCTTACCACAAAAATACGTTTACGAGG
CTTCTAAGAACGAATTAAGAAAAATTTTCGCTTCTACGATAAGACCTTGTAGTTAGCTGACCTCAA
GAAGAAATGGAACCAAGAAATTCGGTGGTGGTGGCCAGAGCAAGATTCCAAAAATCTTACCGTT
AA

FIG. 2 - 11

YDL083C_YMR143W_homolog 142aa (SEQ ID NO 314)
 MSTQSVQTFGKKKTATAVAHVHVKAGKGLIKINGSFITLVQPELRFVKYVEPLTLVGLDKPQIGIDIRV
 KVTGGGHVSQVYAIRQAIAGLVAHQKYVDEASKNELKIFASYDKTLVLVADSRMRPEKPKFGGRG
 ARARFQKSYR

YDL125C_homolog 959bp public: 1..959; CDS: 501..956 (SEQ ID NO 315)
 GTGGTAAGATATAGAAAGCTTACCACCTTGACAAAGTTGAAATAGGATGGGTGAAAAATTGGACAT
 CTTGAACTACTTTAAAATTCTGAACTTGATCACCAGATCCTTTTCTTTTACATAATTAGATATGATGG
 ATAGGTTAGAAATCGTCTTTAAAGAGAAGGTATATATCTAACTGATTGGCGAGGTGTTGGAAGAAAG
 TCATCCCACTGTATATTTCTGGAGTTTACGTACTACAGTTCACTGGGGTGAATACCTAAATAG
 GGGGTAGAAATCGAACTCTCAAAATTTAAGGAGACTATGACCCGAAAGAGAAGAAAAATTTTA
 TTACTCTAAGAACTTTATATACCTCCAACTCACTTTTCTTTAGTTTCACTTCTGCTTTTCTTTT
 CTTACACATCTTAAGGTCAAACTTTAACTTATTAGCTTGGAATAATCTCACTTCAATTCAGGTT
 CTCCTTTCAATTGACATTATAGTATTTCCTCAATTCATTTATGGCTTCTCATGCTTCCTGTATATCTT
 GTAAAAATATCAAGGTGAAATTCCTCTTTTCAAGTTAATTGAAACTGCAAGACTTATTCCTCTT
 TGGACATTCACCAATTTGCTGAAGCCACGTTTAAATTTATCCCTAAACACCATGGGGCAAGTTGCG
 ACAACATTCAGACGACTACCTTAGTGACATTTTACCAGTTGTCAAAAAATTGACAAAAGTCTTGA
 AATTGGAGCAAAAATAATCTCCAGAAAGGTGAAGGTTATAACGTTTACAGAAACAACGGAAGAATTG
 CTCATCAAGTTGTGATCACGTTCACTTCCATTGTAGTCTTAAAGAGGATGAGGCTACAGGTTTAC
 GTGTTGGTTGGCTGCTGAGGCACTGATTTTGATAAATTAGGAAAAATGCATGAGAAATTAAGAG
 AAGAATTGGCTAAGGTAGATAATGAAAAATTATAA

YDL125C_homolog 152aa (SEQ ID NO 316)
 MASHASCFCKIIKGEIPSFKLIETAKTYSFLDIQPIAEHVLIIPKHGAKLHNIPDDYLSLILP
 VVKKLTVKLKDENNTPPEGEYNVLQNNRIAHQVVDVHVPHLIPKDEATGLGVGWPAEATDFDK
 LGLKHEKLKEELAKVDNEKL

YDL133CA_YDL184C_homolog 297bp PathoSeq: 1..297; CDS: 220..294
 (SEQ ID NO 317)
 CATAATTATTACATATAAACTCGCACTATAATTTTTTTTTTCTATCTGTGTGTGTGTGTGTGT
 GAGAGCCAGAGAAACCAAACTGACTGAGTGATCGTCTCAACAATTTATTTCTCTCGTCTTATT
 TTTTCTCTTCTTCTTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT
 CCAAAACACTAGTATTTCAACATGAGAGATAAGTGGAGAAAAAGAGAGATTAGAAGATTAAAGAGA
 AAGAGACGGAAGTTAGAGCTAGATCCAAGTAA

YDL133CA_YDL184C_homolog 25aa (SEQ ID NO 318)
 MRDKWRKKRVRRLKRRKRVRRSK

YDL136W_YDL191W_homolog 1303bp PathoSeq: 1..1303; exon 1:
 501..503, intron 1: 504..943, exon 2: 944..1300 (SEQ ID NO 319)
 TATTGCTGATGCTATACGGCAATGGGCGTTACAAATATACAACTTATATTTGAAAGTAAATCTTA
 TTATTTTCTTCTATCGCTATGCAATACCGATTATATCACAAAGACAATTGCTATTGTTGTGGGAA
 TAAATTTAAATCCTCTTATTTGGTGTCTAGACTTTTGCTTTTGTGGTGATTAGGCTTTAGCCCT
 ATCACGTGAAATCTGTATATAAAAAATTTCTTTATAGCGCGATAAAACATATTTTTTTCCGTATT
 ACACAAATATTGTGTGAAGTTTGTCTCGTGTGTTTCTCACTGTTTCTCTTTTCTTTTCTGTAGTAT
 CAATTAACGCTTAGATCAATCAAGTTTGGTAACTTGACACGAAACAAATCTCAAAATTTGTGTAC
 TGTGTGAACCAACGAAGAGAGAAAAAAACCCATACAAAAATTTTTCAGTATCAAGGAATTAGA
 AGAGACGTTTAAATCAACAAAGTTCAAACTATCAACAATGGTATGTTTAAATATCGATATTATCCA
 TAGATGTACATGTATCTCAATGGGTTTCATATTTGGAAGATTATGTTTATGGAGATTCTATTATT
 TAAGATATGGGATAAGAAATTAAGATATGGATGAGTAGTACAAGACCAACAAAGAGAAATAGCCCC
 CTTTCCCTCCCACTATTCAATATACTCAACAACTATCAAGTTAAAAGTTTCAAGATATACACGTAA
 ATGAAAAGTTAAATACCGAAGAAATCAAAATACCAAGTCCATACCGTGTTTGGGTTTATGATTACTA
 TATTTTACAAGAAACATATTATATGAATGATACCAATCCACAGCGACTTTTCAGATAGCCAAAT

FIG. 2 - 12

AAC TAAGCAACTCAAGATAACATAGGATCATGCATCAATCACAATGAAACATTAACTAACTAA
 CTTTTTTTTTTATTTATTAGGCCGGTGTAAACCTTTGCAATTAAGAACTAAATCTAAGGAACAATT
 AGAATCTCAATTTGGTTGAAATGAAACAAGAAATGGCCACTTTAAAAGTTCAAAAAATTACAAGAAC
 AAGTTTACCAAGAATTACACTGTTGCTAAAAACATTGCTAGAGTATTGACTGTTATTAACTTGAA
 TCAAAAGAGAAAATGTTGCTGCCTTTTACGCTGGTAAAAAATACATTCCAAGAAAGTTTAAGAGCTAA
 AAAGCTAGAGCTTTAAGAAGAAAAATTGACTAAATTTGAAGCTTCTCAAGAAACTGAAAAAGCTAG
 AAAACAAGAATTGCTTTTCCACAAAGAAAAATTGCTATTAAAGCTTAA

YDL136W_YDL191W_homolog 120aa (SEQ ID NO 320)

MAGVITFELRLTKSKEQLVELKQELATLVKQKLRPSLPRHTVRKNIARVLTVINLNQRENV
 RAFYAGKKYIPKDLRAKKTRALRRKLTKEFASQETEKARKQRIAPQRKFAIKA

YDL167C_homolog 2690bp PathoSeq: 1..1640, public: 1641..2690; CDS:
 501..2687 (SEQ ID NO 321)

CTCTGTGTAATTTGATGAAATCCACACAATAAAAAATTTCTTCTCTCTTTTAAAGAACCTAAAAACA
 GAATCAACACTATTGTGCCCATACATATCCAAGAATTAATACCTATTAGTTCTAAGTGGAAATAGA
 AGAAGAACTAAACTTAACACTTACTGTTACGCAACGTCAGAGGGCATTTTTTTAGTTTAAATTTTGT
 TTCAATTTCAAATGTAATCTTAAAGAATCACCGAGTATACATACCTTTCTTTGTATTTTATCAGGGAA
 GCCCATCCACCCAGCTTACATCCCAACAAATCCCTTAATCTTGTCTTGTAGTGTATTTAATTAAT
 CTATTGAAATTTAAGTTTGATATGCGAGAGAAATATTGCGGATGTATTAAGTTTGAATCGGACTGTA
 ATACTTTAGGGGGCTTAATCATATATTGCAATTTATACCCCTACTCGCGGTGTTGCTTACCACTG
 ACTAGTATGACTCTTTCTGAGATTTCTAGCCAATAAATATGAGTGTATTTATATTATTATTCATA
 TTTCTACTACTGTTGATGACTCGCCGACATTTGTGCACTAAGGATTTCTCCGAGTTAAATGAAATTG
 CTTGGGAAACAGTCGATAGTGTCACTTTGGAACCTTTATACAAAGGATCAAACCTGGTTCGTCCAA
 CCAACACACCTTATCACACCTTACTGCTCGAAGATTTCATAGAATAACATGGGACAATGTCAAAAATG
 CTGGGTCGTTCAAAGACGCCATCACAACCTTTGATCAATACGTACAAGAACACATAATTTCCAAGA
 AAAAGGAGTTTTCAATTGTGATGTTTGACATTTCCAATTGAGAGTTCAGTTGGTTCGTTGAAGCTA
 GAGACAAATCCCGTGGTTTTACCCTCGTATCTACAACATCCAAGGATTTTTGATTTACCAAGAGAAT
 ATTTAAATTTGGCAATCTAGCCACCCCTGAAACATTATCATACCCCCCACTTCTTTAACTAATATTA
 TTACTGCAATTAGAAGTTGAGGTTGAGAAATATATCTGAATATGTGCACTTGCCAAACCTTTCTTCCA
 CACCATACCATTCAAAGCTTTCAGCAACAACGACGACGACACTGCAAAATGTCACAGCCATTGACG
 TCCTTTCCAGTGAAACAGAACCAAAATGGTAAAGTCATTGCAAAATTTGCGACGCCAAATTTGCCAAAC
 AATTGATCAAAAAATCATTCCCTGTTGAGAAATCACCCCTAATGTATTTCACAGACCTTTTGATTCGG
 CTCAGATATACCTGCTTTTACATCAGAAAGATCAAAGTACTCTATCTTTCCAACCTTGCCAAACG
 ACACCAACACATCAGAGTTGGAATCATGGTTTCACTCAGTATGGTGGGAAGACCGAGTGGGTTTGGGA
 CTTTTAAAGTCTGCAAGATATAACAATAATAAACAACAACAATAGCAATGGCGGGGAAGGATATG
 AGAATGCGAGAAAATATGGTATTTTACGGGTTTGTGGCCCTTTAATACCTCATGAGGGAAGCAAGTTGATT
 GTTTAGCTTTTGAATGGGAGAGTGTGAATGATCGTCTTATTGAAGTTCAAGGCTGCTTCTAGTAAAG
 GTTTTGATATGGCCATGGATAAATTTGTTGTGACTCTGTTCCCACTCTCAAAGAACAGACCTTAGAC
 CGGGGATTTGGACTTTGTTTATCTTTGTGGGTTTCCCAATTTCCAGAGAGAAACACACTGTTTCAAGT
 GCTCTTTTGGCGCAGTGGGCTTTTCAAGATGTTTAAACAGTAAATACAGGCAATGGCCACCGTAAATG
 GCAATGTTTGGCGGCAACCAACAACCAACAACCAATAGTGGAGCTCGCCGTTGGCATGAATTTACAGC
 CTGCTCAAGCTAATGAGAAAATTTGGAACAGGCAATATTAGTATTCCTTCTTACAACGATCCCAAT
 AGGGTCCAACAGGTAATGTGCTACTAATCACCTCAACAATTTCTGAGACCAATTTACTGAAACACACTA
 ATCTTAAACAACAACAATCATCATAGTAATAATTATCACAATAACTACCATCACCAACAACAATA
 ATAACAATCTGGGGAATAGCAAAATGGTAAACACCATACATGGTTCGTTCCCATATATAAATATGTTTC
 CATTTAGAGCAGGTGATCGGAAATGTGAAAAATGTCATGATATCAAAATTTGCGCAAAATTTGTGTT
 GTTTAAAAATGTGGTGTGCGCAAACTGCTATTAAACAATCAACAAAATAATACAAATTTCAATCGGTG
 ATTCAACGGCGCTGCGCATAGCTGCAGCAACAGCCAGTGGTCAACCTTTTAACTTGAATTAATATG
 CATTTTGGACCTTACGACCAACAACAGCTCTGACTCACACCCAGGTCAGCACCATTAACAAAC
 ATTCTCGTAACAACAATGCTTCTGGGGCATCAAAGTTCAACAATGGCTACACCCCAAGAAATCAGT
 ATTAACAATAATAGCAAGAATCTTAGCAACAATTTTGGTCTTAATGGTATGCATCAGCAAAACC

FIG. 2 - 13

AAAATCAAATTTTGATGTATTCAACAATTTGCAACAACAACAGCAACAACAACAGCAACAACAGC
AACACAGCAACAACAACAGCAACAACAGCAACAACAGCAACAACAACATGATTTAA
ATGGAAGTAGCTCTTCCCATCAACTGAAACTTCAATTGAATAACTTGA

YDL167C_homolog 729aa (SEQ ID NO 322)

MSDIYIIHISTTCDDSPTFVTKDSSSELIEFAWETVDSVLTLETLYKGSNLVVRTPNTPITPYCSKIH
RITWDNVKNAGSPFKDAITNFQYVQEHIIKKKEFSIVMFDISKLRLVQLVREARKDSVVLPYSYLQH
PIFDLPREVLNQSSHPETLSYPPTSLTNIIITALEVEVENISEYVDLPNFSSTPSPSKASATTTT
TTANVTALDVLSSETEPNGKVIANLHAKIAKQLIKKSI PVENHNVVTRFPDSDAQDIATFTSERSK
VLVLSNLFNDTITSELESWFTQYGGRRPGGFWTFKSAADDNNNNNNNNNSNGKGQYQARKYIGISGFVA
FNTHEEAVDCLALNGRVLNDRPIEVQASSKVFDMAMDKLLLSFPLSKNRPFGDWTCCLSCGFSN
FQRRTHCFRCSFAAVAFQDVFSNITGNANGNGVSGNHNHNHNSGARRGMNLQPAQANEKITGTGNI
SIPSYNDPIKGPTGNVTNHLNNSETNLNNNNNNNNHNSNNYHNNYHHNNNNNNHNSNGNITIH
GRSHYNNVSPFRAGDWKCEMCMYHNFKNLCKLCKGVAKPINNQQNNTIHSVNSTAAALAAATAS
GQPLNLNNAFLNLQQQQSQSQPQGHYHNSRNNNNSGASKFNNGYNNPKYNNNNNNNNNN
GLNGMHQQNQNLIMYSQQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQHDLNGSSSSSHQSKLQL
NNNT

YDR238C_homolog 3359bp public: 1..1467/1469..3040/3042..3359,
PathoSeq: 1468/3041; CDS: 501..3356 (SEQ ID NO 323)

AATAGCATTTGAACAAGAAGAGGAGCAACGATGACCAAGGTTGGTTTTAGCCAACTCTGATTAT
GATAGTGATGACAGTTTCATAGACAAATTCACAGCCTTAAATGGATATATATATTTAATAATAA
AGGACTTGTTTTTTTAGTAACATAGTGTGATCTCTTTTCTGGGTGTACATTTTCGGATAGCCAAACCA
GTATATCTTTAGCAGTTTATAGACAGTGTATTCAGTGGGTAATAATAAATAAAGCTCATTGAATA
CTATCTAGTGAAGAGTCGTGTGTAATTCGATTTGAAAAATATAAAACCATACAGCTAAATGAAATG
TGTGTGAAAGTACAACCAACGAAAGAAAGAACAAAAAAATGTTGTCCGCCAAAAAAAAGAG
AGAACCAAAATCAAAGTTTCAAGACTATCTCAAACTCTGTGTGACCATTAACATCAATTTGTTCA
CCTCTTGAACCAACATCAAAATGAAATAAACATAGGATCATGAGTGACAGTGGTTATACATTAATCT
ATGAGCCTAATACGGCTACGAAAGTATCTGTCAATGAATTTAAAAATTTGTGTGAAAGAGGTAAG
ATGATGTGAAAGTAGATACCATGAAGAAGATTTTGATTACCATATTAATGGAAGCCCTTACCTG
ACTTGTGTGATGCATATAATCAGATTGTGTCATGCCCTTCCAGAAATAAAGAAATGAAAGAGTTGTGT
ATCATTTATGGGAGGTTTGTCCAAAAATGGATGAATCAGGTAAAAATGAGACATGAAATGATCTTGT
TGTGTAATGCCATCCAAAGTGTATTACAGCATCCAAATGAATATATTCGAGGCAATACCTTTGAGAT
ATTTGACGAAATTTGAAAGAGCCAGAAATTTATGGAAACTTTAGTTCCTAATGTCCTGCAATGTTAG
AACACCGTCAATGCTATGTGAGAAAAATGCTGTTTTCGCAATTTGCTCTATTTCATAAAGTCAGTG
ATCATTTAGCTCCTGATGCTGACGAGTTAATTTACAGATTTTGTATGAGGAAAAACGATCTGTGTT
GTAAAGAAATGCTTTTGTGTGCTTGGAGACTTGAATAGAGAAGCTGCTTTGCAATATATTCAGG
ATAATATTTTCAGTTATGAGACTTTGGATCCATTGATACAATTTGGCTTTTATTGAGTTTATCAAAA
AGGACTTCAATTTCAAATCCAGCTTTAAAGCAACAATATGCCCAATTAATGACAGAAATTTATGAAA
GCTCTTCAAATGTTGTTATGTATGAAGCTGCTAACACGTTGACTGTTTGACTTCAACCCACAAT
CAATTTTGTGTGGCAGGAACAAGTTTGTGAAATTTGGCTACTAGAGAGTCTGATATAACGTTTAAAA
TTATCACTTTTAGAGAGATAAATCAATTAACAAGCAACACTCTGGTGTGTTTACAAGACTTGTCAAT
TAGAAATTTTACGAGGTTTATCTTCCCAAGATTGGATGTTAAAAAGAAAGCTCTTGATGTACTTAT
TGAAGATTTATCACCACCAAGAAATGTTGAAGATGTTGTGAAGTTATGACAGAAAGATCTGAGCTCA
CAGCTTTATCCAATGATGACAGAAATGCAGATTATAGACAGTTGTAATTAATGCCATCCATCAAT
TGGCTATTAACCTTGGCGAGTTGCTGCCAATGTCATGATTATTTGTGGATTCTATGAGCGATT
TGAATCAACTGCTGCTGACGAGTTATCACAATTGCTTAAAGAAGTTGTTGAGAAATTTCCAGATT
TAAGGGACCGTATTTTGAAGAAGATTGATTTTGGCTTTGCCACATGTAAGAAAGGGTGAAGTTTCC
GTGGTGCAATTTGGGTTATTTGGTGAGTATGCTCTAGAGGAATCATTAATACAGAAATCTTGGAAAT
ATATTAGAGGAAGTATTTGGTGAAGTACCAATTTATGTGATGTAATGAACTGAAAGGCTGAAAGCGTATG
ATATCTGAGGAATCAAGAGGAAAGAAACCGGAGTATGATGGTAAACCTCGCAGAAAGGGTCCAGTTG
TATTGCGAGATTGTCATTCAGCTACTGAGTCAGCATGTGACAGGCGAAACCACTGACTCTTTGGA
GTGACAGCAAGACTCTCATCAGAAAGCAAACTCTGCTGGTGAATTTCTACTGATGGTGTGATTATG
CATCACTTTGGTGAATTTGATTCTCCGATTGCAAGTTTGAACAAACTCAAGAAAAATTTTGA

FIG. 2 - 14

ACGGATTAAGAGCAGAAGCATTGTTGATTATGGTTTCGATTTTAAAGAGTTGGGGAATCTAGCTTGG
 TTTCTAAGAAAATTGATGAGGATTCTGCTGCAGAGAATTTTGTCTTACATCAAGATTTTGAACAGTAT
 AAGAAGACCTTCAGGAAATCAAGACAAGCTTCCCTGAAGATACTAAGATTCGATTAAAGCACA
 TTAATAATGCTGAATTGAAGAAAGCAGAAGCATTGGCTAAGGATTTGCGATGATAACGCTGAACAAA
 TGCACGATGCAATTTGTTTTAGACAGTTGGATTAAGATAACAAAAAGAGTAAAGCTTCTGTGGATG
 ATGTTGCTGCTGCGTCAGGAAGCAATGAATTAAGAAAGAAAAATTTGTCTCGAGATTGAACAAAA
 TTATACAATTGACTGGGTTTCCGATCTATTTACGCAGAGGCATTTTGTCAAAGTTTCATCAATACG
 ATGTTGTGTTAGATTGCTTGTAGTGAATCAAAACCACAACACTCTTTAAGAAACTATCAGTTGAAT
 TTGCTACATTTGGGTGATTGAAGGTGGTTGATAAAACCACTACCGCAATATTGGACCTCATGGTT
 TCTACAAAGTTCAAAACCACTATTAAGTTACTTCGGCTGATACCTGGTGTGATCTTTTGGTAACATAG
 TGTATGACCGTCAACACTCGGACGATTACGATATAGTTATTTTGAATGACGTTACCGTTGACATTA
 TGGATTACATTAAGCCAGGCACTTTGTTCAAGAACTCAATTCGCTAAAATGTGGAGAACGAATTTGAAT
 GGGAGAATAAGATAACCATTAATACCTATTGAAACATTGAAAGAGTACTTTGGATGAATTAATGAG
 AGGGTACAAATATGCAATGCTTGACACCGGTCGCGTAATTGGAGAAGAATGTCAATTTTATCAG
 CAACTTGTACTCAAGGTCAAGCTTTGGTGAAGATGCATTGGCTAAATTTATGTATAGAGAAACAGA
 GTGATGGACCAATAATTTGGTCATGTCAGAATAAGATCAAAAGGTCAAGGTTTGGCTTTGTCAATTGG
 GTGATAGAGTAGCTTCCATTTCAGAAAAGTAAAGAGCACTATTGCTCGTGTTTAA

YDR238C_homolog 952aa (SEQ ID NO 324)

MSDSGYTLIYEPNTATKVSNEFKNLLLEKGDVVDVTKKILITILNGDPLPDLMLHIIRFVMP
 RNKELKLLIYHWEVCPKMDSESGKMRHEMILVCNAIQRDQLHPNEYIRGNTLRVLYLTKLKEPELLET
 LVPNVQRCLERHAYVRKNVAVFALWSIHVKSDDLAPDADELIRYRFLYEENDSVCKRNFVCLGDLN
 REAALQYIQDNISVETLDPQLQAFIEFIKKDSIQNPALKQOYQAQLMTEIIESSNNVMYEAANT
 LTVTLSPNQSIILLAGNKFVELATRESNNVKIITLERINQLHKQHPGVGLNDLSLEIRGLSSQDL
 VTKKALDVTLQFTTTRNVEDVVKLLKELQSTALSNDKDNADYRQLLINLHQLAIKFRGLSNAVNI
 DLLLDSIADLNTAAAYEVITFVKEVVEKFPDLRDAILRLRILALPHVKSQGVFRGALWVIGYEALE
 ESLIQESWKYIRGSIGVEPIIASSELKSKRRDDEESQEEETEYDQKPRRKGPVVLDPDGTATSEAL
 TSETDLSLESDSKTPIRKQILAGDFYLGAVLASTLVKLILRLQSLKQQTQEKILNLKAEALLIMVS
 ILRVGESSLVSKKIDEDSADRILSYIKILNDEEDLQEIKTSFLEDTKDAFKAQINNAELKKAELA
 KDLHDNAEQIDDAIVFRQLDKDNKSKASVDDVAAAAGSSELKKNLSSRLNKIILQITGFSDFPIYA
 EAFVKVHQYDVVDVLLVNQTTTLRNLSEVFATLGLDKVVDKPTTANIGPHGFYKQVTTTKVTS
 DTGVIIGNIVYDQGHSDSRIIVILNDVHVDIMDYIKPATCSESQFRKMMNEFEWENKITIKSPIET
 KEYLDLMKGTNMQLTPGAVIGECCFLSANLYSRSSFEDALANLCIEKQSDGPIIGHVRIRS
 KQGLALSLGDRVASIRKGGKATIAVR

YDR294C_homolog 2270bp public: 1..278/280..2270, PathoSeq: 279;
 CDS: 501..2267 (SEQ ID NO 325)

GTTTGTGATCACAATGTTGTGTAACACTCGGGTAATACAAAATAGTGAGAGAGAGAAGAGGGGAAAA
 AAAAGCAGAACACAAAACATGGAATTTGAAACAACTTTGTAATTCAGATCGGACGATTCAT
 AGCAAAGCTTAACAGCACAATTGTCATTTTAACTTAAATTTGGTGGATTAAATCGGGATCAATCTGAAT
 TCGTTTCCCGTATGTTTATAAACCAAGAAAAAGGATACCAAACTTAAATCTTTCATATTAACTAC
 ACTTTTGTGTAGTGGTCAGTTATATATTAATTAATCCACTGTCTCTCCAAATTAATAAAAAA
 AAGAAAAAAGAAAGCTCTCTCTCCCCCAAAGAAAAAGCAAAGGTAATCTCTCATACACACCTT
 TAGATATCTTCTCTCTAGACTTTCTTTAATACTTGCATCAATTGGAAATATTACTTGTCATCAT
 GGAGTTTTCATTGAACTAAATATTATTAATAATATTATATGCTTGAATTTGAATTCATTTACGATTC
 CTCGGAATTTCACTGAATTTCCAACTCAGCAGCAATTAAGATCTACTATCACTTAAGATTTTATTTTC
 TGGCCACATACCTGCTCAAGGATCAATTTGGCTTGAACGGTTCAAGTCTGTTTACGACAGAGATATT
 TTGTTGGCTATTGTTGTATACACTCAATTAATAAGACTTTATCGAGTATAAGAGGTTACGGTATTG
 TAGATTCTATTTCGAAGGTTATACCTATATGTTAGTTCTACGGTGTGATCTCAAATCTTTTCTACAC
 CATTTATTAATACAAAAATGACAAGGAATTGCAAGCGACTATTGGCAAGATGAGAAGAGAGATTA
 TGAAAAAACGATCCACAGTTATTACAGTTTCCCGAATTTGCCAGAACAGGGTATTGACGCTGACATG
 TTTCTTGGAGTTGGATAAATTACAAAACATTGAAACACTTGACTGGATCAATGGAAGAGTCAGTG
 GAGCAGTTTATCATGGAGGTGAGAATCTATTGTGTCATTACAAAGTTGAAGCTTACAGAAATACTCGG
 TGGCCAATCAATTGCAATCCCGATGTTTTCCAGAGTGTGCTAAGATGGAGGCCGAAGTAGTTTCATA

FIG. 2 - 15

AGTACTGCACATCTATCACCTGGAACCTGGGTAAATCCATTGGATCCAAACATGCAGTATGATATTT
 TTAATGGAAAAATATTGAGCTCATTATTGTTTGGATGGACACAACCTCTCCCTTTCTATCAAGAGTTAA
 TTGAAAGTGGATACGGTGGACGATTTTTCGCAAAATCTGGGTGGACTCAACCGCGGTGCTTT
 CGTTTACTGTGTGCTCAACCTACTTAAACCAAGCAAAAAGTTGATAATTTTAATGAAAAAGTTATGG
 AAATCATTAATAATAAAATCATTTCCGAATTAAGTAACGAAGAGTCTCTCTATCATATCGGTAGAA
 TTGATGCTATATTGTCATCAAAATAGAAATAGGATTCAAAGACACAAGCCCGATTTTGGATTGGAT
 TATTGAGCTCTATTGTTCCGTCATGGGTGAATGGAGTTGATCCAAATTGACACCTTGCAAGTGGAAA
 AGATATTGTGCGCATTTTAAAGAAAGATTATAAAACAAATGGTTAAAGGATCTTTAAAGAAATTATAG
 AAAAGACATTGGTTAACCTCTATTTCGCAAAAATTTAAATTCACCATGGAGCCCAAGAGAAAGATTTTA
 CCAAAACCAATTTGGTAAAGAGTGAAGTTTGTATGATCGAGAAAAGAGTAAGTGAACCTACAGAAAGATA
 ACAAGAAAGGAACTTCTATGAGCAAAAATTTGGAATTAGCTAAATTAACAATTGGAGGATCAAATACAG
 AAGTTTATGCCCATGACTATTGTGATGACATTCCAAAGAGAGGTGATTTTATGCCATTGATTTGG
 GCCAAGTAAATAAGAAAGTTGTACATGAAAGGGTAGTTGATACCAATGGCTTGGTTTATGCCAACG
 CTTTAAAGATATTTCCTATTACCACCAAACTTTTACAAGTACCTTCCATTGTTTAAACACTGTT
 TGACGAACCTTGCTGGAACAGAAAACACACCCATTACGGAGTTGGAACCTAAAATACAAATGTTAA
 CTGGCGGGAATAACATTTAGTTCTAAAATATCGACTGACCCCTATAATATTGAGCAACTAAAATTAC
 AGTATGTGTTAAGTGGAAATGGCTTTGAAAGAAAAGTCATCTCAGTTTATGATTTATGTTGGAGA
 TTTTAACTACTACCAAAATTCGACACAGTGATGAGGTATTAGAAAAAGTTGTGAGTTTATGATTTAAA
 ACATGGGACAAAACCAAACTCAATAATATTGCTGATCGCGGTCACTTTATGCGGCTGCTGTGAGCT
 CACTGAAATTGACACCGCTGAAATACATCAGTGACATCGTTTCAGGTTTGGATGCAAGTTCAATTTG
 TAATGGAGTTGAACTCCCAATTAGAATCAGAAAGGAAAGAGTACTTGGCCAAAGAGATTATTTCCGA
 TATTGCAAGAAATACAAAAGTATGATTGCAAGGTGAATTGAGGTATAGACTAGTTGGAAATCAAG
 AGATTATTGTTGAAAACGAAAAGCTTATTGAGAAATTTGATAAGGATATTCTTCGAACAGACCAA
 CTTTATCGTTTAAACAGTAAACAGATGGTTTACTGGCATTGTTGAACCTCATCAATTACAATCATACAA
 GTGAAAATGCTCTTAGTTAACTTACCATTCAAGTGGGATACCTCTCATAGGTAAAGATTGGCTCTT
 CGTATTTCATCAAAGGATGGTGCTCTTTACAAATATTATCTCAGTTATATTTCTTTAAAAATCTAC
 ATTTCCAAAATAAGAGAGAAAGCAATGGTGATATGGAGGTGGTTTGACATATGATGGGTGGAACGGGA
 CATTAACTTTTATTCGTATCTGATCCATACTCTGTTAAGTCGATTCAAACTTTTGAAGATTCTCT
 TACTGTATGGCACTTGATGCTAATTGGAACGATAAGGATTTACAAGAGGCTTAAGTTTGGCGGTTTTCC
 AAAGCGTCGATGCTCCAAATTAATATCTCTTCTCAGGCTGCTAGTGCTCTTTTGAAGATTAATAGAT
 ATTACTTGAGACAGGAAAGAGAGAAAACCTTTTGGGTACCACCTTTAAAGGATCTCAGAGATCTGA
 CTGAAAAGTATCTTGTGTAATACCAAAAACCTTTGTCACCTGTTATTGGTGACAATGAAATTTTAA
 ATGTCGATAATAAATGGCAAAATAGAAATTTTCAAGTATAG

YDR430C_homolog 1034aa (SEQ ID NO 328)
 MLKTRLKQSRRAISRVVRRYACSHPISPNLDKYPVGLKLHGYEVTQTSPIPEFSLTAVSLKHOTESGA
 THLHLDSPNDNNVFSIAFKTNPPDNTGVPHLEHTTLCGSKKFPVRDPFFKMTNRSLSNFMNAMT
 GHDTYTFYPFATINSKDFENLMDVYLSSVFEPLQNLNTHDFLQEGWRIENQNVHDITSSLEKFGVYVNE
 MKGQYSNSAYFYFIKLESITYPSLNNSSGGDPKKIVDLSYEGLELPHFSKNYHPNNAKTFFYVGLPLE
 DLSLKSIDYFYESFEKKVSSVDVKQPIFSTDKSEIFDVITPGPVDTHMNGKETSEQYCTSTTWNLGNP
 LDPNMGKIFYPKWKILSSLLFDGHNSPFYQELIESGYGDDFSANTGLDSTTALLSFTVGLNLYLTKQK
 VDNFNEKVMIEINNKIIPELSNEESSYHGRIDAILHQIEIGFKRHKPDFGFGLLSSIVPSWNVGVT
 DPTDITQVEKILSHFKEDYKQNGLRIFKELLEKTLNPHSQKFKFTMEPREDFTKQLVXDENLMIE
 KRVELSTEDNKKAIYEQNLLELAKLQLEDQNTVEVLPITLIDIPKRGDFVIAIDLQVNNKRVHVERV
 TDNGLVYANALKDISYLPKLYKYLPLFNCLTNLAGTENTPITELETKIQMLTGGITFSKISTD
 PYNIEQLKLQYVLSGMALKEKSSVYDLWLEILTTTKFDTSDEVLEKLSVLIKMGEQONQINNIADR
 GHSYAAAVSSSKLTPSKYISDVSGLSQVQVFMELNSKLESEGEVLEKLAKIIPILQEIQYVLEQ
 FRYRLVGNQEIIVENEKILEKFDKDISSNRPVLSLTVTDGLSALLNSFYNNHSTENVLNLPFOVG
 YSSLGKIGSSYSKDGASQLLSQLYSFKNLHSHKIRSNAGYGGGLTYDGLNGTLNIFYSYRDPNPV
 KSIQTFRDSLVSGLDANWMDKLQEAKLRFVQSDVAPINSSSGASAFENIDYDLRQERRNFILG
 TTLKDLRDVTEKYLVDNQNNLVTVIGDNEILNVNDKNQIRNFQV

FIG. 2 - 17

YDR450W_YML026C_homolog 1366bp public: 1..1366; exon 1: 501..548, intron 1: 549..976, exon 2: 977..1363 (SEQ ID NO 329)
 TTAAGAAGCTACGAGATGTAAATGTTTTATGTCATTATATAATTGTTAAATCATGTATATAGATT
 TTTTAAATGAATGTATTCCCTAAATAGAACAGAAATTATGATGCTGTTACAGCAAAAACCTGGTTGGAG
 TATTCGGAGAGTGTATAAAGCTGAAATTTGATTTACAACCAAAAACCGCTGCACGCTGAAGTAATTA
 GGGCTTTTATAGGGCTTCTATATATACAGGCACCAAGAAATTTTTTTTATGGGCGATAGAAATATGTAT
 GCGCGCAGATCTTCCCTGCTAGAGGTTTTCTTTTGTATGTCTGTAAACAGTCCGACTCACATAGTT
 AAGTAATTTTAAAGCCAGAGATTGTGTACAGTCGCACGCCCTAATCAATAGATTAAATTTCTCAAA
 CTTTCTCTCTTTCTCTCTTTTGTCTTTCTCCTAAGGAAAAAATAATTTATTTCAATTTGTTGAAAAAT
 TTTTGATAGTTCAGTTTAAACAACACCAAGTAATCAACCATGCCATTAGTTTGTCCAAGAACAAAGGTT
 CATTCACAACCATTTTACGGTATGTGAGTGATTTATAAGATTATTTGAATAGAGATAGAAAAGGGTT
 AAGGAAGGAAAGAAATTTATCCAACACTCTGTTTGGGAAAGATTAAATCAGAAATTTGAATGCAATGA
 AAAAATTTTTCAAGAGATGGATATGGAAACAGATTTCGATTGTATCAACAAATATATAAGAAAGC
 AATGATTTACTACTGTTTGGGAAAGATTTTGGATATGTGTATCAACAATCACTACTATTTTACTTTGG
 AGTAATATGTTTCAATATTTATCAGAGACTTATCAAAAATTTATGAGTTTATTTATTTGAAGTTCA
 ATACCATCAAGCCTTTTTTTTAAACCATCACTCTATTCAACAATCATTTAAATATTTAAAGCTTTTT
 TTTCCCTGTTTAAAGTATTCGATTACTAACATTATGAATTTATTTATATAGTTTGTGTAACACCAA
 CATTTAGGTAGATAATCAAGATCATGTACGCCTTGACCAAGATCAGAGGTCGCGTAGAAGATATGC
 CAACTGGTTTGTAAAAAGCCGATGTTGAATTAACCAAAAGAGCTGGTGGAATTGACCCAGAGA
 ATTGGAAAGAAATGTCCACCATTATGCAAAACCAACCAACTATAAAATCCAGACTTGGTTGTGAA
 CAGACAAAAGATGCAAGTTGATGGTAAAGATTACCATGTTTATAGCTAACCACTTGGAAATCTAAAT
 GAGAGATTGTTGGAAAGATTGAAGAAATCAGATCTCACAGAGGTTATAGACACTTCTGGGGATT
 GAAAGTTAGAGGTCAACATACTAAACTACTTCTCGTGGCTGTTAA

YDR450W_YML026C_homolog 145aa (SEQ ID NO 330)
 MFLVVFQEGSFQHLRLNLTNIDGRKIMYALTKIRGVRRYANLVCKKADVELTKRAGELTQEEL
 ERIVTIIQNPTNWKIPAWFLNRQDQVDGKDYHLVANNLESKLRLDLRLKKIRSHRGIRHFWGLK
 VRGQHTKTTSRGR

YDR471W_YHR010W_homolog 1327bp PathoSeq: 1..1327; exon 1: 501..530, intron 1: 531..946, exon 2: 947..1324 (SEQ ID NO 331)
 ATAGTTATTACATATAATAAAGCAAATAAATAAAGAAATGATAAAGAACCATATTAAACAAAGTT
 TGAACGCTGCTGAAGTAAATCTTGATATACGAGAATATTCATCTTGGAAATATTCTTAAACGATACTG
 GTAATACCTAATTTCTATTGTGTGGTGCATCACGTGCTAGGGCTATAGCCCTAATAGTATATGCA
 GTCGCATACATTAATTTGGTCATCTCATAGTAAATATATAATGTATAGTGTGGCGCGCACTGTAAT
 TTTTCACTAAGTTAAGGAGATGCGAAAAATTTAGTACTTAACAAAATTTGATTGTGTGTGTGT
 GGCTATTGGGCGAGAGCGAAAAATTTACCCCTACTGAGAGGAACTGTGAGGGAGAGAGATACAC
 AAATCTCTGTCGCGCAAGAAGAAAGACAAAAATTTTTTGAIAAAAAAAAAAGAGACAACCAACCTT
 TTATTGTAATTAACATTTTAAGATATCAAGAACTAAAAATGGCTAAGTTTCATCAAACTTGGTAAAG
 TTGGTATGTAATAATGAGTACCTATATGGGTAGACAAATGATAGATTATTATGGCCAACTATGAATGG
 GATAGATATATATGATATGGGAGAGAAATTTGAAGGATTGAAATATTTTATATAAAGAGAGAAG
 GAAGAGAAATATGTAACAAATGAAAAGAAGATACAAATCTGTTAATTTAACTAGAAATTGCCATT
 AAAGATTTAAATGATTACCATCTGTAATAAATTTATTGGAATTTGGGAGATTCTTTGGAGTTAAGA
 AAAAAGCAAGTGATTGATCAATCACTATGGAGCGCTCACAGACATCAACGAATCCCAACAATTT
 TTATTATTCATATGATATGGCAGTAAACAATCATGAATCTACAATTCATTTTAAAAAAGC
 ATTATACCTAACTAAATTTTTTAGCTATTTGTTGAAGAGTTCGTTACGCTGGTAAAAAAGATGTCAT
 TGTGAAACCATGATGAAGGTACCAAATCTCACCCATCTCCACATGTCATTGTTGCTGGTATTGA
 AAGAGCTCCATTGAAGGTTACCAAGAGATGGATGCTAAAAAGGTTACCAAAAGAACTTAAAGTCAA
 GCCATTGTTTAAATTAGTAAACTACAACCATTTAATGCCAATAGATCTCATTAGATGTTTGAATC
 ATTCAAATCTGCTGTCACCTCTGAAGCTTTAGAAGAACCATCTCAAAGAGAAGAGCTTAAAAAGT
 TGTCAGAAGAGGCTTTTGAAGAAAACATCAAGCTGGTAAAGAAATGTTTCTTCCAAAAATTACA
 CTTTAA

FIG. 2 - 18

YDR471W_YHR010W_homolog 136aa (SEQ ID NO 332)

MAKFKIKSGKVAIVVRGRYAGKKVIVKPHDEGTSHPFPHAI VAGIERAPLKVTKKMDAKKVKTKRT
 VKKPFVKLVNYNHLMPTRYSLDVESFKSAVTSSEALEEPPSQREEAKKVKKAFEEKHQAGKNKWWFFQ
 KLHF

YDR486C_homolog 1157bp PathoSeq: 1..1157; CDS: 501..1154 (SEQ ID NO 333)

TTCCAGTCACTCCGAAATGCATAAGCAAGACGTTAGTTGTATTGTGGTTGTTTAGTCTAATCCAAA
 AATACTTGCCATGACGACCCATGAAGTAACAACTGCATTGTGTAAGGCTTTTCTCATCTTATTCA
 ATTCTTTTTCAGATCATTCGTCATCTTTAAGCACAGGGAATAGCAATGGATCATGTAAACAAATCA
 CTTTCGTGATTCGAAAGCCCAAAATGTTTCGTTTAAACAACGCACACATGTGAAACCTTAACCCG
 AGTTAGTCGTCAGAGAAAATAATTCAGTGTAAAGTCGTACCTTAAGCGTCAAAACGTACTTCTGCA
 ACCTCTGGCATTGAGTGTAATTTAAATATTTCATGATAATCTGGAACTACAAGCTACGAAAAA
 GAAAAAGAAAAATAGTACGAGTCTTTGGTGAGATAAATAATGGAGAACACTTTTTCCTCTTT
 GGAGGTTTATAGAGGCAAAACCAATCTAGACAAGGAGATGAACAGATTATTTCGGAACGAAAAAGCA
 CTCGCCCAAAACCATCTTTGGAATGATGCAATCAAGGGAATCGATGAAAGAGTGGGGTCTTTGGATG
 TAAATTAAGCAAGATCTCAACTCGGAATTTATCCACATACCAACAAAAGATAAGCAGAATGAGAGCG
 GACCCGGGAAGTCGGCACTAAAACAAAAGCAATCAAGTTACTAAGCACAGGGAAGCAGATAGAAG
 CTCAAAAGGATCAGTTAGAGAATCAATCTTGAATATGACACAAGCTTCCATGACACACAGATACT
 TACAAAAATCACCATTGCTCAATAAATGCAATGAAAACAGCCAATAAATCTGTTGAAAACAACTTATG
 GAAAAATTAATATTCGATGAATTTGGAAGATCTTCAAGATGAAATGTTGGATTGGATTGATAAATCAA
 ATGACTACAGGAGGCATCTTGACGAGCTATGATGTACCCGATGCATCAGTCAGCTGGAGTTGG
 ATGCTGAATTAGAAGCTCTTTGGCGAAGAAATTTGATTTTGAATGAAATGGGACAGAGATGGGATAG
 GTGCACCTAGTTACTTTAAATGATACAGAACCTACAGCAGCAGATAAATTGCCATACATTATTGACG
 AACAACCAAGAAAGCTCAAAAAATCGCAAACTAG

YDR486C_homolog 218aa (SEQ ID NO 334)

MNRLFGTKSTAPKPSLNDIAKIGIDERVGSLDVLSKINSELSTYQQKISRMRDGPKGSALKQKAIK
 LLRQRKQIEAQKQDLENQSWNMTOASMTTNDLQNTMVTINAMKTANKSLKQTYGKINIDEQLQD
 EMLDLIDKSNELQALSTSYVDVDDISESELDAALEALGEEIDFENEMAESGIGAFPSYLNDEPTA
 ADKLPTFIDEQPEEAQKIAN

YDR507C_homolog 4550bp PathoSeq: 1..1424, public: 1524..4550; CDS: 501..4547 (SEQ ID NO 335)

GAATGAGATTTTTTTTTTACTAAGGGTGCACTACTACTAGTTATTGTGTTTGTGTTGACGATCA
 TAAAGAAAAAATTTACAGATTACACAAAACACTTACTTCTGCTGTTTTTTTTTTATTTTAGTTTT
 TTGGTTTCAATAAATTTAAAAAGAAAGCAATAATTTATGAAATAAATTTATATTTTGGTTTTTT
 TTTTCTTTGGTTTCTTTGAAATTTTGCAAAACCAATCCAAATTTTTTTTGAATAATTTTCTCTCTCT
 TCATTGTGTGACTTTTGAAAGTTTATTATCCATCATATTTCAAGTTGAATAAGTTTCTCAATATCT
 GTCCAACCAAGAGAAACCAATAAACACATCAATTCCAACCTTTGTTTATCATCAACACAGAAACAA
 AAAACAGATAATTTATAGACACTTCAATCTATTCGTTATTTTTTCCAAGTACTACAGCTCTTAT
 TTTTAATACATTTATCATAAACAAATTTATATCAATAATGCCACATTCAGACAACCTTCGATAT
 CGTCATCGATTATGTCCCAATCAATATCATCCACAGAAAGTCCGACCTTGGAAATTAGTATA
 AAACCTTTAGGAAGAGGTGCCACCGGTAGAGTCTTATTAGCTACTCATCAAACTACTGTGCTCAAAAG
 CTGCGGTTAAAGTAGTTTCCAATCCGAATTACAAGACGAGAAACCGAGAAAAATGGAGATGGAT
 TACCATTGTGGTATAGAAAGAGAAATTTATATAATGAAATTTAACTCATCTTAATGTTTGGAGAT
 TATATGATGTATGGGAAACATCTAAGGCTCTTTATCTGTGTTTGAATACGTTGAAGGTGGAGATAT
 TATTGTATTTATTGGTGGAACTGGTCCATTACCTGAAGTCGAGGCTATCAAGTATTTCCGTCAAAA
 TCATATTTGGGTACGGCTTATGTCTATGCTTTGGTATATGTCACAGAGATTTAAACACAGAGAAAT
 TGTTACTAGATTTCTCAATGTGAATGTAAATATAGCCGATTTTGGAAATGCGAGCTTTAGAAAGTAAACG
 GCAATTTATAGAGACTCTTGTGGTTCACTCATTTATGCTGCTCCAGAAATCGTTAGTGGATTGA
 AATATCATGGAGCTGCTTCTGATGTTTGGTCTGTGGGGTTATATTATTTGCTTGTGTGACAGGTA
 GATTACCTTTGATGATGAAAAATTTAGAAATTTACTTCTTAAAGTCCAGGCTGGTAACTTTGAAA
 TGCCCGTTGATGAAGTTACGACAGAAAGCTAGAGATTTAATGCTAGAATGTTAGAGGTTGATCTCA

FIG. 2 - 19

TGAGAAGAATATCTACTGAAAAAATCTTAAAGACCCCATTTGTTAACCAAAATACCCAAATGTCAAACG
 AAGATTTAATCAGTGAAGAAATCATTTACCACATCCACATACCTGGTTACAAATCTTTAGGGTCAGTTA
 GAAACATTTGATAAAGCAGATTTTATCAAACTTGACAAATTTTATGGAAATGATAGACCCGAGAGGAAA
 TTGTTGATTTGTCCTTTTGAAGATGGATCCAAATCCAGAAAAAATCATTTCTATGCATTTATTTGATGAGAT
 CAAAGACATAATCAAGACCAATAACACTAATAACAAATTCACCAAGAAATCAACGAGTTTTCATTAATA
 AAGTGGTACGCAAGTGGGTCCAAATACAGTCTTAATGGAACCCCTAGAGAAAGAAAGAGGCGAGTCAACA
 TAAGTGTGTCAAGAGCAACATCTTTTCCAATACAAGTCTAATCTTGGCGCTGGTGTCAACAGCAAAATA
 GAAATCTCGTTTCCAGACATCTTGTGGCTTCTCTGGCCCAACAAATCTCTCTGTAATACCCATCAACA
 AGTCACCATACAGATCAGCTTTATAGATCACCATAATAATCGCCTTCTAAGAGATATTTCATATAATC
 AATCCCCCAATCAATCTCTCTTACGGAAGAGATCAAAATTCACAAAGACAAATTTGAAATGAACCAT
 TAAAGCCAAGCCCAAGAAATATTATCAATGAGATTTGTTGATGCAACAAAGCAATCTTTCTCTACCTC
 CATCGCTTCCACTTCTTACCTTCAAAAGATTTCTGTTATATGATCGATGAACCCAAATCAACCC
 AGTTTGCAACCACTGCTTTAAGTCAAGTCCCTGAAAAATCTATTGTGTGATGATCCCTGATTTTAA
 TGCAGTCAGCAAAAATTTCTAGTGGAAAGAGAAATTCATTAATAGGAAAGAACCAACCAACAGCA
 ACAGCAACAGAGAATGTCTAAGAGAAAAATCAATTCGTGTCATCTATGACACAGGGGATTTGAAAGAA
 ATTTCCATAACCATGAAATTTGTTATCTACTTATGTCTAAATTTATCAGGTGATGACGATCGGGAATACA
 TGGATAAAACAAACAAAAGAACATCGGCTACTTTTGCAGCATTTGTGTGACAAAATTTTAAATCAAG
 AAGCATATGACGAGAAAGAGCAACAAATTTAGTTGATCTTGAAGAAAAGGAGAGCAAGGAATATGAAA
 GGTTAATGGAATTTGGAAGAAAGAAACATGAAGCTGAGTTGAAGCTAGAAAGAGAAATTAGAAAAGA
 AGAAAGAGAGCAAGAAAGACGCTTCCATTTTGAGTTCTAAGAAATTAAGTATTTTGTCAAGAATG
 ATGCTGATCCAAATATAATGTAACAAGAGTTGGTCGATGAAGGTATATAACCAACCAACCAACGCTCAAT
 CCAAAATTTGACCGCTTTAAGAGCATTATCTGAAGGAAATCATGCATCTGAAGAATTTGACATTTGG
 AAGACGTTGAGAAATTTGAAGAGACGATCAGCATCAACGCGGTTTCCAAAAGAAAGCAACATCTCCGG
 TTTTTCACAGAAGACCTGTATCAAGATTAGATCCATTTAGGCAAGCAACAGAGAAATGAACAGTTAG
 ATAGAGCAAAAGATGCTTTGGAACAAGAAATGGAGGGAATTCACAAAAGAGAAAGTTCTACTGTTAGTC
 GTAAAAAAGTCAACAGAGAGTCGATGATATCAGTTATGGATGATATTTGTTGAAGAGGACCAAGGCC
 GTGTCAACAGGAGATCAACACGAAACACTTACTATGAAGGGGAAAGAGACTATGAATACAGAAAC
 CAATCTGGAAGATTCCAATTTGA CTGATGACTACATGACAGAAATCAGAAAATCAAGACTTTTGA
 ACAGTCAGTTAAATTTAGGGATCCACTTAATGAAAAAAGAAAAATCTGAACCCAAGACTCTTATTA
 GCAATGTTCAAATACCGAGTGTTA CTAGAAAAATCAAGAAATTTCACTACTTCCAACAAAAGGTTGT
 CGGTATTTGCTATGTTATCAACAAAGGAATCATACCGTGATTTGAAATTTCTATAATTAACCTACCCAG
 ATGAAAAACCCGAAACAGCATCAAAACATGAACAAGCCAGCGTTACGAACCAAGATTTGCTGATCTGTT
 TGGATAAAGCTGGAATTTGGCTGAACCAAGATATGAAACTGAGACTGATGTTGTAAGATATAAGTGTCTG
 TTAATGATTTGGATGATCAATTTAGCTGATAGAAGGACTTCTTATTAATGATGATCTGGAAGAGAG
 CATCTAGAGCTTCAACAACATAAACGTTACAATGTTCAATTCAGTTCAGAAAAGAAAGCAAAATCCA
 AAGTCTCTGATTTGCCAAAGAAATGATTATGATGACACATTTGTCAGATAATGATGATGAAATTTCA
 AGCGTCAGTATAAATTCGATGGTTTCTGATGAGCTCTAGTGCATCTGATGATGATTTTGAATAGATTA
 AATTACAGATGGTAAATCAACTAAATCTTTCCATTTGATGAATTTGGCTACCGACGCTGTCAAGATG
 GTCATAGAAAACCAAAGATAAGACATTTCAACCCGGGCCAGAAATGTTGATTTCTCTATTTGAATG
 GAGGATTTAGTGTGCTCTCAACCAATGTCTAAAGTTTCGTGGTAAACATTTCAAGTGGTCAATGATGATA
 GTGTTCCACCCACCCGCGGCTCAACAAGGTGAATAAAAAACCATTTGGAATGATAAGACGAATTTCC
 CTCCACCGAAGTGGATCAAAAAAGAAAAGGTTCAATTTTTTGAAGAACTTTCTTGGGGATCCAAA
 AAACATTTGAAAAATTAATAAAAAACCGCGCCACTAATACCAGCATCAACAAACAAATTACCAGTCTGT
 CTGAATCAAAAGAGGAGAAACCAAAAAAGTTCAATTTTTCAGATGGTTTTCGTCACTTAATACCTCAT
 CTGCTGCTGCTATTCTTCAACATAATTTCAACACCAATTTTACCTTAACATGAAATGTCTACTGCTTTATTTG
 CTTTATTTGAATTTCTTTGGTCTAAATTTTGGTTTGAAGATTTTACGGAATGATCAAGTTGGATTTATA
 TTACTGGTCTATTCTTCAACATAATTTCTTTAAATTTAAAGAGTTGTAATAATTTAGAAATTAAGATA
 ATCAAAGAGATTTTAATCAAAAATCAGAAATTTGTTTGTGTTAGAGTGAAGAGATCTAAAGTTTACAA
 CTGATACTTTATTTTGTGAATTTGAAGAGGCTTACTCAAGAGAGGTTGTTAGATAAATAA

YDR507C_homolog 1349aa (SEQ ID NO 336)
 MPHSPQPSISSSIMSQSNHNHPKQIPGWLKGLTGRGATGRVLLATHQTTGQKAIVKVVSXSELQD
 EETEKNGDGLPYGIEREIIIMKLLTHPNVRLYDVWETSALYLVLEYVEGGEFLDLLVERGPLPE
 VEAIKYFRQIILGTAYCHAIGICHRLKLPENLLLSQLNVKLADFGMALESNGKLLTSCGSPHY

FIG. 2 - 20

TCGCATACACCATAAATCCCATAGAAAACGTGCAAAATGCTCTGACGCCGAAGAAAAACATTTCT
 ACTAAAATCAACGAAGCTATAACCCCGAATCCGAAAAGTCTACCTTGGAAAAGGGCAAGGAACAA
 GTCACCAATACCCCTTGACAAAGCTGTTGGCTCAAAATGTTCCAGATAACCAAAAATCTTTCACTCAA
 ACTGTTGCAGACAGCTGCAACAAGGTTCCGATAAATGCTAAAGCTGATTTGAAGAAAACAAATCCGAA
 CAAGCAGAGGGCGAACAAGAACCCCTTGCTGAAAACAGCTCAAGAATATGTCGAGGTTGCCAAAACGT
 AAATTGAAAAGGCTGCTGAATACGTGA

YFL014W_homolog_1 106aa (SEQ ID NO 340)
 MSDAGRKNISTKINEAITPESEKSTLEKGEQVSTLTKAVGSNVPDNQKSFQTVDASVQGGSDN
 AKADLLKQSEQAEGEQRPLSKQLKNMSRLPKSKLERSSNT

YFL014W_homolog_2 884bp public: 1..884; CDS: 501..881 (SEQ ID NO 341)
 CCTTCTCCTGTGAAAAAGTTTCGAGATGTAACGTTTCCGAGTAATAGAGAGCCAGAAATCCATTTTTG
 TGTACTACAGACAAAATTCAGAAGTTTCAACTGCTGCATATCGCCTAAATGACCTGTAGCATTCGTC
 CAAATTTGAGACCCCTCAATTTACATTTTGTCAAAAAAATTGGTCCCTAGTGTGTGCTATCGATAACGAA
 GGTGAAGGCAGTTTAGCTTGGAGGCATTTAGAGAACTTAGTTACATCTCATCTCCGTTTCGAGAA
 ATCGTTGATTTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCGAGCACCACAGCAATATAGC
 AATCAATAAATAAATTGCCCGCGGTTGACAGTGATATCTTCGAGGAATGGCAACCTTTGCCCCCC
 TCTCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATCTTTGAATCTTGTGTTTT
 TTTTCGACAAACACCAATAAATCCCATAGAAAACGTGCAAAATGCTGACGCCGGAAGAAAAACATTT
 CTACTAAAAATCAACGAAGCTATAACCCCGAATCCGAAAAGTCTACCTTGGAAAAGGCCAAGGAA
 AAGTCACCAAGTACCTTTGACAAAGCTGTGGCTCAAAATGTTCCAGATAACCAAAAATCTTTCACTC
 AAATCTGTTGCAGACACACTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAAATCCG
 AACAGCAGAGGGCGAAGCAAGAACCCCTTGCTGAAAACAGCTCAAGAATATGTCGAGGTTGCCAAAA
 CTGAAATTTGAAAAGGCTGCTGAATACGTGAGTGGAGTTGTACCAGGTGCTACCGAAGGTGCCAAAA
 CCGCGCTGATAGTACTAAAAAATAG

YFL014W_homolog_2 127aa (SEQ ID NO 342)
 MSDAGRKNISTKINEAITPESEKSTLEKGEQVSTLTKAVGSNVPDNQKSFQTVDANVQGGSDN
 AKADLLKQSEQAEGEAKTLAETAQYEVVAKTEIGKAEYVSGVVTGATEGAKTGADSTKK

YGL011C_homolog 1244bp PathoSeq: 1..1244; CDS: 501..1241 (SEQ ID NO 343)
 GAAGGGCAGCATATGAAATCGACTCACTTCAGGATTATAATGGTATGAAACGTTGTACTTGTATT
 TAGTGGCCAGGATGATTAGGATCATATATTGGGGTGTTTTCTCGAGTCTGGTATCGGTTGTAAAGC
 TATCTGTTTCACTTATCAGTATCGTCAATTTATATTAACTACTTTTCTCCTATGGTTATATATGGT
 AAACAAAAGAAACAAATATAAATAGAAAGAAAGTATAGTTTGAATAATGCTTAAAGTAAACAAAG
 AATGAAAGAATGTTGAATGAAAGAAAAAATAATGAAAGTGAGTGGCAGATATGTAGAAAAA
 TGTCAAATGTTTGAATTTTACCATTGAGTAGTTGTGTACTGTAGGAGGAAGAAACCAAGAA
 AGAAAGAGAGAAAGAAAAATTTCCGCCACTACAAATATCAACAAGTTTCAATATAGTAATATAATCC
 CAATTTGATCATTTACTTTATTCACACAAATTCATAAACAATGTCCAATTCAGCAGGTTTGTATAGAC
 ATATCAATATTTTTTCTCCTGAAGGTAGATTATACCAAGTAGAATATGCTTTTAAAGCTATCAAT
 CAGCAAAATATCACCAGTTTAGGAATCAGAGGTCAAGATTCTGCGGTTATTTATCATCAAAAAGAAGA
 TCCAGATAAGTTTATTAGATCCTAAAACCGTGTCAATATTTTAAAAATCACTCCTGATATAGGAA
 TGGTTGCCACTGGATCAATTGCTGATGCTAGAGCTCAAGCCATGAGAGCAAGATCTGAAGCTACAG
 AATTAGATATAAATATGGTTACGAAATCGCGGTGGAAAAGTTTATCAAGAAAGAAATGGCGAATATAT
 CTCAATTTGATATCTCAAAGAGCTTATATGAGACCAATTTGGGTGTTGCTTTAACTTTTATTTCAAGTTG
 ATTTTGTCTGATGAAGGTGAGAGGTCCACAAATTTTAAATGTGATCCTGCTGGATATTTTCACTGGGG
 TGAAGCCGCTGGCCACTGGTCCAAAAACAAGAAAGCAACGACTTTTATAGAGAAAAAATTCAAAA
 AAACCGATGCTGTTAAAGAGGATTGGCAAAAAACTGTTGAATTTGCAATAATTTGCTGTGAGTTCTG
 TGATTGGAATGCAATTCAGAAAAATGATATTGAAATTTGGTGTGGCACTGAAGGAGCAATTTAGAA
 TTTTGACACCAGAAGAAATAGACGAAAAGATTGATTTCAATAGCTGAACAAAGATTAG

FIG. 2 - 22

YGL011C_homolog 247aa (SEQ ID NO 344)
MSNSAGFDRHITIPSPGRIYQVEYAFKAINSANITSLGITGQDSAVIISQKKIPDKLLDPKTVSY
IFKTIIPSTGMVATGISADARAQAMRARSEATEFRKYGYEMPVESLSRRMANISQLYTQRAYMRFL
GVALTFIQVDFADEGRGPQIFKCDPAGYFTGVKAVATGPKQBEATTYLEKKFKKTDVKGWDQKVT
EPAITALLSSVIGTEFRKNDIEIGVATEGEFRILTPPEIDERLISIAEQD

YGL031C_YGR148C_homolog 968bp PathoSeq: 1..968; CDS: 501..965 (SEQ ID NO 345)
CATTGTAGGTACACCTGTTTTGCTCAATGTACACACACGACCAGCAGTAGGAAAAAACA
AATTTAAATGAAAAATCATTTTCGTTCAATATTAAGCTTCTTAAGATACCAACCAATTAATGTG
TGTGACATACCATATAAATAAGCTACAAATGGGGATAACTATGTATTTTAAATGATAAATGAATGGA
AGACCCAGAAATGTAAATGTTATAAGATAGTATTATATTGAAAACACCTTAAAAAATCAACCA
CCCATCTAACCGTCGAATTGGAAATGTCAATTTAGTTAGCATCGAAAATCAACAAAGACATGGGGA
ATCATTTACATATAAAATAATGAGAGAGAAATACAACTGCTACGTTATGTTTTGTTTCATTATGTC
TTGTTTCATTATGCTCTGTTTCATTATGTCAAAAAATCTATAGTTACCTACCTCTACATCAATTTAG
GTCTGAAATACATAACATTTTATTTATTTATAGTAAAAATGAAGATTGAAGTTGACTCTCTTTTCAG
GTTCTAAAAATCTACCCAGGTAGAGGTACTTTATTTGTCAGAGGTGACTCTAAAAATTTTGTAGATTCC
AATCCTCAAAATCTGCTTCTTTATTTCCAAACAAAGAAAGAACCCAAAGAAATTTCTTGGACGTGTT
TGTAACGAGAGACACCAAAAAAGGTATTCTGAAGAAGCTGCTAAAAAGAGAACACAGAAAGACCG
TCAAGCACCAAAAGAGCTATTGTGCGGTGCTTCTTTGGAATTGATCAAGAAAGAAAGAGTCAAAAC
CATCTGACAGAAAAAGCTGCTAGAGACTCTAAATTTAGCTAAAGACAAAGAGCTAAAAAAGCTGCTA
AAGCTGCGCAAAAAGCTGAAAAAGGCTAAGGCTGTTGCTTCTGTTGCTTCTGTTGTTCTTAAACAAC
AAGCTTAAAGGTTCTTTCCAAAAAGTTAAAGCTACCTACCTCCGTTAA

YGL031C_YGR148C_homolog 155aa (SEQ ID NO 346)
MKIEVDSFGSGSKIYFGRGLTFVRGDSKIFRFQSSKSASLFFQORKNPRRISWTVLYRRHHKIGISEE
AAKRRTRKTVKHQRAIVGASLELIKERRSQKPSDRKAARDSKLAKDKEAKKAARAKAEKAKAVA
SGASVVSKQQAQKSGFQKVKATSR

YGL043W_homolog 1418bp public: 1..436, PathoSeq: 437..1418; CDS: 501..1415 (SEQ ID NO 347)
AATCTACCATTAGGCAATGTCATATAATTAGATTACGAACAGCTGATGACGAGTTTCATTATCT
CCATAATTTTAAATGGGCATACCTTTGGATTTCACCTGTTAAATTCATCAATAATAACTTCACATCT
AATACCTGCTGCCAAGCTGATCTTGCAATATCCCGCACCTGTTCTTCAGTGTAATCAAAATGGAAATTTA
CCTATTGAAAACACAAGTGCTTTTACTATCCATATTTAGTTTGAAGCTGCCTAGTTTTCCTGATTCTT
GGTAACAAAAAATCTATAATTATTTAACAAATTTATCGATAGAATCTCTTCCAAAAGTCAACCAATTT
CGATACATTTTTCCTATGAGATGTTTTCCTCCCTTTGCTCTTAACTAATGTATTTGGGTACACT
AGCTGAACCTACCAAGTTTCAGTTCAGTCTAAAAAATTTTATTTATTTGTTGTTTGTATTATACCC
TTTGATATATTTACTAATATTTATCTTACCTTTTCATCATGGATACAAAGGAAATTAAGATCTACCG
TATCTAATCTTGAAAAAGCAGATAGATGACACCAACATTTTAAAGTTGTTTGAATATCTTGAATGATG
GGGTAAACCATCCGAAAAATCTTGAGAGAAACCAAGTAGGTGATGCTGTCACAAATTCAGAA
GTACAGCAGGTGCCGAAATCAACGGTTTAGTTAAAAAATGATCAGAAATTTGAGAGATGCCGTGTC
AAGCGGAAAAAGAACCAAAAAAGAGTTAGCAATAGCAGCTGGAACAGGAAACAGGAAACACCTTCAA
GCTCAGCAATTTTCGCCAATCTATCTCGGGTTCTGGAAGTACAAACCCAAACCATCAGAGTCAACCA
CACCATCGGCTGCCCGTAAAGGTCCAAAGAAATCCAAAACTGACGGTGTAAATACTCAATTATACG
AAAAATGATACAGCAATTTGAGAAATAGCTATTGAAATCGAGGCTGAAGTATACAAAGAGCGAATACCTGA
AAGTAGGTGACAGTTTATAGAAATAGGTTTAAAGAGCTTTACCATGAATTTTCGAAATTAAGAAAAAC
CAGAATTAAGAGAAAGACTTATCTGAAACAAATTTTACCTGCTGCGCTTCAATTAATACCCCTTA
ATGAAATGGCTCTCTGAGCAATTTGAAAAAGAAATTAAGAAATTTGCAACAAACAACTTTGTTGTATG
CTCAAGGTGCTACTGAAAAAGAGACAGTGACCGATAGATTCACTTGTGGCAAGTGTAAAGCACAAGA
AGGTCAGTTATTATCAATGCAACACAGATCAGCGGATGAGCCTTTAACTACATTTTGTACTTGTG
AAAAATTTGGGCAATAGATGGAAGTTTTCATAA

YGL043W_homolog 305aa (SEQ ID NO 348)

MDTKERISTVSNLEKAVDDTTILKLLNINLNDGVKPKSEKLLRETKVGVAVNKFRRSHSDAEINGLVKK
MIRNWRDAVQAEKNNKKLAIAGTGTGTFSSSAISFSSSGSGSTTPKPSSESTTPSAARKGPRNPK
TDGVNTQLYENDTRNASVSALYTSLAVDRDDSPKHILRIATIEIEAEVYKSEYSKVSYSRNLRLSF
TMNLRNKNPELRERILSKQILPAAFIKMTPNEMAEALKKIEKLHKQNLFDAQGATEKRAVTD
FTCGCKRKKHVSYQMQRSADEPLTFTCTCENCGRNWKFS

YGL103W_homolog 1301bp public: 1..688, PathoSeq: 689..1301; exon
1: 501..548, intron 1: 549..899, exon 2: 900..1298 (SEQ ID NO 349)
ACATTATTTGTTGGCTATACCTTTCCCAAGTTTAAAGGAATGGTTAGGCGGGTCAGTCTACTTTATT
TTTACTGTAAATGTGTTTGCCAGTGTATGGTTTATCAAGACTAAAGTTCTGTAGACAAAGGTAAG
CATTCGTACCAAGGAAGTCTGGAATTAACCGGTAGTTACTTCCAGTATATATGGTGTTCATGTGTT
TTGTGTCTAAAGTTGGTTAGGGCTAAAGCCCTTAATCAATAGTAGTGTACTTTGTTTGAAGAAAAA
AATACATGCAAAATACTGCATATTAGAAATTATAAGGGAATGAAATGAAAAAAGAAATAATTT
TGTAGATCGCATAGTGTGAGCGCCACACACACAACTTTGTAGTGCTACAGTTTCTCTCTTTC
CCATAGCTCTCCGAGTCGCACGCTTGACAAAAAGTTAATTAGAAATAGAAAAATTTCTCATTTCTT
TTGAGTTTTCCACCAATACTAACTAGTAATAACCAACATGCCTACTAGATTAACTAAAAACAGAA
AACACAGAGGTAATGTTTCTGTTATGTACAAATTTTCACTAAAGTTTAAACGGATGAAGAGTATTGA
ATGTTTCAAGGACATATGGAGATTTAGAGAAAAACATGGAAAACTAATCGAAAAATGAATATGAATGG
AAAAATTTTAACTGAATATCAGAATTAGACACACACAGATCCAGAGTCAATTTACATGAA
TCATACACAAACCAAGCAATGAATATGAGTAGTTTGGGAAACCAACATACAGAGTATTTTTCAGAA
CAATCAAGTTTATCATTTACAGAAAGACAGTCCATCAATATGTCTCCAAAAATACTCTTTGAAGTCAAT
TAAAGTCAAAATGAACGAATTTACTAACTTATTTTCTTTTACGCGGTAAAGGGTAGAATTTGGTAAAC
ACAGAAAGCACCAGGTTGTAGAGGTAAAGCTGGTGGTCAACATCATCAGAACCACTTGGATA
AATACCATCCAGGTACTTCCGTAAAAGTTGGTATGAGATACCTCCACAAACCAACCACTTCT
GGAGACCAGAAAACTCACTTGGACAAATTTGGTGGTCTTTGGTGTCTGAAAAAGAAAGACGAATCT
TGAGCAATCATCTGCTTCTCTCTCTCCAGTCTATCGACACCTTGGCTACGGTTACGGTAAAGTTT
TCGGTTAAAGGTAGATTACCAGAAAGTTCCAGTCAATTTGTCAAAGCCAGATTTGTTTCTTAATTAGCTG
AAGAAAAATCAGAGCTGTGGTGGTGTGTCGAATTAGTTGCTTAA

YGL103W_homolog 149aa (SEQ ID NO 350)

MPRLTKRKHRGNVSAGKGRIGKRRKHPGGRGKAGGQHHRTNLDKYHPGYFGKVGMRYPFHQQN
HFWRPEINLDKLWTLVDSSEKKDEYLSKSSASAAFPVIDTLAHGYKVLGKRLPEVFPVIVKARFVSK
LAEKIRAVGGVVLEVA

YGL147C_homolog 423bp PathoSeq: 1..423; CDS: <1..420 (SEQ ID NO 351)

GCTATCAAAATCACTGTTCACAATGGTGACAGAAAAACAGTTGCTGCTTTAAGAACTGTCAAACTCT
TTGATTGCTAACTGTATCACTGGTGCTACTAAAGGTTACAATACAAGATGAGATTGTTTATGCG
CATTTCCCAATTAACTGTTAACTATTATAAAAAAGATGGTCAAGATTACGTTGAAATTAGAAATTT
TTGGGTGAAAAAGAGTTAGAGAAGTTAAAAATCCATGAAGGTTGCACCATGGAATTTCTTCTACT
CAAAAGGATGAATTTGATTGTTTCTGGTAACTCTTGGAGCTGTTTCTCAAAATGCTGCTGATAT
CAACAAATCTGTCGTGTGAGAAACAGGATATCCGTAAATTTCTGGATGTTATTTATGTTTCTGAA
AGAGGTACCATTTGTTGAAGAACTCTAA

YGL147C_homolog 140aa (SEQ ID NO 352)

AIKTTVNHGDRKHVAALRTVKSILIANLITGVTKGYKYMRFVYAHFPINVNIIKKDQDQDYVEIRNF
LGEKRVREVIHGEVMTSEISTQKDELIVSGNSLEAVSQNAADIQICRVNRNKDIRKFLDLGIYVSE
RGTIIVEI

YGL213C_homolog 1655bp PathoSeq: 1..1655; CDS: 501..1652 (SEQ ID NO 353)

GATGATCGCTAAACAAGGTACCCGATTATTATCATCAACAAAGAGCTACTTATAGAAATGATTCTC
AACCTTAAATAGCTTGTAGTTTATTGATTGGGACTAATTGTGTCAGCATGCAACAAATATGCCAGT

FIG. 2 - 24

TGCATAGAAATAAATCGGTATTATTACGGCATACCAATCGATTGTAGGGGGTGAAGCTGGTGCTAA
 TTCFGGGGTGTGTGCATTTCCAGTCCATAAACGTTGAAACACAAAATTCGTGTGTAATTTGGTGAAAT
 GAAATGATCAGATGATCTTATGGGTGGCATTTGAAGTGTGTCGTCAGATGATTTTCTAGGATA
 ATGAAGGTAACTACGAACCTTATGAGTTTTCATTCTCTCGATGTTTTTTTTTCTCTGTTTTCTT
 TTGTCGTTGTAGCAAGAAGAAAAAAGTGCTTCCACAGTCTTGGACTCAATTTTCCACCCT
 CCACAAATCAATTTCAATTAACATATCAATAATCCAATATGGGTAAACAGATATATATACCGCTCA
 GTGCATCTCAGGCTCATAGCTGGATATCTTGGGTAGCTATTACCAATAAGTTCAGCTGATCCG
 TGTCTAGTGTGATATGCGAAATTTTGGGACAAACGAAGACGAAGTTTCATCTGCCATAAGAAT
 TTGTCCAACTGGTATTATTAGATAAAAGCGGAATCCATGCGGTGGCTGCTACGAAAAATGTTTTGCG
 CAAGCTCTCAATTGAAAGTGACATTATTAGCAATTGTCATGTTTCAATGGATCTATCATCTTCAGAT
 ATTTATATCAATGATGACTTTTCAACTATCGAAAGTCTAACTGATGATAAAAAATCAATTTGAAAGCA
 ATTTGTTGGACCCCTGGCTTTTATCGCGATCCGAATCCAAACAAAGCATATTTTATTAACAACCGGA
 CCAATGGCAGTACAGAGGTTTCATTTATTGAATATTTGTTGATGAAAAATGAGAAGGCTGTAATCACAT
 TTGAAAAGTTTGGGCAATTAAAGGAAACTCTTCTCTTCCCAAATCTTTGGCTATATGTGCCAA
 CAGAGATAAAAAATGTGCTGTGGGTACATCAATGGTGATGCTTGTGTTATATGACTTTGTTAGCT
 TGAATTTGATATACACATTTTCGTTGAGTGATTTGGTGACCAGTAGAAATTTCCCAATCGACGCTTA
 TACCTAGGTTGTTGGCATTTTCCCTGCTGGAACCTTGTGGCTGTGGCAAGAGCAATCAAGCTG
 CTGGCTCAATTACATATACGACGTTGACATGGTGAGAATGTGGGCTCTTTGGCCACACCTCAC
 ACTCGGCCAAATCTGTGTTGGTGGGTTTGCACATCAAGGCTGGATTTTGGGGTTGAGTTTTGATG
 AGGAAGGTAAAGCATTTGGCTAGTTTGGGATTTGACAAATGCATAAGAGCTTCGGAATTTAGAAAACAA
 GCGAAAGGGGAAGCAACAAATAGTATATCTATACAGACTTAGATGACTACATATAATGATCAAG
 ACGAGAGTGTGCTCTCTGGTGTGCTTTTATTAAGAAAGGGGTTAGAGGTGGCTCTGGTGTGACAA
 GCAATGAAGGATTATGTGTGCGTAGTTTCGATAGAGGAATAAGATGGTACCGAGAGGACGAGGAA
 TATAG

YGL213C_homolog 384aa (SEQ ID NO 354)

MGKQYISTVSASQAHKSDILGVAITNKFTVSVSDGYAKFWDNKQDEVHSPKEFVQSVFIDKSGI
 AVAAENVLPSSTLKVTLALAFACFNGLIFRYIINDDFSTIESLTDIKSFESNCWTGPFYRDPES
 KQDYFITTKNGTTEVHLLNVIDENEKAVITFEKFGQLKGNSSSPFNLSAICPTENKKCAVGYING
 DVLLYDFVSLKLIYTFRSDLVTSRNSQSTSIPLVAFSPGGTLLAVARDNQAAQSITLYDVEHGE
 NVGSLATPSHSKSVVGGFAHQGWILGLSFDEEGKHLASCGFDKCI RVWNLETSSEREATISISISD
 LDDTTHNDQDESASGVAFIKKGVRRGSGSDSNEGLCVVSFDRGIRWYREAGGI

YGR085C_YPR102C_homolog 1418bp public: 1..1418; exon 1: 501..503,
 intron 1: 504..896, exon 2: 897..1415 (SEQ ID NO 355)

ATAGAGATGCTTATCTCGTGGTTCAGTTAATTTATATCATGTCACTGAACAAAGTTGGACTTATC
 ATGGTAATTTCAATGTCTGGTGATCTCTTTTGGGAAGTTAAAGAAAAGGAACAAATTTGTAAGT
 TAGATGATGATAAAGTAAAGTGTGATGTTATAAAAAAGAAATGCAATTCAATATATAAATTTACAAATCT
 GATAATAAATCAGTAACTATATATGCCAACAAATGGAAGTATCTGTGTCAGCTGATTAAGGCTCA
 AAAGCCCTTAACAGGTTCACAGTGATGTTGATTATTTATCCCTGCACACATTTGAGTTTTTTTTCTA
 TGGTGAAAAATTTAGTGAGACGATGTTGTTCGCATTTTACCACACACTTCACTCAGGTGTGTC
 CATACTAACATCTCTCACACTATACACAAAAAATCTTTGTTTGAAGAAATTTTGAAGGTGAT
 GTTTTCTCAATGATATATCCATACAATAACTGCCAAAGATGGTATGTTCAAGTGTTTAAAGAGATC
 GAAATGTTTGTGTTTAAATGGGAAGTATATCAATGAGAAAAATGAGAAAAATAGAGATGAGACCG
 AATTAATTTGAAAGAGTTTCTTTTGGGGAATGGGTTCAATAAGATTTTTCAGATTTGGAATCAAAA
 TTATGTGAGATGTGAAGAGAGTAAATATAACAAGAAAGTTCAAATCTGTTCAAGAAATTTATGTAAAT
 ACAACGATTTATCAATTACAGTCAACGAATAGAAATAAAACAAAAGCCAGCATATAACAGATACCAGT
 GATTCATCCAGTGAATAATAAATGATATTCAATTAAGAACAAATATAAGACATTTTATTTATG
 GATCAACAAAACTAACTATCTTTCTTTTAAATAGTCTGACAAATCCCAAAATGTTATGCGGTG
 AATTCGATTTGAAAAATAGTTTAAACATTTGTGTTGGTGAATCCGGTGATAGATTAAACAGAG
 CCGCCAAAGTTTGAACAAATATCTGTTCAAAACCCGATTCATCTAAAGCTAGATACACTGTGCA
 GAACATTTGCGTATTAGAAGAAATGCAAAATGTCGCTCCACGTTACTGTACAGAGGTCCAAAAGCTG
 AAGAAATCTTGGAAAGAGGTTTGAAGTTAAAGAAATATCAATTAAGATCTAAAAACTCTCTGTCTA
 CCGGTAACTTTGTTTTCGTTATGATGAACATATGATTATTAGTATCAAATATGATCCATCTATTG

FIG. 2 - 25

GTATTTCACGGTATGGATTCTTCTACGTTGTTATGGGTAGAGCCGGTGCAGAGTACCAGAGAAGAAAGA
GAGCTAGATTCCCATTTGGTAACTCTCACAAAACCAAAAGAAGATACCATCCAATTGGTTCAAGA
CCAGATACGATGCTGAAGTTTGGATAAATA

YGR085C_YPR102C_homolog 174aa (SEQ ID NO 356)

MSDKSQNVMLRELRIEKLVLNLCVGESGDRLTRAARKVLEQLSGQTFVQSKARYTVRTFGIRRNEKIA
VHVTVYRGPKAETILERGLKVKEYQLRSKNFSAITNGFGFIDEHIDLGIKYDPSIGIYGMDFVVMVG
RAGARVTRRRKRSTIGNSHKTNKEDTIQWFKTRYDAEVLDK

YGR118W_YPR132W_homolog 919bp PathoSeq: 1..919; CDS: 482..916 (SEQ ID NO 357)

TATTGCGTAATCGTTATCAATGTTTGGATTGTTGCAACGCTGGGTTGTGTATATGCGAGAAAAATG
AGTAATTTGTTTAAAAATAATCGATGCAGCAGTCTGCCACTAAAATAAAATGTCATATTGCAT
GATAAGGATTATCAATACTGTTAGGCTCTATAGCCCTAACTTTAATCATTTACACGTGATACAAA
AAGTTGTTTGTATCCCGCAGCACTATGAGTACGCACTCACTAATTATAGCCTGAAAAAAAATTTTC
CACATAGTAAAGGGGATTTGTATGGTGGTGCCTGCCTAAGACGTCTGCATACATTTTCTAAAGT
CACACTGATATAGGGATGTTGTGGTAGTGATTGTGTGTTCCACCAAAATAACTTTGCGGACACTCT
CATATACATCAATTTTCTTCAAAAAATTTTCTTCTTCTACATTTTCTCAAGAAATCTCTCTTTA
CAATTCAACAACATCAATCATGGGTAAAGGTAAACCAAGAGGGCTTAACCTCTGCTAGAAAAATTAAG
AGTTCCAGAGAGAAACACAGATGGGCTGATCAAGCTTATAAAGCTAGATTATTAGGTACCGCTTT
CAAACTCTCTCCATTTGGTGGTTCATCTCACGCCAAAGGTATCGCTTTTGGAAAAAATTTGGTATTGA
ATCTAAACAACCAAACTCTGCTATCAGAAAAATGTGTGAGAGTCCAATTAATCAAAAACGGTAAGAA
AGTCACTGCTTTGTTTCCAAACGATGGTGTGTTGAACITTTGTTGACGAAAATGACGAAGCTCTGTT
GGCTGCTTTTCCGTAGAAAGGTTAAAGCTAAGGGGGATATCCAGGGGTAGATTCAAGGTTGTTAA
AGTTTCCGGTGTCTCTTATTAGCTTTATGGAAAGAAAGAAAGAAAGCAAGATCATAG

YGR118W_YPR132W_homolog 145aa (SEQ ID NO 358)

MKGKPRGLNSARKLRVHRRNNRWADQAYKARLLGTAFKSSPFGGSSHAKGIVLEKIGIESKQPN
AIRKCVRVQLIKNGKVTAFVFNDCGLNFVDENDEVLLAGFRRGKAKGIDIPVRFKVKVSGVSL
LALWKEKKEKPRS

YGR277C_homolog 1164bp PathoSeq: 1..724, public: 724..1164; CDS: 196..1161 (SEQ ID NO 359)

AATTCATTGTATCTCTAAGAAGATGAACAGGCCCTTGAATGGGAGGGGTGGTTCGACTTCCACGAA
ATGTGGTTGGAAAAATCTGAGTCTCAAAAAAGGTTCTCTCGTAAAAAGGCCAGAGAAAGAAAAACC
ACCAAAACCCCAACCAACCTAACCTTTTCTTCCATCCATCTCTTTCTTACTTTGCGAAATG
TTGAATCCAGTTTATTCATTAAAGATCCTATAAAATACGATTATTCACAATTTATATATCTTTA
CTCCGGAATTTCAATTAATGTAAATCGTATTGATTAGTTATATCTTTGTCAAATCACCGCAATCAAA
CAATTGAATGAAATTTATGTTTATTTATCAATTAATTCGTAATCATAAGAATAATGGAGATCT
GATGGAGATACCGACAGTTTGCTTATGTTTGATTATCGATTGAAATTAATATATTTATTTAATTTA
TCAACAAAAAATTTGAATCAATTTATGTTTAAATTAATTTGAATTCATGATATATTTGCGGAAGGTAT
AATGATAACAGTCACTTGTGTCATCTTTGCCATTTGTCAATTAACACAAATATCAAACTTTGAAAT
CCAACATCCAATCAAGAGCAAAATAGTAGTAGTGTCTATAATGATGAGGATGATAAAATTAATCT
AGTCGGAATATCAACAAATTTAAACACTGCTGTAGGTGGAACATTTGATCATTTACATGATGGT
CATAAAAATTTATATCAATGGCAATTTTCTTAACTTCAAAATAATTAATTTATTTGGTATTAATCTGT
TCTAATTTATTAATTAATAAAAAATTTAAATCTCAATTAACAACTTTTATATCAAGACAAAAATTTA
GTTATTCAATTCATAAAATTTATTTATTATTGAGTGAACAGTGTATTTTCTTGAATTTATGAA
ATTAATGATGTTTGTGGTCCAATGGTTATATTAATGATATTGATAATTTAAATTAATCTCAAGAA
ACTAAATCTGGTGGGAAATTTGTTAAACAAATTTGTAAGATCATGGATTAAATTTATTAGATATT
ACAATATTAAAGTGATTGGTGGGAATTTGAGAAAAATTCATGGAAAGGTAATTAAGTTCAA
CTGATATTAGAGAACAAAGATAATATCGATTATTAATCAATA

FIG. 2 - 26

AAACATCATCCAGATAAAAAATCCGCTAGTGGTGGATTAGAAAAACGATGGATTTTTCAAAATATTTC
 AAAAAGCCCTTTGAAGTTATGTTGGACCCAGTCAAGAGAAGACAATACGATTCTATTGATGTTGAAA
 ATGATGCCAAAACCAACAGCTCCAAAATCCAAATACGATTCTTTGAAGCTTGGGGTCCAGTATTG
 AAAGTGGAAGCAAGATTCTTCTACATAAACCAACAGTTCATTGTTGGGAAATTTAGAAAGCACCAAG
 AAGAAGCTTGATGCTTTCTACAGTTCTTGGGGAAGATTGACTCTTGGGAAGACTTTTGAATTCAAAG
 ATGAAGATGTTCCAGATGACACTGCCAACAGAGATCACAACCGTTATATTGAACGTAAGAAATATTG
 CCCAACAGAAAGAAATTTGAAGCAAGAAGATCACAAGAGATTATCGAATTGGTCGAAAGAGCTCATG
 CTGAAGATCCCAAGAAATTAATTTGTTTCAAGAAAAAGGCCAAGAAAAAGAGGCTGCTAAGAAATGGG
 AAAAAGATCTGGATCAAGAAAAAGCTGCTGAAGAGGCTGCTGCCAAAAAGGCTGCTGAAGAGGCCG
 CTGCTAAGAAAGCCGCCAAGAAAGCCGCCGCTTTGAAGGCCAATCTTAAAAAAGCTTAAAGAAAGCTG
 CTAAGCTTGCTTAAAAAGAAAAAAGAGAAACATCAGAGCTGCTGTTAAAGACAATAATTACTTTG
 GTGACTCAGCTAAATCTGCCGACATTGATGCTGATGCTGATTTGTTAATCGAAAAATTCGACGATG
 TCAAAATTAGGTGAAGTTGCTGATAAAGTTAAAGATGCTGATGCTGCTTCAAGTGAATCTACTTTG
 TTGAAGTTGCAAGGAATTTGGTTGGAGCTGGTTCTTTAGATGCTTCCTATTGGAATATTTTAACT
 AGATTTTCTTTTCTAGGAAAAATAATATATATAGAATGAAACTATCAAAAACAATTATACAGAAG
 CTGAACCTCAACAGACTAAACAGCAAG

YGR285C_homolog 427aa (SEQ ID NO 364)

MSIVLPSTGTTDGFKAVSKYSAPVRRPIEPVGRYFLAHASRTLRLGHTWSEFEKLEAEKNVKQIEVNE
 DEDLDGEDEQSEELLEHDPREWKTANLYAVLGLSHLRSKATEDIQIRRAHRKQVLKHHDPDKKSASGGL
 ENDGPFKIIQKAFEVMLDPVKRRQYDSIDVENDPKPPAPKSKYDFFFAWGPVFSEEARFSTKQVVP
 LIGNLESTKEEVDAFYSFWRGFDQWKTTFEFKDEDVDDTANRDHKRYIERKNILOOKEIEARRSQE
 IIELVERAHAEDEPRIKLFKEKAKKEKAKKWESEGRKAEEAAAKAAEEAAAKAAEEAAALK
 ANSKRAKEAAKAAKKNRNIRAAVKDNNYFGDSAKSADIDADVLLIEKFDDVLKLEVDKVKDA
 DAASVKSTFVEVAKELVAGSLDASLYLYFN

YHR021C_homolog 1178bp public: 1..537/917..1178, PathoSeq:

538..916; exon 1: 501..503, intron 1: 504..932, exon 2: 933..1175
 (SEQ ID NO 365)

TTTCATTGTGAGGCATTGTGTAGAATGTGGACTGTAGGAAGGTGCAAAAATATATATCCAATAAGTC
 ACATCTCAAAATGGTAGTAGAAGAAATCAACCTTGGGACAGATATTCTCTGCTTAAAAATGAGTTTAC
 TGATCAAAATAAAATATTGGCTCAACCATTTGAAAAGCTATTCTTGACACTTTTTCAGTATTGATTTT
 TGGTTGTTTTCACAATTGAAAAAAAATGTTGAGCCCTAATAGCCCTAATTGTTTGCACGTGATGT
 ATTGCTTTGAGTGAAAAAGGTGTACATTGTTACACACACAAAAAATAAATACTTCTCCCCCA
 ATATGCTGCGTATAGTGAGAAATCTTCTTCTCTTGCCTACTATCGCATTTTTTTTTTGGTAA
 CTCACGAAACCTAATTGGAAAGAGAAAAAGAAAAAATAAATACTTCTCCCCCA
 AGTTTGTGAATATACATATTAGAGAAACAGTTAACAAATGGTATGTTTCAATTAGATTATACCATGAG
 TTATGGAGGATATTCTCGGATGATCAGAAATATCATAATATAGGAGTATATTTTATCGGAATC
 AAGATATAAATGAATTGAAATAAAATTTGAATAAGAGGAAGCATAGAATAACGGAATGATGATTAA
 CATCAGAAAAATTTGACTACCCGAATTAATGAATTAGGATCAACATATTAATATCAACTACTACTT
 TAAAAGAACAGGAAATGAGAGAAGAATCAGCATGAAAGTTTACCACCTCAGAAAACGTCAGAAAGTAA
 TATACTTTTGGTGTGGATCCATGTTGTTATTACTGAAATCATCGAAACGAATATAACCCCTCTTTT
 CCACATTGACATACCTCAGACACAATTTTCAAATAAACATGTAACTAATTAATTTTCTTTT
 TCGTATAGGCTTTTGTGTTCAAGATTATTATACATCCATCTCCAGCCATGAAGCTTAAACACAAAT
 TGAAAATTTTGTGTTCAACAAACCAAGATCTTCTTTTGTGAGCGTTAAATGTCAAGAGTGCTTTAATA
 TCACCACGTGTTTGTGTTCAAGCTCAAACTGCTGCTCAGTTGTGACTCTTGTGTTTGTGTTGTTGTA
 CCCCACCTGGTGGTAAAGCTAAATTGACTGAAGGTTGTTTCATTGAGAGAAAGTAA

YHR021C_homolog 82aa (SEQ ID NO 366)

MVLVDLLHSPATEAKQHKLKTLVQQPRSFMDVKQCGCLNITTVFSHAQTAVTCDSCTVLCTP
 TGGKAKLTGECSPRRK

FIG. 2 - 28

YHR141C_YNL162W_homolog 1179bp PathoSeq: 1..1179; exon 1: 501..503, intron 1: 504..861, exon 2: 862..1176 (SEQ ID NO 367)
 501..503, intron 1: 504..861, exon 2: 862..1176 (SEQ ID NO 367)
 TTTATATGTGTTTGTGTTCTCATGTATAGTAATTATTTAATTTGATGTCCATTATTCATGTAATT
 GTGATGTATTTTGTGTTGGTCTCTCTTTCGTGTTTTCATATTTTCGAGCTGGTCCGATCATACAA
 ATTTGGAAGGAGCTACCAAGCAGAAATGATAGCAAAAAAAAAACAGGAGACTTTTGGAAATTTCTTG
 TTTTAGGCGTTAGCCCTAATGCCTGTATATAATTGATTGATGCTTTTAAATTTGTGGGGTCAAAA
 ACAGAAAGCGAAAAAAGAGCTGGAAAGTGTGATTAAACAACACGAGGGAAGAAAAAATCTTAA
 TTAGGTGAACAAAAATTAATGTGTGAGCGGTGACATGCACAAATTTTCAATTGGTTATTTCACGCA
 CTAACAAACTCAACCTCCATTGTGAGAAAAAGAGATTTTCTTTGAAAAAATTTTACATACATATC
 TTAGTTCACATAGTAACCTTCGAAGACAACATAGACAAGATGGGTATGTTCCAGTATAGCAATATTC
 AACAATGAGATACAGATATTTCTCCAATACAAAGAGATTAAATGGTGTGTTTGTATAGAGTGTAAAG
 CCATGTGTTTAAATAGGAATGATTGTTCAGGGGATAAGATGAAAAGTGGAAATTTGTCCAAAGCAAA
 TGAAACGAATTTTCTGGGATAGCGTTCACAACTCAACCTATCCAGGTTTCTTATGCAATTTAAG
 AAAACAAGTCAATATTATCAAGATGGAGTTTATAAGGAGAGATATTGAAACATCAAAATTTGTGA
 AAGAAATAGCCAATATTGGCACCATTTCTCTGTGATCATAGAAATCTAACAACTCTCTTGTGTGTT
 ATAGTTAACGTTCCAAAACTAGAAGACCTACTGTAAAGTAAAGAAATGCCGTAAACATACCCAA
 CACAAAGTTACCAAATACAAAGCTGGTAAAGCTCTCTTGTTCGCTCAAGGTAAAAAGAGATATGAC
 AGAAAACAATCCGGTTGTGGTGTCAAAACAAATTTTCCACAAGAGAACCAAGACTACCAA
 AAGTTGTGTTTGTGAGATTGGAATGTGTTGTCTGTAAAAACCAAGGCTCAATTACCATTGAAAAGATGT
 AAACATTTCGAATTGGGTGGTGACAAAAAACAAGGCTCAAGCTTTTCAATTTTAA

YHR141C_YNL162W_homolog 106aa (SEQ ID NO 368)
 MWNVFKRKYCYCKGCKRKHQHKVYQYKAGKSLFAQGGKRRYDRKQSGYGGQTKQIFHKKATTK
 KVVLRLECVVCKTKAQIPLKRCXHFELGGDKKQKQALQF

YIL112W_homolog 3583bp PathoSeq: 1..3583; CDS: 365..3580 (SEQ ID NO 369)
 GTGCGAATAATACAAGCGATCGTTTGAATAATCCAATGATTAGCTCTGATCAACGAATTCAAAAAT
 TTCCTCTCAAGGACGTAGTACAAACAGAGATGAGAAGGGGTTTGAACCTGTTTGTATTTCAGAGGAGA
 TGACGGTGCAAAAAAGATCTACCAACCAAGAGACACATAATTTTGAATGATTTCACGAAAGAGTTT
 CATTTAGTGATATCTCAAGCCAAAAATTTTCAAGGGAAAGTTCCCGTAATGTTTTCACGGGAAGCAG
 CAGGCGAAGTTCAATAATAAAAAATTGATCATCATACTAATGTGGACGTGTCAACGAAACCGGAAAA
 TATAAATAGCAGAGATAACAAAACTGAGAAGAATATGACTTTGAGTTTCAGAGTCAACCAAAACCGAG
 GTCTGAAGAAGTTAGTAAATCTTTGAAACCAACAATTTACCAAGAAAACTTCATTCACTGATTAGCTT
 AAAATCTGCCAAAACTAAGGCTAAAGAAGAAAAAGTTAACCAATCGAAAAAAGTGACAAAAACGATTAA
 TTTGAGAAGAACGAAAAACGGAAACCAATTTCAACAAAGCGAGCAACTTTTAAACGGACAAAAAGGATTA
 TAAACTGGAAACCCAAATAGTGAAGTAAATTTGAAAGCAATAATGACGACCTGAAAGCTTACAGCTGG
 CTGTGCCCTAGGACCTTAGATAAAGTAATCTGGAATAACGATTCAGATAAATCAGAAACGACTCAAC
 AAACTTGCCCGCTCAGAAATCATTTTCCCGATACATCATTTATTGTCTCAAGTTAAATGAGATGATPAC
 TGATTTTCAATTTCAATGAGTTAGCAGAGATACCGGAAGCAAGGATGGTTTCAGTTTGTGCGCAGCAA
 TGTCTGAGAACATTTGATGAGAATCAAAATATTTTCAAGAGCTGAACTGTTTATAGCAGACTTCC
 TCCACGCTCTGATGAAGGAAGAAACTTTTACGTGAACAAACAGCAGATGTAAAGAGACATTAAT
 GAAGAAACCAAAATTTGAATACTATTTTGTAGTTCCGATGAAGAGGAGGAGGAGATTCAAGAACAGGA
 TTTTCAACTCCAGAAACCGAAAAACTACCAAGAGATGACCAACTCTGATTTTTCAAAATTTCAAA
 AGCAACACAGAAATCAGTAACGATAAAACAGAAAGTAAATAGCCAGAGAGTGAAGAGAGGTTTGGCGA
 GAAAGAGAGAAATTTACCAACTAGAAGATAGATTACC AATTAAAAAAGAGAAATTCGGCTGCGAGAA
 TGCAAGACACTTTGAAACCGGTGTGAGTTTCAAAATCAGAATCTTAAGATTTCAGAACTGCAAGAAACT
 ACCTTTACAAGTTTAAACGTGATTCAAGTGGTTCGATCATTTTCAACAGAGCTTCAAGAGAGGTTAA
 TTTTGCAGATGTTCCAGATTACATAGAGAGGGGTGTGAGTGCCTTCAAGTGAAGAGGATTTCTGTGGATT
 CACATGCTTGCATGAGGCGACATTGGAAGGTGATACACAAATTTGAAATATCTCATCGAATATGG
 TGCTAATGTAAATGCGAAAGCTGTGTAAGCTGGTGTGATTCGAGACACCATTTGATCGATGACAGCTGA
 AAACAACACTCTGATTGTGTTTAAAGTGTACTAGAAAAATGATGCTGTGCTTACTGATTATTTTCAATAT
 TGATGGAATCACCGCTTTAACTAAGATTATAATGAACATGAAGGAGAGAGGATATGATGAAT
 TATTCAAGTTCTAGAAGAACCACTGCAAACTATAACAGTCGTTTACCAAGAGAAGTTTCAGTTTGT

FIG. 2 - 29

ATCAGATGCTCCTATTGGTAGTGGACCAATCATGGAGGATCCAAATGACAACTATTTTCAGAGCT
 AATTAAAGGTAAGGAATAATAAAATACGCTGCAGAGAATTCAAAAGAGAAAAACAGCAGAAATATTT
 TGTGTGCTCGTCATAATTTAGAAAGGAAAAACAGATATTTTAAATTTTACGTCTCTAGAAACGGCCACAC
 AGAAGCTTGTGTGATATTAATACATAGGCTTAAACCTACACCTTTTAAATTTGATACCCAGGTCAAGTTG
 TGGTGTACTGTCATTATTTGGCCAGTATTTGGACGCGGTCTATTTGAAGTTGTCGATTCTCTGTGTCTG
 CAAAGGTCGTGATCCATTCAGAGCAAGAAAAAAGATGGGTTGAATGCTTTAGAAATTCACCAACA
 CTCGCCACATTTTGAATTCACGGGAAGTTAGTGTAAATAGAAATTCAGGAGAGAGAGATGGGAAC
 CAAAATTTTGTCTGGTATTCCGTCAAGGCTAGTATCTCGTGCAACATCTCGTGACCTCTCTGTCTCC
 CGTATCATCAGACGAAGATGACGTAGTGGAAAGAAAAAGAAATTACAGCACACACAGAAAATAAAG
 TGCTGAAAAGAGCTGGAGGATAAAATCACGAAAAACAGTTAATGAGCATGTACGCAATCGGAAAC
 CCACGAGTCTACAGGTCGAAAACTTGAAGAAGCTCATAGCAATGAGGAAGAAGACGGAAAAACGTTGA
 ATGCTCAGACGATGAACCTAAAGAACACATCTTTTGAAGAAGTCAAAGTCTGATTGTAAATTTGAA
 ATCACAACATAGAGAATTCACCTCTGATGATCACCAACACAGTGAAAGCCATTCAGATTCTTTTGC
 AGAAAAAGAAAAATTTATCGGCAACGCCACCTGCTCTCCGCCACCAACCAACCAACCAACCTTC
 TCAAGCAGTTTCAAGGCCAAGAAGAACAAAAATCAAAGATGCTGAAGAAGCTAGATTGTGGCA
 AGAAAAAGTGAAGCTAAAAAGAGGGCTCGAAGAGAAATGTTTTTAAAGTCCGAGAAAGAGAAAA
 GGGGTTGCGACAACAGTGCACATTTAGATCATTTATCTCGGTGGATTGCGTTATTTGCAAGTTCGA
 AAACCCAAATATCTCGGCTGTGTATAAATTTTGCCTTTCTATGTATTGTAATTCGACGATTAATAA
 GTATGCTGTGATTCTCAAGTCTCCTTGATCAGCTCAACGGTTGTGACGAAGCTCTCAATACTGT
 ACAACCTCATCAGAGAGAGAAATAAATGCACTGAAAAAGCAAAATTTGGAAGCTCTTTTCAA
 GTTTATTGGTATTGATCTCAGGAATCCAAATTTGTGATCAAGAAGCTCAATAACAATGGTCAAAA
 ACAGTTTCAAAATTTTGTGCTTCATTTTGTGGAGGTAGATTGTGCTGAAGAATTTTAAAGGAAT
 TCCAGAGTACGATCAAAAAGCAAAAGATAACCAAAATGATGTTAGTTTAGAGCTTTTGAAGTGGGT
 TTCTGATTGCGTCAAGGATGATATAATAGTTGATGGAATCTGAAATGATATTGATTTCAGAA
 AATCGAAAGTTTATCTCTCATTTTGAATACTAGGAAAGACATTATTAGGACTGTCAGTACTTT
 AGCACCCCATATGTTGA

YIL112W_homolog 1072aa (SEQ ID NO 370)

MTLSSESTKPSVEEVSKSLKPTITKKTSTFDLYLSAKTKAKEEKTIEKSDKTINSEERKTEPIQQ
 SEQLLTDKDKONKSEPNSEVNLDKNDSDSKATAGCALGPDKNKTGKNDSDKSETTPKLRASEFADT
 SLLSPVNESDTPNPNELAEIPEAKDGSVVAANVSENIDENENISEAETVIADLRLDEBKLLLR
 EQTADVKRHLKKTCLNTIFSSDEEEIEIQEPDFKLQEPKLPEDDQHPDFQNSKATTEISNDKTE
 VNKPEVKEVGEKERNHQLDRLPIKKEKMRSENAKTSENGVSSEKSEKISKSKLPIYKVRDSSGR
 SLLQRACKGNFADVDQYIERGASANEKDFCGFTCLHEAALEGHTQIVKYLINGANVNKADEAG
 DSETPFLIDAAENKHLDCVKVLENDADPTIFNIDGFTALTKIYNEHEGEEGYDEIIQVLEATANY
 NSRLPREVQFVSDAPIGSGPIMEDPNDNYFAELIKGKIYKYAAENSEKTAEYFVAGHNLGKPD
 ILILAARNGHTELVDIILGLNPTPFNIDTESSCGVTALLASIGRHFVVDLSLLSKGADPFKTRK
 DGLNALEIAQHSPhFDSREVSVIMKFMEKSGTKILSGIPSRVVSRASTRAPSVVPSDEDDVVEE
 KEITAHTELSAEKKSSEDKITKTVNEHVSNRKPHESTGRKLEKTHSNEERKRKRKREWSDEPEKPHL
 LKKSNDLKLKSLHREFTSDDHHTSEHSDFSFAEKRHLSATPPAPPPPPPPPPSQAVIKAQEEQK
 IKDAEERALKQEKVEAKRRARREMLKSEKEKEQKRKEEELRAQEEKRIAKAQEEQERLAREAE
 EKSKELEKKVGLRQQLLDHYFVGLRYCKFDGNPNISAVDKFLPFYVVIDDKYAVDLQVSLTIT
 STVVSQVINTVQPHQKREINATEKSKLWKLFKFIIGIDPRNFNCQQRSSITNGQKQFQNLHLHFVE
 VDLAEELKEFPEVHSAKADNQIDVSLLESLSGFSDVCVDDIIVDGNLEIDIDSKIEKFIPLHLNT
 RKDIIRTVSTLAHPLW

YIL148W_YKR094C_homolog 659bp PathoSeq: 1..659; CDS: 501..656 (SEQ ID NO 371)

TAGTTTCTTTTGGCGGTATATCTCACTCATGATTGATGTATTGCCCCACTAAAAAGAAAAACCAAT
 GAAACAATAAGATTGATTGATAGATTGGTGTGAATTAATCTGATGCTTTCAACATCTGATTTTGT
 CTGCTGCTCGGTGATTGAGGTTGGGTAATTTCTTCTTTGAGAAATGTGAGCATGCAATGAGTGTG
 CATGCAAAATATGATGTCGCTCAATTGCGACATACTACTTAGGGCTATAGACCTATTGCAAGTGCCT

FIG. 2 - 30

TAGTTTTAAACCTAAAAAAACAATTTTGTGCAGTCGTGCACCATTCGTTCTATTTTCTACTGTGA
 TTGACGTACAAACCTTCACAGTTCACGCACACTTTTGTGCATTCTCAAACCTCTCTCAGCGCTTG
 GTAGGAATGAAAAAATTTTGGTAAAGCGGAAAAAATAAATTAACATTGAATATTTTGGAAATC
 CCGCTTTTGGATTACTACAATAGATTAAAGTAACTAAAGATGATTGAACCATCTCTGAAAGCTTTGAG
 CTTCAAAATACAACGTGAAAAATCCATTGTGCTAAATGTTACGCTAGATTGTCACCAAGGACCA
 CCACTGTCGTAGAGAAAGTGTGGTCACACCAATCAATTGAGACCAAGAAGAAATGAAGTAG

YIL148W_YKR094C_homolog 52aa (SEQ ID NO 372)

MIEPLSKALASKYNCEKISIRCKYARLPFRATNCRKRKCGHTNQLRPKKKLK

YIL150C_homolog 2297bp PathoSeq: 1..1162, public: 1163..2297; CDS:
 501..2294 (SEQ ID NO 373)

ACTCAGCCTTTTGAATTCATCTTTGGTAAAAGGATATGTAATGAATCCGCATAATGAGCATTTCT
 CTAACCTCCATATTTGTTGTTCTACCCCTCTTGCATAGAGACTTTGATCGTGACATTTTGTAAAGTGG
 TAGAGGTATGGGTAAGATTATTTTACCACCCGTTTCTTTAGCAAATAGTCTAAAGCATTTTCTG
 AATTGTTGAGTTTTCGGTACATCATTAGCTATCTTTTGACAAATGATTTGCTTCTACCTCTAGTCA
 TGGAAATAACAAGTTAAACAGCGTGTTTTGTGGTTTGTGGAACAAATAAATTTGGTGGTGTAAAT
 GTGTGTGTTTGTGTTTCTTTTACCAGATTTTGTCTTGTCTTAAATAAGAAACAGCGCAATGAT
 TCTTTTCATAGTTTCTTTTTCATACATACTTCTGACCGGTGCATCTATATCTGCTAACATCTACT
 GGCACCAACAAGAAAGAGAAATTTGAACTAATCCGAAGATGAACGACCCGAGAGATGAACAAATG
 ACTCCGATGTGATTAACAGAGAGATTCTATGTAATGAAGGACCTTGGTGCAGGAGTTTGAAT
 TGAATAATGCAAGATTAAGAAAGAAACAAAGCCTTGAAAAACGCTGCTTCAAGTCCACCTGGGAAG
 ACATGCTGAATAAACAAGAACCCCATCAACCCGAGGTCCCGAAGCCCGAAGAAAGCTTAAAGTCC
 ATTTGGATAAGTGTACTAGAAGAACCAAGTAATTTTACCAAGAGGACCTCTGGGATTTCCA
 AGATAAAGAAGATCAAACTTCTTAAACAAACTCTACGAGACAAGTAATAAGACATGATAAAGAAGATG
 CCCATAAAATAGATTTTCAGTAAAGAAAGGTTTGGTGTTCATTTGGATAAGTATATCTTTACGCCAA
 AAGAGCTTGTGTGATGATTTAGAACCAGATATCCAAGCTTTACTTGCAGCAAGAGATACCTTGCCCAAC
 TGCATAATGGCCGACATTATTGCCGAAACTGATAGCAACATGAAATTCCTTAAAAATTGACAAGTTT
 TAGCGAAAACCCCATAAATCAAAACAACTATGCTGAACCCCAAGTATTGTAATTTGGTGTCTTGTTCCT
 TTGTGTCGCGCAAGGACCCAGTGCAGGTTGCTGCCAACAACTCTAAATACATCAAGTTTGAAGGTTG
 GAAATTTTATGAATTCGTAGACTTGTATGCTTTTGTGATAAGGCTTTTCAGAAAAACGGGAAAAATCC
 AACCAGGTGATTTTATTTATTCATTTTGAATCCATTGATCAACAAGTATGAAATACAAGTTTGGCAAGG
 GCCAGTTTCAGTGTGGGTTCAATTTGAAAGTAGAAAAACCAATGTGCTCAAGTATTTTAGAGATAG
 GATCGTTAAGAGATTTTGGGTTTTCGAAAGTTTACTAGAAAAGCTAGATAATAGCAGATGCAAAAAGGG
 CCATCAACAAGAGGACGCAAGAAATCTGCGATATACATTTGGATATGAAGTTTAACTCTAGTACAA
 GAATGGAATTTAAATGGAAGTGTTCGATTAGATCCCCGCAAAAAAACAAGAAAAAGATGTACATGA
 ATAAAAATGGGCTCTGGCTTTTATTAAGCAATATAACGAGGAGAGTACTGTTATAGGAACAAGCTAGC
 GTTCTCCTCTTGTATCCAAAAGGTACCAAGACCCGAAAGTACTCCAGAACCAAAATCAAGCGCGCA
 AACTAATAGACGACAAGGCAAGGAGATGCTTGAACAAAAGCTATCGAAAATAGGTTTCGGCTTCAT
 TATTGAACAAATTTACAATTTACTGAAGAAAGAACAGATAAACTTGCAGTGTATCGTCTGAAGA
 GCAAAGGATTTCAACAACAATGATTTACATATTGGGTTTGTATCCAAACAGGTACATCTTTGAACC
 AAAATAGTACCTCTGCTGGCAGCAAGCTGATGGAATAATCTCGAGCACGGGAATTCATGATTTTGA
 GTGTGTAACATCTGGTCTAAGTTCGTTGTCTTGTCTTAAACAAGATCGCCAGTGCAGAAAGTTGCA
 AATGGAACACGAATATCAGAACTTTTACAAATTTACGATCGACGAGTTTACGAGGCATCTCTTGAGTA
 CTTCTCGTCGTTACAGAATCTTGTAGGAAAGCAACACACGCTTACTAGTATGAAGAAAGAA
 GAGTGGTTGTCTCAGATGATGAACAACCCGGGATGGAAGAAGATGAAGAAGACATTGAAATCCAGT
 TTGACGAGCAAAAGTCTAAGATGCTCATGAAATGACTGGAGCCAGGTA

YIL150C_homolog 598aa (SEQ ID NO 374)

MNDPRDEQIDSDVLTEDSDDELKDLVQEFELKYALKKNKALKRRRSQSPSEDMSNKQKPHQPEV
 PRTPEKAVHLDDKVVEEPKQRIFTKKEPRDSIKESNFLNKLYETSNKHDKEDAHKIDFSKRFRF
 QLDKQITFTPKDQVDDLEPI SKLYLRRRYLAQSQIADI I AETDSNMKFLKIDKFLAKTHKSNRYAEP
 KYCNWCLVAFVVRKDPQVQVANN SKYIKLVGNFMNSVDLMLFDKAFQKNGKI QPGDLFLILNPLI
 NKYEITQVGKGQFQSGFNLKVENTNVSSILEIGSLRDFGCFKTRKLDNSRCKRAINTRTQEFCDIH

FIG. 2 - 31

LDMKPKSSTRMELNCSVSIRSPOKNNKKMYMNKNGSGFIKQYNEESTVIGTSYVGSPLDPKRYQDPK
VLQNOIKRRKLIDDKAKEMLEQKLSKLGSASLNNLQLSKKEATDKLASDRSKSGKFTNTMISHIG
FDPTPTGLNQNSTSLGSKSMEKSRARELHDLVSVETSGHKSLSSSKQDRQSKVAKWNTNRTLQNYD
RRVASHSLSSTRRLQLNLVGKQTHATLVDKRRKRVVSDDEQPGMEDEEDIEIQFDDKSKMSYMKM
TGAR

YIL167W_YIL168W_homolog 1499bp public: 1..1499; CDS: 501..1496
(SEQ ID NO 375)

TTTCTTCATCAACTGCTCAAATGCTTTGAAAGTGAAAGCTTACTTTTTTGGTTTCGTTTAGGTG
GCATCAAGGTAAAGGAGGGAGTTTGGTATAGTTAGGTTTGTGACTTATTTCTCTTTTGTAGATAGA
TATAACAGAACTACCAAAAGTGAGCCACATCTGTTAATCTTGAAAAGCAAATTGAGAAAACCAT
TTATGCAAGTCGTACTGGTGATATCTTGGTCAATTGCTACACTTTGTAATGAATACTGTAAT
GTAGCGCACTGGTGTGAANAATATATATTTAAGTATATAGAATCAGGTCAATATAAAATTTTGA
AATATAACAAATCTTTCAATCTAAACGTATGGTTAAGGATTATAAATCAAATCAGTACTGCTT
TTGTTCTTAAAAAACCCATCGTGGTGGTAACTGTCAGGAGACCCGACATCAAATGGAATTCACACA
ATCAGTCTCCGAATTTATTACCCTTGAAACCTTAACCTTAATGAAAGAGCTTCCATCACTACTACCT
TTGTTGAGGTTTCAGACAAACTTCTTACAAGCCTCCGTGACGGGTGTTTTCAGAAAGTAGATAG
AGCAGCCTCCGCGACCTGCAAAATTAAGAGGCATGGGACATCTGGTGGCCAGCTCATAGATGTGG
CCAGAAAACCTTGCAAAATCGAACGTAGCAGTTTTCGTCATCTGGTGGTAAATGACAGGATTAGCAG
CTGCTTATGCCAGCCAGTTTTCGGAGTATCGTGCATCTGGTGTGGCTGAAAGTTTCGAAAGCCAA
CTGTTATAGAAAAGTTGAAATCCTTGGGTGCAGATGTCATTATTCATGGGAAACATTTGGGAGAGG
CCGATAACTATTTAACTGATTTTGTATTAAAAAATCTTGACAAAACAGCTCTATCCGGTCTATTGTC
ACCTTTTGTATGACCACTTGTGTGGGAGGGTCATAGTAAGATCATACCGGAAATCATCGATCAAA
AGCAATTACCCAATCTTGATAAAGTTAAGGGGGCTCATTTGTTTCGTTAGGAGGGGGTGGCTTATACA
ACGGAATAGTTGAAGGTTTGGAAAAATCATAAAGAGATACCAAGTGTGGCAATGAAACTAAACAAG
CGGCAAGTTTTCAGAGGGCGGTCAAAGAAAGTTAAAGTTGTTTCATTACAAAAAGTGCAAACTTTGG
CCACTCTTTGGCTTCGCGGTACCTTTCTTCCAAGGCATTAGCAAACTATATTGAGCGTCTTACAG
TTCTGTGCTGAAATTTGATGACTTGGACGCTGTTAAAGGTGTGTTGATGATACGACCTTTCGGAT
ATATGGTTGAGCCTGCATGTGTGCATCCGTTCATCAGTGATGCACAGGCAAGATTATTTGAATA
AATTTGGTACATTAAGTCCAGATGATATTATCATTTGTTGTATGTTGGTATGAGTCCGCTATCAACA
AGTATATTATAGACGAATATAGAAGTTTATTAGAAAAAGACTCTTGA

YIL167W_YIL168W_homolog 332aa (SEQ ID NO 376)

MKEPSITTTTVEVTDLPTKPPCRVFFKNEYEQPSGSVLRGMHVLQSIDVARKLGKSNVAVFS
SSGGNAGLAAAYASQFFVGSCTTVLPESSEKPTVIEKLSLGLADVI IHGKHNGEADNVLDFVINKL
DKTVYVYVCHPFDPLLWEHSHKIIETIIDQKLPNFDKVKVICSVGGGGLYNGIVEGLENNKEI
PVLAIETKQATPHEAVKEGKVHLQKVQTLATSLASPLYLSSKALANYIERPTVLAIEDDLDAVKG
VDVVDYDFGYMVEPACGASVASVMHRQDLLNKFGTLSPDDIIIVVICGGSAINKYIIDEYRSLEK
DS

YJL034W_homolog 2564bp PathoSeq: 1..806/1401/2504, public:

807..1400/1402..2503/2505..2564; CDS: 501..2561 (SEQ ID NO 377)
TTTTTGAAAACAGAGAAATGAATGAACAATTTGATGACCATAGAAATGAAGTGAAGAACACATAAATCT
GGGACACTTCAGCTGATAACAACAAGTGACATGAACAACAATGTCGTTTGTATATTTTGGCACA
TTTGTGTTTCAAGCCAAAAAGAAAGACAGAAACAGAAAAAGAAAAATCTCAAAGTTGCCACGT
AAGCACAATTAATCTTTTATGTTGTAATCATTTCTAGTATATTCTACGTAATAGGTAGAGTCCCT
ATATGACAGACACACAGGTTTTCACAGATGTTGACAGAGTGTGAAAAATTTATTCAGCTTGAT
TATAAAATATACAACCTTACCTCCACGGTTTTTTTGTGATTTTGTGATTTTGTGAATTCCTCTTCT
TTTTTTGTGATTTATTTATTAACATCTCTGTGTAATACTTTTATGATAAATTTTACAAGATT
TAATTAGATCAATTAGATTATAGAATCATTTCAATATAATGAGATCATCACAATCTTCTGTGTTAC
CAGTATTTGGTTTATATATGTTGGCGTTAGTTATACTTATACCATTTTGGTTTTCACCGAAGCAGC
CATTTGGCGTTGCTGCAGTGAGCGATGATGAATCCTCGACAGATAATTTAGTTGACAGTCAATGGTA
TAGATTTGGGTACCACTTATCTCTGTGTTGGTGTATTAAGAAAAACGGTGAAGGTTGAAATTTGGCCA
ACGATCAAGGTAATAGAATCACTCCATCATACGTGTCGTTCAATGGCGATGAAAGATTGGTTGGAG

FIG. 2 - 32

ACGCTGCCAAGAATCAAGCTTCTCTTAATGTCAACAACACTGTTTTTCGATATTAAAAAGATTGATTG
 GTTTGAAATATAATGATGACACTGTGCAAAAGGAACCTTAAACATTTGCTTTACAAAATTGAAAAATA
 AGGGTAAACAACAGCTGTTTAAAGTTGAATACCAAGGTGAAGAAAAAACTTTCTCCCTCGAAGAAA
 TTTTCATCTATGGTTTGGGTAAAATGAAGAGTATTGCTGAAGATTACCTTGGCAAAAAGATTACTC
 ATGCCGTTGTCACTGTTTCCAGCTTATTTCACAGATGCTCAAGAGCAAGCTACTAAGATGCCGGTA
 CTATTGCTGGTTTGAACGTTTGTAGAATTGTCAATGAACCTACTGCTGCCGCTATTGCTCATGGAT
 TAGACAAGAGGCCACCAAGAAAAACAAATTATTGTTTACGATTGCGGTGCTGCTACTTTTGATGTTT
 CTTTATTGTCCATTGAAAGGTGGTGTTCGAACTTGTGCTACTGCTGGTGATACCTCACTTGGGTG
 GTGAAGATTTTGATTTCGAAGATTGTGAGTACTTGGCCAAACAAATTCAGAAGAGAGCAAGCAATAATTG
 ATATCACTGCCAATTCTAAAGCCATTTCCAAATTGAAGAGAGAGCGAAAGGCGGAGCAACTT
 TATCTTCTCAAATGAGCTACTAGATTGAAATCGACTCTCTTGTGTGATGTTATTGACTTCTGTAA
 CTTCTTCAAAGCCAAAGTTTGAAGAATTGAACATTGCTGCTTTCAGAAGAGACTTTGAAACCACTG
 AACAAAGTGTGAAGAGCTGGTGTGCAAGAAATCCGATATTGATGATATTGTTTGGTGTGGTGTG
 CCACCAGAATTCCAAAAGTTCAAGAATTATTGGAAGGATTCTTTGATGTTGAAAAAGCGCTTCAAAG
 GTATTAAACCAGATGAAGCTGTTCCTTATGCTGCGCGCTGTTCAAGCAGGTGTTTTGAGTGTGTAAG
 AAGGTGTGATGACCAATGTTTTGTTGGATGTTTAAACCATTGACTTTAGGTATTGAAACTCTCTGGT
 GGGTTATGATCACCTTTGATCAAGAGAAACACTGCCATCCCAACCAAGAAATCTCAAATCTCTCAA
 CTGCTGCTGATAACCAACCAACTGTTTGTGATCCAAGTCTATGAAGGTGAAGAACCAATGCTGTAAG
 ACACAACAGATTTGGGCAAAATTCGAATTGACTGGTATTCCACAGCTTCCAAGAGGTGGTCCCAACAA
 TTGAAGTCACTTTCTCATTTGGATGCCAAATGGTATCTTGAAGTTGAAGCTGCTGATTAAGGAGTAA
 GTAATCTGTAATTCATTACTATCAACCAAGAGGGTGAATTCACAGGATGAAATTTGATAGCTG
 TGGTTGAAGAGCTGAAAAATACGCTCAACAAGATCAAGAATTGAAGAGAAAGATTGAAGCTAGAA
 ACTCATTTAGAAAACCTATGCTCATGTCTTGAGAGGTTCAATTGAGTGATCTTCTGAAACCGGTTTAG
 GTTCTAAATTTGGATGACGATGACAAGGAAACTTTGGATGACGCTATCAAGGAAACTTTAGAAATTTA
 TTGAAGATCAACTTTGATGACTGCTACTGCTGAAGAATTGAAGAACAAAAACAAATAATTATGACG
 TTGCTAACCCTATCAGACAAAATTATACGGTGGAGCTGCTGGTGAAGGTGCTGGTGGCGCTGGGG
 ATGCCAAATTCGGTGATGATTGATTCAGATGATGAATTCGATCACGATGAATTTGATG

YJL034W_homolog 687aa (SEQ ID NO 378)
 MRSSQSSWLPRIGLLYVALVILPFLVSPKHAFVAVAVSDDESSTDNYGTVIGIDLGTYYSCVGM
 KNGKVELLNDQGNRIPTPSVFNCDERLVGDAAKNQASSNNVNTVFDIKRLTGLKYNDDTVQKEL
 KHLPHYKIKENKNGKNPVVVEYQGEKFTSPSEETSSMVLGKMKSIADLYLKKVTVHAVVTVPAFYND
 QRQATKDLGATIGLNLVRLVNEPTAAAIAYGLDKGDQEKQIIVYDLGGGTFDVSLLSTEGGVFEVL
 ATAGDTHLGGEDFFDKLVRYLAKQPKKKNHIDITANSKAI SKLKREAEKAKRTLSSQMSSTRVEIDG
 FVDGIDFSETLSRAKFEELNLAAFRKTLKPVQVLKDGKVKSSDIDDLVLVGSTRIPKVQELLE
 FFDGKKASKGINPDEAVAYGAQVGLVSGEEDVDIVLLDVNPLTLGIETSGGVMTLTKRNTAI
 PTKKSQIFSTADNQPTVLVQYVEGERTMAKDNRLKGFELTGLPPAPRGVQPIEVTFSLDANGIL
 KVEAADKGTGKSESITITNEKGRLSKDEIDRMVEAEKYAQDQELKEKIEARNLSYLAHVLRGQ
 LSDTSETGLGSKLDDDKETLDDAIKETLEFIDNFDPTATAEEFEQKQLLDVANPPTAKLYGGA
 AGEAGGAGDAKFGDDSDDEFDHDEL

YJL035C_homolog 1346bp PathoSeq: 1..125, public: 126..1346; CDS:
 501..1343 (SEQ ID NO 379)
 GCCCCATGGTGACAGAAAAATGATTGATCCAGGTTTCTTTGAAGGTTTGTAAATACGTTTAAACTTG
 TGACCTAACTCACTTTTCAATAAAATCTTGTATAAAATTTGGTTTCTTTGAATTGTTTGTAACTCTCT
 AAGATTGCTCGTCTTCAGTGTTTGCAGGTGGAGCTGCTATTGCCAGCTCGCGCGCATAAACAGCAGGT
 TCTGGTATGTCACTCTTCATCTACTAAGCCGGACAATCCCAAGCCGCTCTCTTGTCTCTTTATTTCT
 CTAAGGAATGCTTTTATGTAGTCTGACATTTCTTGCCTGTAAGGAAGTACAGATTAAAGCTCGAAA
 CTCATTCGACAACAAAGCTCTTAATTTTCTTCTATAGTAATTTGATCTTTGGTCCCAACACAAA
 AGATACAGAGAGAGAAAGGAGGCGCTTAGGCTGACAGAAAAAAAATTTAGTACCTGCCAACACAG
 TAGCTTCAACCCCAATATGATTGATGATGAGTTGAAGTATGCTGACAGATCTTACTTTCACATCTTC
 AGTACATGGCTATAAGCTTGTGTCGGTTACAAAGCTTACTAAATATGAGACACCAAGTGTCTAT
 GTATAGTCGTGGATTCAAATCAGATAAAATCATTAGCATAGGCTACAATTATACCAACCACTCTC
 TAAATGGTACACAACACCGAGAATTATTGCTTTTACAACGATTGTTGGGAACAAAAAAGTGAATTTG

FIG. 2 - 33

ACTATAATGATTTAAATTTGTATGTGACAGTGGAGCCTTGTATTATGTGTGCATCTTATTTCACGTC
AGTTGGGCATCAAAAAAGTAATATTTGGTTGTGGGAATGATAGATTCCGGAGGAAATGGTACCATT
TATCAATACATAGTGACATCACCTTGCCTAACGCAGCTTATCCAGTATCGGGGGTATATGTAGGA
CAGAAGGAATCCAACTATTACGAAATTTTATATTCAACAAAAATGAGTCGGGCACCAATCCAAAAA
TCAAAAAGAACACAGATTTGAGAGTAAGGAATCCACAGAGAATCAGTTTGTAGCATTTTCAAAAG
ATGAATTTATAGAGTTTACGGAATGAAAGAGTGATATTACGATGGGAAGATTTTGAATCA
CTCCATTACAAAACAAGGTTATGATATAAAAGAATTGATATCGTTGGATATGATGCAAAAAGTTC
CATTTCTAGAGGATGAGTTGGGACAAATTACAGATGAGCAAAATTAATTGAATTTCACAACTTATTTT
TCAACATAAATGATGATGGAACGGTTAAATTATAAAAACCAATAGGCAAAATATAACAGTAAAAAGA
GACACTTTGCAACGATGAAGAAATAG

YJL035C_homolog 281aa (SEQ ID NO 380)

MSTDLTSHFQYMAISLFGVYKALLNNETPVSCIVVDSKDKIISIGVYNTNHSNGTQHAEFIALQ
RFGEQKSSIDYNLDLILYVTFPCIMCASYLRLQIGKVIKVCNDNRFGNGNTILSIHSDITLPNAA
YSSIGGICRTGEGQLLRNFYIQNESAPNPKIKKNTDIESKEYPENQFCSIISKDEFIEFYGNERNV
IYDGKIFEITPLQNKGYDIKELISLDMMQKVPFLEDELQITDEQIIIEFHNLFNINDDGTVNYKK
PIGKYNYSKKRHFAHDEE

YJL180C_homolog 1504bp public: 1..938/940..1504, PathoSeq: 939;
CDS: 501..>1502 (SEQ ID NO 381)

CTTTATCTAATTGATTAAATAATTATTAACATTAGTACCAATAAATGCTTTACCAACAACCTTGCC
AAACTTTTTTCATTGGATTGGGTATTACATAATTTATTTAAATTTAGCATTTGTAGTATCAATTTATG
TTAAATTTGTTCATGGCTCGATCAAGTTGTAATTAACCATGGATAATCTCGCTTGAGATTTATTTA
ATTGATTATCCATTTCAAGTAGGACTTTTGTAAATGCTTCTGATTCAATGATTAATGAGACGAGT
GTGTGTGATGGGCGATGAAGCTGAAGGTTTTCAGTATTTGGAATGGAAGCCCCAAGAAGAACACAGGG
AAAAATATACAATCTATAATCAGTATGTTTCAGTTTGGAAATGGAAGCCCCAAGAAGAACACAGGG
AAATTAATAATAAAGGTTGGAGAAAAAATAAATGAACAGAGAAGATTCATCCTTTTAGA
TCAACAGAAATATATCTTACCATCCCCCCCCCTCCAAAAATGCTTAGATTTACTAGGACTACTGCTT
GGAATTAAGATCTATTCATTTGCCACTATTCAATATAGACAATTTACTTATCCACTATATGTT
ATCAATTAACAAACCTTACTCCATCTTAGGAATAAATAATACCATTGAATCCAATATACCTTCAG
AACTAATAGATTAGCTAAACTGGTACTAGATTTTGGAAAAAGGTTGAAGTAAATTCATTAATG
AACTCAAAAAATAGAAATTCATTTAGATGGGAAAACTCTACGCACACCACTTGGATTCCCAATTAG
AATTAACCAATCAATAAAAACAATTTGCAATTTAATTTGCTCATGAATGGACTCATTTACCTGATA
TTAAAGTGAATCAAGTACTTTACCAATTAACAGCTTTAGCCACTAGAGCTATAGATTTTGGTCAAC
AAATGTTTGAATGATATGAAGACAGAAAAAGCTGAAGAAATGTTAGCATTTGGAAGATATTAATTTAC
AAATGTTTGAATATCTTTGACTGATACCTTGTCTTATTTGCTACCAACAAGAAATGATGATGTA
AATTAAGAAAAAGACAGAAAGAAATTTATCGTCCATTAATTAATGAATTTAATGAATTTTTCACAA
TTTATGCTCATATAATAAAATTTAATCCCTCGCAAAAAATCTAATGAATGAAATTTAGATTTGTG
AACTGATAGGATTAAGAGGTAATAAACAAGATGAACCACTCAATTAGTTGATTTGGATTTGGTTAA
ATCAATTTCAAAATTTATGATTTAATTCGCTTGGAGAAACAATCTAATCACTAATAATCATTTTAT
GTGGAATTTACTTTATTAAGATCAATGCTTAATGATATGAACCTTTAAAGAAATTTATCAATTTTA
ATAAAATTTCCATTGATGAAGATTATATCATAAACCTTTAGAAGAAATAGTTGAATTTAGGAAAT
TAGAACTATTATTCAACTGAAGAATGGGTGAAGTAGAAGATACCTATGA

YJL180C_homolog 334aa (SEQ ID NO 382)

MLRFTRTTAWKLRSPATITQYRQFTYSTICYQLKLTLPSPSLGINNTIESNIPSETNRLAKTGTRFW
KKEGVFKNENETQKYEIQLDGKTLRTPLGFPLELPINKKQLAYLIAHEWHLDPDIKVKSSLP/LTAL
ATRAIDLSQQLHSDMKTEKAEMLEALEDIKLQMLRYLDTDTCLLATNKECDGLKRRQEEIYRPL
INEFNEPFTTYAHNNKLI.PKQKSELKYLDCETDGLRGNKQDETQLVLDWNLQPLIYDLIALEK
TILTTKSF.LCGTTLRSNVNDIETLKELYQFNKNSIDEDYHKTLEELVELGNLETTYQTEWGEV
EDTH

FIG. 2 - 34

YJL187C_homolog 3689bp public: 1..452/3414..3689, PathoS Q:
 453..3413; CDS: 501..3686 (SEQ ID NO 383)
 TATTATATATATAATCTAACCAACAGTACTATCCCTTAACCTATTAGCTCAATGTCATTCTTCATTA
 AACAAAGAGATATGGTAATTGTTGATTAGACAAACAGTTGGGTATCCCAATTTGTAATTGGAACCGCTTC
 TTAACCTCTGCTGTTTATTGTAATAAATATTGTCGCTCTTCTTCATCAACATATTATTGTAACAGCTCTC
 TAACGTGTAATGTTGGGCTGACAGTAGAGTATTGCGGTCAATTTTAGGAGTGATTATAAATCTCTGT
 GAGAAACGCAAGCAACAAAAAAGAACAAAGGAACCAACATCATGATTAAATATATTAATAGTAGA
 AACTCAAGGGTGAGCTAGATGACTGAGCGTGCGAGAAAAAAGAAAAAACATCATCCAAAGTTTAA
 CAAAGTATTTCTTTTTTTTTTCAATTTTACAACCAAAGATAAAATAACTACACACCCCAACATTA
 CAGCCAAAAACACATACTCTGTGCAATATTACGCTCCAATGGATTCAAACCCGCTGCAAGACGTAT
 CGGGTGATACAGTAGACACACCAATGGCCAAACAATAATCCCACTAATGACAGCACAATCTCTCTCT
 AGAACCAATTTCTAAACCTGGCTTGAGAAACACCAACCAACCACTACCAACCAACCTGCAACCTGC
 AAATGCAATTTCTCATTCACAGCAGTCACCTTATATTAATCAATTTGGAATACTTTACCAATAACAGT
 TTTCCGCTCTTTCAATAGTTTAAATTTTGGAGGATGCCAATGATGCCAACCAACCAATAGTTTCAA
 CAACAACTTAAATAAGAAAAACCAATTAACAAGTCACCACTTCAATATCAAGCAGGACTTATTAA
 ACGTAGTAGTACGACAGTTTCTTGATAACTCCAACCGGAACAGATAGAAGATGGAGACGTCACAA
 CACAGCAGCAGCATCAGATTTTGTGATGAAGATATTGAAGATCCTGAAAGCATGCGATACACCC
 CAACTTGGAATATCTTGAAATCCAAAAATCGATAGCTTCAATATTATCTAGCAAGCATAGAA
 AGAGCAATAGTCAGATTACCTACAATCTGCACGTCACGGAAGCCATCCGAAGAAGATAGCTCATCAT
 CGATGGCTCAACAATAGGTTATCTTAACAACCTCACAAGGTTCAATTAAGAGATCGTCAAAGATTGTA
 ATTTATCTTAATGATTCCCAATTTGAAAAACGGTTGATGGAGGTAAAAATTCGGATGAAATAGATGACA
 TTAGTTTGAAGCAAAATAGATGTTGTCAGTGGCACCCTAACGATTTTCAATCACCACATTCAGCAGAA
 AGCCGGAATATTTTGTGCTATAACTGCAGCAACCGGAATTTCCAATCATCAATTTAAAGGGCCAC
 ACAAGTTGGTTAGTACCTGCCCTTCCCGCTGCTCAAAGAATAAGTTTTCGCATATCATCATCAACCA
 CATCTTCTGCCACAGTCTAACTTGCAATTTCACTTCCAAGTTGGGACTGAAGAGGATTCAAAATGTTTA
 AAAATGCAAAATAGAGAGCGCATTAATGTCGTCAAGCAGAGTTATGACTCCAGAAAAACCGAAAAATGG
 TATCTAAAAATATTTGGCAAGTCAGCAAAAAATAGGCGAGCTTATACCCCAACCCATCATCTACCC
 CAATGGCTGCTCTCACTCAACCCCTCCTTCATCATCTCACTGAATTCACCAACCGGCAGCAATAA
 CATCTACAAGTCCAGCAGCTGATGAGCATTTATGATATTGACAACTGTCAGACGTCGTCACAAAA
 ATAGAAAACTGTCTAATATTCTGCACTCTCAATATTATTTATCAAGATGAAAAATCATATCAAGT
 CAAATCATGCTAGAAAAATCTAGTAATCCAATACCATAACCTCCGACCGCAACCACTACCGACAAATA
 TTTCTGCTCTCTGGCTGAAACAGGGAAAGGGTCAACTACAACATAAAAGCAACCTATCTAAGGGTT
 GTCCCTTATTGATGATAAAGAGAATAAAGCTTCTTATCAGTTTGTAAACCAATGCAAAACAGCTT
 TCAATCTCTCGGGTTGGTCAAAAAGATAGCATAAAGTGGTCTGCTGGACAGGAAACCTACCTCCAG
 AAACA CCAATCAAAAGAAATCCATTAATGATTTTAAATACCAACAAAGTTGACCTCCATATAGCA
 GTGGATTTGCTGAAGGAAAAAGATGTAATGGGTGATCAACATGATATATATTTCCCATTTCCATGTC
 AAAATCAACAGTTTTCCTGGCAGCGTGAATCCCAACACTACTACGAAACCAACCAACATCAACAGC
 ATCATGATGATGATTTCTTCTTATGAAGTTGGAAGGAATAATCTTATGATGCCAGTATGACATGCA
 TCAATTAACACAAGATTATATCAAAATTTTCCCTTCTCGGAATTGAAGAGGAGCAGGTGCTTCAGC
 GACCAACAAGAAGATTAGAATTAGTTTCAATCTGCAATTGAACTAGATGATAACATTAATACAGC
 AAACACCAACCAAGAACTGCTACTACCGAAATACGACACCTCAACATCACTTACCCCTTTACACGC
 AATCCAGAGTCTCAATTTGTAAGTTTGACACTGAGAAAGATGGAAGAAAGGAATTTGTCAATAGTCT
 TAGATAAATCAAAATGCAACTTAAACGAGAAATTAAGGAATGCGAACCAACCTCAACACCAATATGTCT
 TTGCAAGAAATAGTTTAAAGAAACCTATGAATAATGCTGAAAGAGGTGATGACCTGTAGTAGTATAA
 TTGCTCAACGCATAGATATTATGCCATCGTTAGATGAAGTTGACTCAGTGTCTGTTATCTCTTCAA
 AGATAGATGAACATTTAAATTTGAAAAGTTTGGAAATGAAGAAATCAAGATATTGGATCGGGAGCAAT
 TTTCCATTTGCTTTTGAATGTTTATTTAATAACGAAAAAGTTTGTCTATCAAAAGAACTTAAAGAACCCAC
 TTATTTGAAAAATTTGGAGAACAAACATATAAAACGAGAAATTTGAAGAGTTAGAGAGTGTGGAACAGCA
 TTAAGAAAGATGAAGCAACATTAATGCAAGAACAGAAAGAAAGAGATCTAGTTTATTTTCA
 TTGAGGCTCGGGATTTTAAATAATTACTACTATATAATGACAGAAATTTCTGTGAAGGTGGTACATTTAT
 TGAATTCTTAGAGAAAAATAACATTACAAAAATGATGAATTTAGAAATTTGGAAGATCTCTAATTTG
 AAATTTCTAAATTTGGGTTAAAAATTTATTTATCTGAAAAATTTTATTCATTTGGGATTTTAAACACGAA
 ACATTTTATCACTTTTGAAGGGTCATTGAAAAATTTGGTGATTTTGGGATTTGCTAATTTGCTTAAATGCTA
 TACTAGAAAGGACTTTGATCTTGAAGGAGATCGTAATTATATTGCCCCGCACTTAAATGATGACA

FIG. 2 - 35

AAATTTTACTCCGTTTGCAGATATTTTCAGTCTTGGATTGATTATATTGGAGATCGCTGCTAATA
TAATTTTACAGATAATGGAACGCCATGGCTAAATTGAGAAGTGGAGACCTTGAGTGATGCTGGCC
GATTATCAAGTGATAATATTTCAATGTTTTCACACCAATCCAAATACCAATGCAATATACAGTG
GCAGTGAAGTAGAAGTGGTAGTGGCAGTACAGGAGGCAATGGTAGTCTGGTGATTGA

YJL187C_homolog 1062aa (SEQ ID NO 384)

MDSNFCQDVSGDTSSTPMANNPTNDSTISSQNHKSRTGLRKHQQQHHQSHSQMHSQSQSPYIN
QLEYFTNNQFSRSPNSLLLEDANDANTNNSSTTLNKKTKINKSPFNIKQDLLNDSIDTFLDNSNT
ETIEDGVDVTTDDDDHDFDDEDIEDPEAVQYTPTLNLIKSKKVDSPNIISSKHKRSNSQITYNSHVR
KPSEEDTSSSMATIRLSNNSQSSIKRSSKYLNLSDSNLKTVDGGKIPDEIDDIISLNEIDVAVAPN
DFSSPLSARKPDIFAAITAAANGNSNNQFKRPHKLVSQSPSPSSKKNKFRISSTSTSSPQSNLHSPSK
LGSKGFKMFKNANRDAIMSSSRVMTPEKPMKVSIFGKSAKIRRAYTPTHTSTPMVSSLNPPSS
TSNSTTAAITSTSPAADHYDINDDCDPSKNNKSSNISASSIIYQDENHIKSNHARKSSNPPIPY
PPTPEPLPTNISASVAETGKGSTTTKSNLSKGCPLFDDKENKASYQFVKPLQTAFNSSGLVKKNSIS
GSSDRKLPETPIKRNPLMLINTNKVVPVYSSGFAEGDKVMGDQHDIIYSHIPQCNQRFPGSVNPNPT
TNNNNNTQQHSDLSIEVGRNNSYDASSSTINNTSYIKIFPSSSELKKEQVLQRQEDLELNVNSD
IELDDNIIIPETPKKSLLEPNQHHQHLPLYTQSKSPLLKFDTEKDGRRNLISVLDKSNATKREISE
PPSTPINMSFAKNSFKKPMNNAERGDDPSIIAQRIDIMPSLDEVDVSVPKSIDHEILKFGMK
NKIYIGSGAFSIAFECFLNNEKFAIKRTKKPLIGKLEKQTIKREIEALRVLTISKEDENATNMQEQE
GKEYLYVYFIEAWDFNNYYYIMTEFCGGTLFDLFEENKHYKIDEFRIWKILIEILNGLKFIHSKN
YLHLDLKPANIFITTFGSLKIGDFGLATKLPILEKDFDLEGRNYIAPELINDKIYTPFADIFSLG
LILEIAANIILPDNGTPWRKLRSGDLSAAGRLSSDNISMFLQHNFNTNNSISGSGSPSGSGSTGG
NGSAGD

YJL189W_homolog 887bp public: 1..666, PathoSeq: 667..887; exon 1:

501..506, intron 1: 507..737, exon 2: 738..884 (SEQ ID NO 385)
AGTCAAGAAATTTATGATGACTTTGGAGGATGGCTGATTAAAGACTTGTCTTTTACAGATTTTTTC
AGCATTTGGATGGCGTTTAAAGCATCAGCTAAGACGGAGGTTCTAGTCATGGGTGATTGCTCTGT
TGATAAAAGAAACCGTGAAAGGAAGTATTGTGAAAAATCGATTGATATATTTTATTTTCTCTCT
TCTCCACTGTAACAGTAGTAAACACACTAGTTACAACGATGACCTGATATAAATCTTCTG
AAAAAATTTTCTTCTCTGATTTTGTAAATCTTCTGCTCTTCTCTCACTCACTCACATTTAAT
GAATGAAAGGTTTGGTGCTTACAAAATCTCACTCACTGTCGCTCAAGACACACA
GACCCACAGCAAACTTCTCTCAGAAAACAGAAAAAAATTTCAAGCAAAATTTTCTTCACT
TAGATTTTCTTCTCTCAGAAATATCAAGTAACTTTAAAGATGCTGTATCTCAATAACAGATGTTAT
AATGATGCTCTTCTCTGCTCTTTTATGGGTGATTATTATAATAAATGCGAGATGAGAAATATATTGGA
TAATAAACCTTGCAAAATGAATCAGTTGACCATTTTGAAATAATGACCATTTAGCAATACCCAGAT
TGCTGGTAACAAAGCAGAGAGAAGTACAGCAACTCAGATATAATGAAACATCATATCACTTCACTC
ATTTCTTATAGTCTCAAAAATCATTGAGAACTAACAAGTATAGCTAAGSGCTCAAAAGCAAAAAC
GACCATTTCCACAAATGGATCAGATTGAGAACTGACACAAATCAGATACATGCTAAAAGAAAGAC
ACTGGAGAAGAACTAAGTTGGGTATCTAA

YJL189W_homolog 51aa (SEQ ID NO 386)

MPSQKSFRTKQLAKAQQRNPLPQWIRLRTDNKIRYNAKRHRHRRRTKLGI

YJL190C_YLR367W_homolog 893bp public: 1..893; CDS: 501..890 (SEQ ID NO 387)

GATTTTCATTGCAAGGTTTATTATCCAATATATTTCTCATCTGCCATTATTATAATAATCACCCA
ATAAAAGACTGAAAGACATCATTTAACTGTTATTGTACATACAGGCATCTTTAAAGTTACTTGT
ATATTCTGGAAGAAAGAAATCTAGATGGAAGAAATTTTGTCTTGAAATTTTATTTTCTCTCTG
AGAGAAAGGTTTGTGCTGTGGGTCTGTGTGTGTTTAGGCACAGAGTGAGATTTTGTGTAGTGAGTT
TGTAAGACACCAAACTTTTCTTCAATTAATAAGTGTGAGTGAGTGAGAAAGAGCGAAAGAAATACAA
AAATACAGGGAAGAAATTTTTCAGAAAGATTTATAATATGCGAGTCACTAGTTGTAACATGATGT
GTTTACTACTGTTTACAGTGAGGAAGGAGGAGAAAAAAATATCAATCGATTTTTCACAAATCTTC
CTTTTACCGTTTCTTTTATCAACAGACAAATCAACCATGACTAGAACCTCCGTCTTAGCTGATG

FIG. 2 - 36

CTTTAAACGCCATCAACAATGCTGAAAAAATCGGTAAAGACAAGTCTTTAATCAGACCATCTCCCA
 AAGTCATCATATAAATCTTCGATGTCATGCAAAAACACCGTTACATTTGGTGAATTCGAATACCATTTG
 ATGATCCACAGATCCGGTAAATTTGTTGTTCAATTAATATGCTAGATTAAACAAATTTGGTGTCTATTG
 AACCAAGATTCAACGTCAAAATCAACGACATTGAAAGATGGACTGACAACTTGTGTGCCAGCTAGAC
 AATTCCGTTACGTTATCTTAACCACTTCTGCTGTTATCATGAGACCACGAAGAAGCTAGAAGAAAGC
 ACGTTTCTGTGTAATAATCTTAGGTTTCGTTTACTAGT

YJL190C_YLR367W_homolog 130aa (SEQ ID NO 388)

MRLTSLADALNAINNAETKQRKQVLIRPSSKVIKFLVTVMQKHGYIGEFYIDHRSGKIVVQLN
 GRLNKCGVIQPRFNWINDIERWTDNLPLPARQFGYVILTTSAGIMDHDEARRKHVSGKILGFVY

YJL197W_homolog 4619bp PathoSeq: 1..3041/3260..4619, public:
 3042..3259; CDS: 501..4616 (SEQ ID NO 389)

CAACGACAAACAATAAGAAGAAATCTTTCCAGATATTGTAAAAATCCTTATATTAATGTTAATA
 GAAGCCTAAAAATTTGCTTGAATTGATAGATTGCTGATCTTTTGTCTAGAAACACGCGTTATATTA
 CTTATCTCTTCTGTAATTTCTTGATCTCTGTTTGAATCAACACGCTTTGTTTCTCTTTCTGCC
 TCCCTCTGCCACCCAGTTTATTTGTTTGTCTTGTGACGCTGCTGCCAAAAAATAAATTTGAGTTC
 TCTCTCTCTTTTACACAGAGAAGACAAAGAAAAAATAAATCAATAATTAAGATTCAAGC
 TTTTCTTTTGTAGTTTCTTTTAAACAACAAAATTTGAATTTACAATCCTTGAATTTACAACCTTCATATTC
 AGCTCTAAATCAATAAATATAACAATAAATTAATTTGAATTTATCTATAAACCATCGATATTTGAT
 TTTATCTTTTATTTTGTGTTTGTCTCCATAATTTGTGTCATGCTTGACAAATAGAAGACATCGATCCG
 AGATAACCTTCTGATGCAAGGAAATTTTGACTACAAATGAAATTTGAAGCAACAGATTTCAGAACATA
 CAACAAATGTGCTAATAATGAACCTCCCTCAAGGTGAATCCAAATGAACCAACAGGAGATCATCAAAATG
 ACAACCTTGCATCCCAACGTCATTAATTAATCAATGATTATTACACAATGATCATTTGTAAGAAGGAA
 CAGAACGTTCATCATCTCCCTCAAAATTTCTTACATGAATTTTGAATTTTACCATTTCGAATTTTATA
 GTGATTTGAAGATCAACTTTGTTCTATTGATTTCCACTCATTTACTTAATGAACAAAGTAAATTTAT
 ATCCCGAAGATGAAGAACCAAGTCACCTTTTGTCTATGATCGCCAGAAGTATTTCAACATTTTGGGTG
 AATGGTTTGGAAATATTGGGCCAACCAATTTATAGAGCTATCATTTATTAATCCAGACACCAAGAAA
 AACAGATTGAAGATTTCCCGCCATTATTTTGGGTTTCATCAATTAGGTAAAAAGACGCAACCAACAT
 ACTTGCACACCGTCTAATAATGAAGCAACCAACATCATCATCACCATTGGTTCATCAGATTACACCA
 TACCAGTATTGCTTTCCAAAAACAAGCACTTTTCATAGATTAAATGGATGTTATACGTTATAATGTTCT
 TTAAAGCACCAGAAAATCGACGAAGATTTTAGGATTTGGTTTATTTGTCCCAAGAATAAAGGCT
 TACAGTATTTGATTTCAAATACAAACTTTTATGTTTGATATCTCCAAAAAATCTTTGGTTTACACCA
 ATATGCTTGAGGATGCTTTGAAGATTCACGGTATTGTGGCCAGTTCCCTATAATATAATGGTAGAAG
 CAAAAGAAAAACATCAACAGAAATTTCCATATTGATCAATTTATTTTATCTCATTTCAACAGCATATG
 AAGAAGTATCACAGGGTGGTGGACACCTTTGGATTATCAACATGCGGGAACACATGTTTATATGAAT
 CGGCTTTTACAATGTTTATTACACGTTCTGAAATCAACTATTTATTTTACAACTTTTATAAAA
 AAAAAATGAATTTTGACACCCCTTTGGGATATCATGGAGATGTTGCCAATGCAATTTGGTTCACTTT
 TAGAGATTAATTTCTCGATGTTTCTGCGGTATCTTCAACAGATTTCTCAAGAGTTGTTGAGTTGGC
 TATTAGATGCTCTTTCATGAGGATTTGAATAGAATTCACCAAAACCATATTGTGAAAAGCCGAAT
 TGAAGAGTAGCAAAATTTGATGACCCCAAGCCATCACCACAACTTGCCAAATCTTGCTGGAATCAAC
 ATAGGCAAGAAACGACTCGGTGATAATTTGATTTATTTACTGGGTTGATCAATCTCATCAATCATTAATCT
 GTCCCTGATTGTGGTAAAGAATCCATAACTTTTGATCCCTTTAATGATTTAATCTTACTTTTACCCTA
 TCAGTAGAAGATGGTATCACACATTTACAATTTGTTGATTTGTCTCAATCAAGCGCTTATACCGGAAA
 GGATTAAGAGTTGGTAAAGTTGAGTTGAATAAAAACATCCAATTTGATGATTTACTTAGCTATTTGA
 GTAATTTCTTGAATTTGATCTACTGAGTTGTTTGCTTATGAGATTTTCAAAATGCCAATCTATA
 GTGACCTTCCAATTAGATTACACCAAGAACAAGTTTTCACCTCATGATGATTTATCAGAGATACAG
 ATGATGTTTATAGTGTACATTTGTTCCACATAACCTTGCCGTTGACATCATGTGTCGACAGTTTCAATG
 CCGTTTGAAGATGCTGATAGTTTCATATCAAAATGGTAAATTTTGTGAATCCCATTTATTTGTGGTGA
 TGAATTAAGAAGTCGATGTCAATAGTTTGTGTTTATTTAGAAAGAAATTTATAGAAACAGTTTCTT
 TATTGAGTAAATAATTTGATTTGGTTGATGAATATGAAAAATAAAGAGGATTAAGAGATTACGTTG
 AAAAAAGTATTTTACAAAAACCTGGATTTCCTGCAATTTGTCACAGCCATTAGAAACCTCCGATTTGTG
 AAAAAACAACAATAATACTAGCGCAACGACGATGAGGATGCTGACACCATGAAGGCTATG

FIG. 2 - 37

ATAGTGAAGTGTCTTTGGCTAACCCATACCTTGGAGCTAATTTTGGGTTCAAAATCATGTATGTTCT
 ATGACTATAGCCCTAAATTTGAATTTCTAACCTTCGTAGCAGGTACAATCATGACCAACCAACAAAT
 TCAAAACAAACAGAGAGAGTTATTAATGTTCTTACACACAAACCTACTTTTAGCGATTTCAAACCTT
 TATCGGACCAATTTATCAGAATCAAAACGCAACTATTATTTTATCCTGATTATAAAAGATGGATG
 ATGAGATGGACCAATTTGGTGGAGGAAGTGAACCAAAATTTGGCAGAGCAANGAGAGCGGAGTCAT
 CGGGGTGAGAAATAGTAGTAGGCACTGGAAGAACAGATGGATTGTATTATTAATAAATGAAGAGG
 ATACTCTCAAGCAACCAATCAACTGTACTGCTGTGCTGAAACCGGTACCTCCACCACTTACTCGTTA
 GAAATTAATCTGGAGTTCACATCCCGCTCATCCGATGAAGAACAGAAAGTGAAGCTAATTTGGGAA
 GTTTGTTTGATTCACATCAAACTTGGCGTTGCTCCACCACTCATATTTCCGATTCACAAAC
 CTTTGAATGTAAACTCCCTATGGAAGTAACCTTTGAAAGTTCATCAGCAGACTTGAATTTCTGGTA
 CAACATGTATATCGAAGGACACAGTTTGTATGTGATTGGGATAAGGAAATTTATCAAAATGTCT
 TTGGTGATAAAGAAATTACAAGCATGGGAAAAACATATCGAATTTACCGAATCCAGAAATGGAGAAAA
 ATAGAGCTCATTTTGAAGACAAAGAAAAAGCTAAATTTACATTATCTGATTGTCTTAAGAGTTTCA
 GTACCCCTGAAATTTTAGTGAAACATGATTTATGGTATTGTCCACGTTGTACTGAACATAAAGCTG
 CCACAAAGACAACTCAACTTTGGTCAACGGGTGATACTCTCACTATTCTTTGAAAAGATTTCATA
 GTGCTCGTGCAATTTAGTGATAAGATTGATGTTTGTGTTGATTTCCTCAATTTGAAGGTTTAGATATAA
 GTTCGATGTGTGCAATACTGATTGACACCTGAAGATTGTTTATACGACTTGTATGTCCTGTGATA
 ATCATTATGCTGCGTTAGAGGTTGCTCATTACACTGCCCTCGGTAAGAAGTTCCAGAGATGATAAAT
 GGTATTATTTTAAATGAGTTCAGTCACTGAAATTAATACTCTCAAGAAGTCTGAGTCAATTTCTG
 CTACTCTTTTATTTATAGCTCGAAGAAAGTTCGAAGGAGCTGGTATTTTTGGGAGGAGAAACCTTTA
 TCGACTTGCTTCAAAAGAGTTCGAGAGGAATACCTCTGAGAGTTTGCAGAAAGAAAGATTGGTCTCT
 AAAATGTTGGCCAAATGCTCAATACGTATGCCAAATTTGAACAAAGATAAATTTGATAAAGAACAG
 AGAAACAGAAAGAGGAACAAAGAACAGGAACAGGAACAGGAACAGGAACAGGAACAGGAACAGGAAC
 AAGAGCCAGTTCAAGAGCCAGATCAAGAACAGAGCCAGATCAAGAGCCAGATCAAGATCAAGATC
 AAGAGCCAGATCAAGAGCCAGATCAAGATCAAGAGCCAGATCAAGAACAAATAAAAAATCTAGACCAT
 TCGATGAATCAAAACCATCAACTAGTGAAACAAATAACCAACAAACAAACAACTCAGTTCACTTTG
 ATGATGAAGATAATGATTACGATTATGAAGCAGAAGTAGAAGATTCCAATATTCGCAACAAAGAT
 TACTTTCAAAAGAAATTAACGCAATAAATTTGGTGCAATTATTAAGCAATGTGTCGCAAGAGTAC
 CTTTCATCACCAGTACCAATTGAAACTGATGGTGACACTGATGTAATGATTCCAATTCACATAG

YJL197W_homolog 1372aa (SEQ ID NO 390)

MPDNIEDRSEIPSDAKEIVTTNEIEATDSEHTTNVDNELPQGESNEQTGDDSDNDLASKRQLINDL
 LHNDHFEETERYII PQNLHFEFLNLPIDNFDLKDQLGPIDFHSLNLQGNLYPENEEPTVFCV
 SPEVFOHLEWGFILGQPIIRAI IINPDTKKEQIERFPPLFWVHQLGKKTQPTYLRHRRHNGSNHH
 HHHGHDSPIPVLLSKTSTFHRLMDVIRYNVLKAPRKSTKDFRIWFIWPDQKGLQYLSIQTFPMFD
 ISKTLTVSPNMLEDALKDGHIVASSYNIMVEAKEKHQTEFPIDQFILSHSNAYEEVVSQGGGHLGLS
 NMGNVTCYMSALQCLLHVPEINYYFFNYIYKKELNFDNPLGYHGHDVANAFGSLLKQAFDVKHNSSS
 ISPREFKSTIGRYSMSFSGYLQDQSQELLSWLLDALHEDLNRIHQKPYCEKPELKDDIEDDPAQAT
 KLANTCNQNHKARNDSVIIDLTGLYQSTLICPCDGKKSITFDFNDLTLPLPISKKWYHTFTIVD
 LSNQGVIPERIMKLEVELNKTSNFDLLSYLSNFLNVPSTELFAYEIFQNAIYSDFQLDYTNNKFL
 PISDIIRDSDLVIVYVPHNPVAVDIIVPVFNAVEDADSSYQMVNFFGIPLVFVMNKEVDVNSFGFI
 RKKLLETVSLDKIDLVDYEYIKRSNEDYVEKVYFKSDFPALSQLFSTSDCEKNMNTSDGNDH
 EDADNDEGVDSEVSLANPYLGANFGFKIMYVHDYSPKLNSNLSRYNHDQTTKFKQTERVINVP
 KPTFSDFKPLSDQLSESKRNYFFPYDYKKMDMEDQVLVEEVNQNLAEQKEARSSGSENSSRASEQ
 DGFVLINKEDTLKQSTPVAAAEVTPPPLVPRNNTGVHIPSDEETESSEANLGSFLDSTSNLPLPP
 PSTYESTKPSNVNSPMESNFESSADLNSGTTLSIKDTVLLCDWDKEQYKCFQCGDKELQWLEMIS
 NLPNLEKKNRAHFERQKAKITLSDCLKSFSFTPEILGEHDLWYCPRCEHKAARTKTLQWSTGDI
 LTINHLKSRARAFSDKIDLVLPFPIEGLDTSYVANTDLTPEDCLYDLIAVDNHYGLGGHYTA
 SVKNFRDDKWYFVNDSRVTEINNPOEVVANSAYLLFYRRRSSKGAGILGGENFIDLLQKGRREEYS
 SLQKKRLVLQNGQIVNITYAKIEQDIIDKETEKQKEQEQEQEQEQEQEQEVEQPEVQEPDQEQEP
 DQEPDQDQEPDQEPDQEQBNETIKSRPFDEKDLKPTSETNNQQQTTFQNFDDDEDNDYDYEAEV
 EDSNIRKQRLSKENNSNKLVIKSNRGEVTSPPVPIETDGDITDVTDSNST

FIG. 2 - 38

YJL198W_homolog 2693bp PathoSeq: 1..899/1285..2693, public:
900..1284; CDS: <3..2690 (SEQ ID NO 391)
TTCATTTCCTAAATTCAAATGAATTATCATCACCAATGCCACCATCATTTTCATTAACTATGGTA
GTGAATGGGATTTAGAAAATCATTCAAACTAGTTTAGATAATGAAAAAGAAATCAGAAATCAATCAT
TTACTGGTGAATTAGAATATATCTCAACTTCCTCCAATGGTGAACATGACACCACCACCCTGCCA
CTAAACATGAATTGATATTACAAACAAATTTTGAATTCTAATGATGAATCATATATTAATCTCTAAAT
CATTAACATTTGATTCATTAAAAATTTTCACTAAACAAATTAATTTGGTGAATTAATTAATAATTAATC
AATTTTACAAATTCAAAAGAAATCGGAAATTTTCAAAATTTATAATAATTTAAATTCATGATTTACAAA
ATCAAAATATTAAATATTGATGATGATTTAAATTCACCTCAAGCTTATAATATTCCGATCCCAATA
TAATAAATCTGATGATCATCATCATATCATTTTAAATCAACTTTATCAAGAAGACGATTCATATG
CTAGTGATATTGATACCATTAATCATATATGATATGATATATGATAATAATAACACCAAAAGA
ATAATTATGATTTTGGAGAAACAAAATAATACTACAGTTGCAATTCATGATGATGATGATTCAGAA
ACGATGAAGAAGAAGAGGAAGAAGAACTCATAGTCATGATTCAGTATTACTTAATCATACACATT
TTAATGTTTAAACAACAATTAATAATTCACATTTAAACGTAAGCCATTACATATTATTATAAATCTTT
CTGAATTTAAATCATTTTATGAAATGAATGAATTTGGAATTCAGGAAAATTTGTAAAAAATTTGATA
AAACTTGTGGTATTTCAAATTAACCAAGATTTTATTAAATGAATTTTACCTCAATATTCTCGAGTAT
TTGAAAATGATACCATTTGAAGAATTAGATTATAAATGAATCAAAATTTATAAAATTTATGCCTTTT
TATCAATTAATAATTAATCTCAATCAACCAACTAAAGAAGATTTGGATATAATAAATTTGAATTTAA
GATCTTATTATTACGGATCATATATGATTGTAAGAAATACCGTTTGGAAAGATTTTATTATACATTA
AAAAGAAATCTTATAATATTGATTAGATAATTCTGTGGTTCAAAATAATAAATTTGGGTGATGAAG
GTCATATAATTAATTCAGTAGTAATTTATCCATGAAAAGAAATTAATTTACCAACATGCTTAA
AATGATTAAATATGATCATATGATATTTCACAAATTTTATTAACACTCTCAAAATGCTTAAATTTA
TATTATTGTGTCATGTTTCTTATTATATTATGACAGTGAACAACTTTTAATGATCCAGTTCAAGGCT
GTGTGTTTACGATATTAGTTGCTGCTGCCATGCTTTGGGCTTCAGAAGCATTAACCTTATACACTA
CAGCTTTATTATTAATCCCACTTTTGGTGTGTTACTTGTAAAGTTTGTAAACCTCCGGGAACCGATC
CAATGGATGCCACCAGGATCACAATATATTTTGGGCAATGTGGAATTCACCAATTTATGATAT
TAATTTGGTGGGTTTACATTAGCTGCTGCATTACAAAATATAATCTTGCCAAAATATTATCATCAT
ATATTTTACGATTGACAGGTCAAAATCCAAAGAAATGATTATTGGCAATCATGTGTGATCATATT
TCTTTTCCATTTGAGATTCTTAATGTGCTGCCCGCTTTATGTTTTCATTTCAATCAACAGCTTT
TAAGAAGTATCCCAAGATTTCCCGCTTGTCTAAAGCATTAGTGTAGGAGTCCGTTTGGGCTGCTG
ATGTTTCTGGTATGGCTTCCAAATTCATCTCCCAAAATGTTATGCTCTTGATCAATGAATC
CTAATCCAGGTTTGGGGAAATGGTTTGTGCTGCGCATTAACCTGTGGCAATCATAGTTTAAATTTAA
TTTGGGTGGAATTTATCATGACGCTTAAATCAATAATGTTAAATCAACAAATCAACCAATTA
AAGAAAAATTAACCATGAACAAATGGTTTGTATTGCGGCTACATACTACTATCTTTTATGGT
GTGTTATGCAAAAATGATGGAACATTTGGTGAATCAGGTATAATCACTCTGTATCCCAATTTGAT
TATTTTTCGGTACCGGTTTATTAATAAGTTGATGATTTAAATTAATTTATCTTGGTCAATTTGATGT
TAGCCATGGGTGGTATTGCAATTAGGGAAAGCCGTTACTCTCTCAGGTTTATTGAAAACATTTGCTT
TAGCATTAACAAAACGAATTTATGCAATTTATGATGCCATTGTTGATTAATTAATCATTTTGGAGCATTA
TTTTGGTGGTAGCTACATTTGTAAGTCATCTGATCAGCACTTATTATTATCCCTTGGTTTAAAG
AAGTTGGAGATTCATTACCTAACCTCATCATTAAATGCTTATTATGGGTGATGATTTAAATGCTT
CAGGGGCAATGGGATTACCAACTCAGGATTCCTTAATGTGACGGCAATTTGGGATGAGAGATGAAG
TTGTTAAACCTTATTGACGGTTAATTTATTATCTAGAGGGGTTCCGCAAGTATAATTTGTTT
ATGTTTGTATTATCACCATTGGTTATGTTATGTCATCATTTGAACCTTTTAA

YJL198W_homolog 896aa (SEQ ID NO 392)
HFLNSNELSSFPMPFSINYGSEWDLLEIIQTSLDNEKESETKSFTGELEYTSTSSNGEHDTTTTAT
KHELILQQLINSNDESYINPKSLTFDPLKIFTKQLIGELIKINQFYSKESEIFKINYNLHLDLQN
QINILDVFKFTQAYNSDPENINTDDHHQYHLKSTLSRTVTNVAASVDFDTINHIDNDYNNNNNNKQ
NYLEKQNNNTVAIHDDDDSEDEEEEBEETHSHDSVLLNHTFHNKQQLKTLKRAATLFLNLS
ELKSFIELNRIGFTTKCKFDKTCGYSIKQDFINEFLPQYSRVCFENDETBEELYDLNQLIKIYAF
SNKLTQSTTKEDLDNFKELRSYLRDHIIVFRFENVTWKDLLSLEKXSINI.DLNSVQNNQMGDEB
HIINSMMNLMSKRLNLPQCLKRLIKYDHIDIPQLLTTQMLKIIIVIVIFILLAVKTFNDFVQGR
CLAVLVAAAMLWASEALPLYTTALLIPLLVVTCVKCTPGCTDDFMDATKASQYIFGTMWNSSTIMIL
IGGFTLAAALSKYNLAKILSSYILLAGTNPFRNVLLAIMCVSLFLSMWISNVAAPVLFCSLIQVPL

FIG. 2 - 39

RSIPTDSPVAKALVLGIALASDVAGMASPIASQPNVIALESMPNPNWGKWFVAVALPVAIISLILI
 WWELFMTFKINNVKIKQPKPIKEKLTMKQWVFVAVITITILLWCVMQKIDGTFGESGIITCPIVL
 FFGTGLLKVDLNNVPSIVMLAMGGIALGKAVTSSGLLKTIALALQKRIMHYDAIVLLIIFGALI
 LVVATFVSHVTSALIIIPLVKEVGDSLKPHPHMLIMGVALIASGAMGLPTSGFPNVTAIGMRDEV
 GKPYLTVNSLIFTRGVPASIIIVYCIITIGYGMSSLF

YJR049C_homolog 2279bp PathoSeq: 1..839, public: 840..2279; CDS:
 501..2276 (SEQ ID NO 393)

TATAAAGTTTCAAGTATATAAAAAGCGTTTAAAAATAATTCTTGTGATTTAAATAAGTTAAATCTTT
 TTTTTTTTCTTCTTTAGTTTTCGCTTTTACCGTTTTCACCAAGAAAGGAGCAATACTGTTTTCAC
 CCTTCCCTCTCCAGTTCATGGCCGCCGCCCTCTCAACAGTTGCTGTCGCTCTCGCTGCTGCT
 ATTTTCCAGCCCATACATTATATGACTAATATCCGTTGCTTATTATTAAGTCCACAATACATT
 GAAAGATGAGAAAGCAAGCTGCAAAAATAATTTTTTTTTATCATCATTTCAATACCTTATATCC
 TAAATTGATAAACAATAGAGTAATTGATCTTTCGAAGGACAATAAACAGATATATTTATATAT
 TAGAGTGAAACAATAGCGATTGCCAATCAGACAAACAGATAATTTATCTTCTCTATTCATTTCG
 ACAATTAAATCCAAAAAAGAAATCGAATTCATATGTCGCAATAGACTCAGAGCCAATTTAT
 CTTCAAAATGAAAAATCTGAATACCTCCACCAATAGACTTCAACTCAACTCAAGTAAACAATCCA
 TGCTTTCTGCAACCAATCTGCAACCGCAACAACACAACTACACACAGAGCAAAAACGGAGGCCAC
 AAACCATACGCGCTCTGCTACTTTTACAACCTAGTGGCAATTCATCATCTTCGTCGATATCTACCTTTAT
 CAGCAGATATCATTTCAACCACTTCATCACTACTGATAAATAACAACAACTTCAACTGTGACGCAAC
 CAGCGCCACAAAGCTCATCGTTTCAACGCGCAACAACATCCACAACGTTTCAATCGGAATCAACTCA
 ATGTATACACTGACTTCAATAGTACTTACTTCTGCTTCAAGCATTAGTAGTTTCAACCAAAAGTT
 TCTTACACAGAGAGCCACCGGATCCATAGTAAATGATATGTGAAGAGATTGCTTCTGCCAATA
 ATCGAGCTGCTAAAGAGGTTTATCAGCTTTATCTACTGATGAATTCGCTTCAAGTTAAATACATA
 CTGAATTAGCTGAACTGCTAATGGAGTGAGAAATGTTAGCCAAAAATTTATCCCGAGCAACCATTC
 AATTAGACGTTAGAGCTATTATGATTACTAAAGCTAGAGATAATGGCACTTTATTATTAAACAA
 AAGAAGTTGTTGAATGGATTTTGGATCAACATCTCATATAACAAATTTATGCTGATGAGAAATTAG
 CAAAGTCGAAAAAGATTCAATCCGAAAGTATTATTGCCAATTTTCCAAATGGTTGAAGAAATTA
 AATATTGGAATAAAAAATTAACACGAAAAATCCAGAAATTTTCGATTTAGTACTTACATTAGGTG
 GTGATGGTACTGTATTATTGTCTCAAACTTATTTCAAAAAATTTGCCACCTATACCTTTTCAATTT
 CATTTGGGCTCATTAGGTTTAAACCAATTTTGAATTCACTGCAATTAGAACAGTATTGAGCAAAAT
 GTTTTGATTCTGGAGTTAAAGCAAAATTTGCGTATGCGATTCACTTGTGAGTACACACTGATGAAG
 GGAAGTTGATTTGTGAACAACAAGTGTGAATGAATTTGGTAGTTGATAGAGGACCTAGCCCATATT
 TTACTCATTTGGAATTATACGGCGATGGATCATTTGAACGGTTGCCAAGCTGATGGGTTGATTA
 TTGCAACTCCAATGGTTGCACTGCTTATTTCATTATCTGCTGGTGGGCTCTTAGTTACCCCTGGTG
 TGAGTGCCATTAGTGTACTCCAATTGTCTCCACACCTTATCGTTCAAGCTATACCTATTAGCTG
 ATGGGATGTTTGTGAAGTTAAAGTCCCACTGAGCAGTAGAGCCACTGCGTGGTGTTCATTTCGATG
 GTAAAGTGGCTACTCAATTGAAGAAAGTTATTATGTGCTACTATTCAAGCTTACCATTGCCCTTAC
 CTACAGCTAATGTCTCCAAAACAGAATAATTGATTCTGTCTAGTAAATTTACATTGGAAACATCA
 GAGAGCAACAACAAACCTTTAGTTTATATTGAAACCAAGAACGCGACAAGATTGCTGCAAGATG
 AAAGATTGGAATAATTACATATTTCAGTGAACAAGATGAATCGAATCATGAGGAACCTGAAATAA
 CTGAAGATTTTGATATTAAATTACTGACAATGAAGCTGATTCTTCTAGTTCCACTCCTAGTGAAG
 AAAGCAACGAAGAATGTGCTAATACCACGACATAA

YJR049C_homolog 592aa (SEQ ID NO 394)

MSHKTQSQLSSQMKNLNTPPIDFNSTSSNNTMPSEPNQPOQQSQPEAKTEPQTRPATFTTSGN
 SSSSISTLSADIQLHLQSLINNNTSTVTQPAQSSSFQRRNPQRFNRNQLNVYDTFNSTPSSA
 SSISSSPKDFVTRFPRHISKLICEEIASANNRAAKELQSRHSTDELRSVKSHTELAEANGVRML
 AKNLSRATIQLDVRAIMIITKARDNGLIYLTKEVVEMLDQSHLITIVADEKLAKSRKRFNPESIIA
 NYPNFGCKKLKYNNKKLTKNPEIFDLVLTLGGDGTVLFSANLQKIVPPILSFLSGSLGLTFNFE
 SFRVTLSKCFDSGVKANLRMRFTCRVHTDEGKLICEQGNELVLDVRGSPSYVTHLELYGDSGLL
 TVAQADGLIIATPTGSTAYLSAGGSLVHPGVSAISVTPICPHLTSFRPILPLDPMGLKVKVPSSS
 RATAWCSFDGKFGYVYVITQASFPFLPTVMSSKTEYIDSVSRNLHWNIRERQKPPSSYLKP
 ETRQSTAESERLDNLHISSEQDESNHEEPIETEDFDINYNTERDSSSSTPSEESNEECANTTT

FIG. 2 - 40

YLR048W_homolog EMBL_entry 1042bp public: 1..1042; CDS: 28..786
(SEQ ID NO 395)
ATAGCGGCGCGCATATPATAGAGAATATGTCATTACCAGCTTCATTGACTTAACTCCAGAAGAT
GCTAAATTTGTTATTAGCTGCGCAACGTCCTATTGGGTGCTAAGAACGCTTCAAGTTCACAAACAAACCA
TATGTTTATCAAAACAGCAGATGGTATGAACATCATCAACATTGGTAAACTTTGGGAAAAAATT
GTTTTTGGCTGCCAGAAATTATTGCTGCTGTTCCAAACGCTTCTGATGTTGCTGTTTGTCTTCAAGA
ACTTTTCGGTCAAAGAGCTGTTTGAATTTGCTGCTCACACTGGTGTCTACTGCCATTGCTGGTAGA
TTCATCTCCAGGTAACCTTTACCAATTATATCATCTCGTTCATTCAAAGAACCAAGATTAGTTGTTGTT
ACTGACCCAGAAACCGATGCTCAAGCCATCAAAGAAATCATCTTATGTTAACTTCCAGTTATTGCC
TTGACTGACATGCGAGTCTCCATCTGAATACGTTGATGTTGCCATTCCA TGTAACAAACAAAGGTAAA
CACTGTATTGTTTAACTCGGTGGTGTCTGCTAGAGAAGTCTTGAGATTAAGAGGTTATATCCCA
GACAGAACTACCGAATGGTCAGTTATGCCAGATTGTTACTTCTACAGAGACCCAGAGAAGCAATTTGAA
CAAAATGCGGTGCGAAGAGCTAAAACCTGAAGGAGTTGAAGGAGCTCCAGTTGCTGAAGCTGAAACC
GAATGGACTGGTGAACCTGAAGATGTTGATTGGGCTGATTCTGGTGCTACCCCCAGCTGCTGAAGA
TGCTGCTGCTTCTATCTGGTAAACACTGAAATCTACCAATAAGAAGTAGAAGTAGAAGTAGAAGAA
GAAACAATAACAACAATAACAACCAAAATAAAAAAAGGTTTAAATGATGTATATTATCGATAAGGA
GAAAGAAGAGATTTTCTTTTAAATATAGGATGCCATTTTATACAAATCCAAATTTGTAATTTAA
GAAAGATTAAATAATATAATATATATATACTAAAAA

YLR048W_homolog SWISS-PROT_entry 253aa (SEQ ID NO 396)
MSLPASFDLTPEDAKLLLAANVHLGAKNVQVHNKPYVYKTRPDGMNIINIGKTWEKIVLAARIIAA
VPNASDVAVCSSRFTFGQRAVLKFAAHTGATAGRFTPGNFTNYITRSFKEPRLVVVDPRDTDAQA
IKESSYVNI PVIALTDMSQSEYVDVAIPCNMKGKHCIGLIWLLAREVFLRLRGILIPDRTEWVSVM
PDLFYRDPFEEIQNAVVEAKTEGVGAFVAEAEFTWGETEDVDWADSGATPSC

YLR088W_homolog 1335bp public: 1..80/494..776/821..1335, PathoSeq:
81..493/777..820; CDS: <1..1332 (SEQ ID NO 397)
TCGGGGCTACAAATTTGCTCCATGAAATTTGGGTTCCGCCACCAATACTTTGTATGCGATTATGCAT
GCTCCACGAGGTGAAAAATCCGAGGCAATGGCGTTGGTTGTGCCATGGACTAAATTTGACCAACGAG
TACAATGAAGGTGCTATGAGTTTGGCGGTGGCTTTGGCACGGTACTTTTCAAAGATGTCGATCTGG
TCGAAAAACATTAATTTTGTATTCTCTGAGACGGGCCACAGACCCTTGAGGTCTGGGGTTGAGGCA
TACCATACGGTGTGGACGATACTGCGGGGTGATTGAGCGCGCGATTATATGAGTAGCGGCAAG
AACCGTGATTATTTTGTAGATTACGATATGTTCTACGAAGGGTTGAATGGCGAGTTGCCGAATTTG
GACTTGTGTAATACGGCCAATGTAAATGACGATATCATGAACAGATCCCTCTGCCATGCAAGGGATG
TCGGATAGGGTTATCAATTTATAGCACCCGGTTGCGAGACTTTGTTTAGGGGTATCCTCAAATTTGACG
CTTGTCGGGTTGACTGATGAAGTTCTATGGGTGTGAAGCATTTTTCGGGGTGGCAGATCCAGGCATTT
ACGATCAAGGTAAGGGGACTGAAGGGAAGATGTTACGCGAGTTTGGCCGATTTGTGATTTCTACG
TTTAGGTCGGTTAACAATTTGCTTGAAGTTTACCAATCGTTTTTCTTTTACTTGTATGTTGTGCG
CCAAACACTTTGTGCTATTGCGGACGTACTTGCCGTCGCGGATTTTGTGGCAGTATCGTATGCG
TTGAGCTCTGTCAGTGGCGGTGGTGGTTGCCGGGTTGATTTCGAAAGCATATATTTTGTGGTGGTG
GTTGAAATTTGGGTGTGCTATTTTGGCGTTTGTCCCGTGAACAGGTGATGCTTTGAGCGATTCTG
CGGGTGGTGTGTTGCGCGCCCAAGCCATCTTTTCCAAAGCAGCGCGCTTTTTCGCTAATTTCTAAT
GCGTTTGTGGCAGTGGCATTAATTAACCGCCCTTGTGATTTGATGATTAATTTGCAATTTGGCGTTTGT
ATTGGGATTTTAGCCCTTCCATTTGACATTTTGTCCGACATTAATGAAGAACAGTCTAGGCTTAACA
GCTTTTGTGTTGGCGGTGTCGAATCCGTTTGTGATTTTCGTTGCTGGGAAAGTGTCTGGCCAC
CCCGAGCTATTGACCGGTTGCTACTGCTGCTGCGACATACAGTGTGGACATGGTTTATCGTT
GTTTTGGGGTGGTTCCGAGGTGGGTGATTATCACATAAGCTACTGTGGCTACAGCCAGTTAAG
GAAAAAGGTGAATAG

YLR088W_homolog 444aa (SEQ ID NO 398)
SGLQLSSMKIGFATNTLYIAMHAPRGENTEAMALVVPWINSNDNEYNEGAMSLAVALARYFTKMSIW
SKNIIFVFPETGHRPLRSWEAYHTVLDDTAGSIEAAIIMEYGNKGDYFEYDMFYEGNLQQLPNL
DLLNTANVMTYHEQIPCAMPGMSDRVINYSTRLQLFRGLILKLTGLVGLDEVHGCFAFSGWQIQAF

FIG. 2 - 41

TIKVRGTEGKDVTFQGRIVDSTFRSVNNLLEKFHQSFFFYLMLSPKHVFSIGTYLPSAILLAVSYA
LSSVSAVVVVAGDFRKKLYFVVVVEIACAILAFVVPNVQVMLVAISAVVLLPRQAIKFSKQAAFLSISI
ALLAVALLITALLIVHFALAFSIGILALPLTFVPTLMKNKSLRTAFCLAVSNPFFVIFVAGKVLGH
PELFDRLVTTAWSIDIQCWTFVIVLWGFPAWVITLTSYCGYKPKVKESE

YLR167W_homolog 1190bp public: 1..1190; CDS: 501..1187 (SEQ ID NO 399)

TAGGTCATTCTATAACAATTGATAGATGCAAGCTAATTGGAATGAAAAATCCATCTTGATCAAAAAC
CCTTTGTTCTCATAGTTAATCCGACTAAAGAGTGTCTTTTCTTTCTTTTGGCTATATC
CTAGTTGCCCTTAACGACAGTAAATAGTTAAAGCGTTGGGAAGTAAATGGTGAACCTCGAACCATTTGGT
TGACGCTGACGATTAATAATGTGAATTTCTTTTCTTTTGGTGTAGTAATTCGTTGTTGTTGT
TGTCTAAATTAGGAAAATGTCGTGACCTTACGTACAGCACACATACCACTGTGTCGTGACATGACC
AACACCAATCGCGTGTTAATCGATAACCAAAAGATTATAAATAGGGGGTGGGAAGGTGCCCACTGTT
TGAAATGAATCAACACAGTCTTTTCTTCTTGTCTTTTCTTCTATTTTACATATACAAATTCGTA
CAATCGTCAACTAACATATATATACAAATCTACAAGCAATGCAAAATTTTCGTTAAAACCTTTGACTG
GTAAACCAATTACCTTAGAAGTGCAAATCTTCTGACACCATCGATAACGTCAAATCCAAGATCCAG
ACAAAGAAAGGTATTCACACGACCAACAAAGATTGATTTTCGCCGTGAAAACAAATAGGAAGATGGCA
GAACCTTGTCTGACTACAACTCATAAAGAAATCTACTTTACATTTGGTTTAAAGTTGAGAGGTG
GTATGCAATCTTGTGTTAAACCTTAACTCGTAAGACTACTCTTGGGAAGTCGAATCTCTGACA
CCATCGATAAGCTCAAATCCAAGATCCAAGCAAAAGAGGTATTCACACGACCAACAAAGATTGA
TTTTCGCCGCTAAACAAATGGGAAGACGGTAGAACCTTGTCTGACTACAACTCCAACAAAGAACTCTA
CTTTACATTTGGTTTAAAGATTGAGAGGTGGTATCAAACTTTGTTTAAACCTTTAACTGGTAGA
CTATCACTTTGGAAGTCGAATCTTCTGACCATCGATAACGTCAAATCCAAGATCCAAGACAAAG
AAGGTATTCACACAGATCAACAAAGATTGATTTTGTCTGTAACAAATTAAGAAGATGGCAGAACCT
TGTCGACTACAACTCCAACAAAGAAATCTACCTTGCACTTGGTCTTGAGATTGAGAGGTGGTTTCT
AA

YLR167W_homolog 229aa (SEQ ID NO 400)

MQIFVKLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQQRILFAGKQLEDGRITLSDYNIQKEST
LHLVLRLRGGMQIFVKLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQQRILFAGKQLEDGRITL
SDYNIQKESTLHLVLRLRGGMQIFVKLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQQRILF
GKQLEDGRITLSDYNIQKESTLHLVLRLRGGM

YLR234W_homolog 2390bp public: 1..2390; CDS: 501..2387 (SEQ ID NO 401)

TCCAGAATAGTAATTAGGGACTTTAATTTTATTAGGAGTGGATTGCATAGAATATGCTATCTAATA
GATACATCTTATTATATTCTTATTCATGCGAAAGCACCAGTATATGGAAATGCTGCCCAAGGTAGT
GCACACAACAACTAGTTTACAAGTAAATTCGAAGTTACGTCAAAGCTTAGAATGGTTCTTATA
GTAGTTGCTACTCTATCAAAAAACCCATAATTTGCTCTATAAACGTAAGGATCACTATATGCTGT
TGAGTAGAAGAAATATGTTGCGAGCCGTACCGACAATGGATTGGCTGAAACTTGTCTCATCAAACTT
GCAAAACACTTTGGAGACGCGCGCGCTTCAACACACAATAAACCAACACGAAATAAGGTAGAGAA
ACAAAACAAAATAAAGGAACCTTTAAACAAGAAGTAATCCCCATTAAACACTTGTATCAAACTTTT
AGGTTTCCGATTTCGCCATTTTCTTGACTAAATAATATGAGAATCATATGTGTGTCGCGAAACAC
CATCGATTTCAAAAGAGGTGGCAAACTTTTGGGAGGAGGGCGAAAAAAGTAAGAAACTCAGGAG
AAAAATTCATCAAAACACTACGATTTCACCTTCACTTTCAACTCTGAAGATTGGCCATGTCAAGTAA
CCATGACTCTCGTGGCTGGACATATCACAGGACTTGATTTTGGGCTCGCCTTTTCGTGGGGAAT
GTGTTCCCGGCGACTATTGAAGCAGACATCAAGACCATTTATCCACAGAATACTATTTATGAAA
ATATTGCAGAAGAGGTGCAAAACGCTGATAAGTTGATGATCTGGACAGATTGTGATAGAGAAGGAG
AATACATTTGGATTGAAATATGAATGCTGCAAGAAATACAAATAGGAACCTTGGGTTAAACAAATA
TTTGGCGGACTAGGTTTTCACACTTGAACGAAATCACAATTTTCGACGACGAAATAATCCCGTGA
ATTTGATATGAGTGCAGTTTCTGCACTTCTTGTGCTATGCGAAATCGATCTTCCAGTGGGTACCA
GTTTTCACAGTTTGTGATGATCAATTGAGACAAAGGGGATAATTGAAAGAAATGAACATGCTTT
CTATGTCATGTCGAATTCGACATTTGGGTTTGTGTGATCGATGACAAACGATCAAGAGTT
TTACACCGGAACCATTTCTGTTATATTGAGATTGAAACTAGGAAGAGAAATAAAGACAAATTTTCA

FIG. 2 - 42

ATTGGGTCGAGGTCATTTTTTCGACAAGATGTATGTGGTTATGCTTTATGATCGATGCTGCAAAA
 GTGGAGAAATTTGGAACCATATCAAAAAAGATAAGTCAAAACCGAAACCAATTTTCGTCCTATCCCAT
 TGACAAACCGTGGAGTTTACAAAAAGATGTGCTAGATTTTAAAGATGTCTGCTAAGACCGCGTTGG
 CAGCTGCTGAAAGACTTTTAAACCTAGGGTATTGTGCTGATCTCTAGAACTGAAACTGACAGGTTTG
 CCAAGAAACCGATTCTTAAGAGCTTTACTAGAGGTGCACAAACAGATCCGGCTGGGGAAGCTATA
 CAACAAGAGCTTTTGAACGAAAGTTTCAAACTCTCGAAGCGGTTCATGATGATAAGGCGCAT
 CTCCAATCCATCTTCAAAATATGTTCTTGGACACCTTAAACACCTTCGATGATAAGAAAGTGT
 ATGAATACGTTGTGCGACGCTTTATTTGCTGTGCTCCAAAGATGCTGTGTGACGCAACCGTGG
 TGACTTTAAATGGGAGATGAATTTCTTACCCTCAAGTGGATTATGTGGTATGAAAAAATTTATT
 TGGAAAGTGATACCTTACAAAAAATGGGAAGCTCTAAACACTACCGAAATTTACAGAGGAGAAC
 AGGTCAAGTTGTGCGATGGAAATTTGAAAGACGGTAAAAACAGTCCACCAATCATATGACCGAGC
 CCGAGCTAAATGTCATTGATGGATGCCAACGATTTGGAACCGATGCTACTATCGCTGAAACATATTA
 ACAAATAGAGACTAGGCCTATATTAATAAATTTGAAAGAGGGGAAAAATGAATATATTTCTTCTTA
 CTCCTTTAGGAATGGGGCTTATAGAAGGCTTTGAAAAAATGGAATTTGAAGATGTATCACTACGTA
 AACCATTTTTGGGGAAGTGTGGAACGATCACCTGAGGACATAGCAACCGGGTCCCGGGCCAAAG
 TGGATGTTTTGAATACAAATAGGCGTATATGTGACGCTTATAGTGTGTTGTTCTCATCAGATAC
 TGTGTTTGTGCAATGAATGTAGGAGAATTATACCTTGGAAATAGCAGTAACACACACACACATA
 ATAATAACGTAA

YLR234W_homolog 629aa (SEQ ID NO 402)

MRILCVAEKISKEVANILGGRRKKVRNSREKIFKNYDFTTFNSEDGPCQVMTSVAGHITGLD
 FGSFAFSGNCPVRLFEADIKTIITKKSIYENIAEEARNADKLMIWTDCDREGEYIGFEIMNAARK
 YNRNLGLNNIWRARFSLERNHIIIRAAKNPVNLDMSAVSAVSCRMEDIDRVGTSFTRLITDQLRQK
 GIIEKNELASYGTCQFFTLGLFVVDYRKRVKSFPEFFWYIEIETRKENKKTIFNWVRGHFFDKMYV
 WLYDRCKSGEGFTISKIESKRKNFRRPFLITVELQKDCARFPMKSAKTALAAERLYNLMGLYS
 YPRTEDRFAKETDFKSLLEVHKQDPRWGSYTKLNLNEGFFTPRSGSHDDKAHPFIHPIKYVSLDT
 LNTLDEKKVYEVVRRFIACCSDAVGTQTVVTLKWGDEFFTAGSLMVHEKNYLEVYTKKWESSK
 QLPKFTTEGEQVQLSSGILDKGKTSPPNHMTPELIALMDANGIGTDATIAEHINKIETRYHINKLV
 KGNKEYLIPLTPLMGHLIEGLEKMEFEDVSLSKPFLRKSLESLIEDIATGSRPKVDVLTNTIGVVVD
 AYSVCSHQIILVLCNECRRIILGNSNNNNNNNNNT

YLR241W_homolog 3098bp public: 1..827/2190..3098, PathoSeq:
 828..2189; CDS: 501..3095 (SEQ ID NO 403)

ATATATAGAATTATGGCTTAGTGCCCTTTATTAACATAAATAGAGGTTACATTAATACAACTTAAC
 AAAACAAAGGAACATAACATCCACGTATAGGGCTTCTTATATTAATATACCTAATTCACCTGATTAT
 ATTGCCCTATATACAGCTTGTAAAAAACACATAAGAAAGTTTACATCTCAAGATGAATTTATCCCC
 CTATTGTAAAAAGTACATCGCCTAATGATAGACATCATAGAGTACTGGCGACTCCTTACATGATGG
 TAAACGACAAACACTACAAACAAAAAACAATATCTTGACGGTATAATTAGTAGTGTGCGAGAGG
 CACACGATAAGATTTATCAGTTTCTTTCTCGTTGACCTTAATCTGTTTTGTATAGACTTTAT
 TTTTGTGTTTTGACCAACCCACTTTTAAATATCAAGAATATTTAACTGATTATAGAAACAA
 CAACAAATAACCCAAATACGTTAAACCACTTTTATACATATGATAGACAAATATAATCAATAATTTGC
 AAATCACTACTACAGCAAAATGATGATAATTTACATCCCCCTACGACGATGTGATATCTGACAC
 ATTCTGCTCGTGTAGCACGATCAAGTAATAATTTGCACTACATTTGGGACTCACTGGCCATTATAC
 TATTTTCTTCTATTTACAGATTAATAATATCCCAAAATATATGTGGGCAAACTTTAATCATTTGAATTTCA
 GTCTACATCTGCAGCTCAAGAGGAATTTACCTGAATTTGCTTCAAAATCATATTATTTGGTGGGATTC
 CTACAGTTTACAAAAATCTAGAGCAAGAAATTTTGGAAACATGCTGGATTAGATGACAGTTGTGTTT
 TGGAAATTTTAAAAATGTGCATTCGAATAATAAGCATATGTTTAGTATTTTGGCATTTATTTATCATAT
 CTCATATCAAGTTTATACAGGGAGAGTAGATGAAGATTATCCCGAGCTGATGATGACCAACG
 ATACGATGATGGAAGTAATAATATGTTACCAATAATTAAGCATATAGTGTGACGTGGAATTC
 TGGTGGCAAGTAAAAATAACGATGGAGAACAGTATCAACAATTTCTTTGGTTATACACTATTTTCA
 CCTATGATTTTACATTTTGTGTTACTGTTTCTATTTCAAAACAAACCAATAGGATTATTTCTATGCG
 GTCAGAGATATCTTGGATCGCAAAATTCAGTACCGGATAGAACGGTAAAAAATCTCGGGATACGAG
 GATCATATACGAGATGAAGTGGCACTCGCACGGCACTTGACCGTTTGAATATTTGGTGAAGTGGATT
 CTGTGTTGATTGTGCAAGGATGGCAAAATCTAAACAACTATTCAAAAGGAAGGAAGAATGTTCT

FIG. 2 - 43

GAAAAATTAGAGGAAAGTTGGGTGGAATATTTGAAAAAATGGGATAACCAATAAGAGCGATTGGA
 TATCGTTGCATCCCCAAGTTGGCGAACTGATCGTTTTTCCAATAGGTATCTGATGATCGAGAAG
 AATCAGACACTGGGGACCTCAAAATTCGAACCTCGCACAAAGCTTCAATTAATAGATCAAGACTCAG
 AATCTGTTGAAGGAGATTCTCTGACACTTTGAATCGCTTGTGTAATGATGAACCTGAGAACAAGC
 CAACTCTTCGGAAAGGTTGGTTCGGATTGTTTGGACCTAAAAGTGGATTCAATAAACTACTACACCG
 ATAAATTTGGAAGGTCATAGATAAAGAGATTACCAGGGCCGAGAAGCTAGAGAATATCCCGCCACTTCGA
 CTGCATTCTTCTACATATGAAAAACCGTGGCTGAAGCACAAATGTTGGCACAGGCGAGCTCTGGATCCAA
 AAGTCAATCATCTTATACCAACCTTGGCCCCGTCTCTCATGATATCCGATGGGATATTTGTCAT
 TAACTAGACAGTACAGAAATACAAAGATCCTTGCTGTACAGATATTTATTTGGTATAATGAGTTTGT
 TGTGTTGTTTATCCAGCTCAGATTTATGGCTAGTTTTTAAACACTAAAAGCAATCTTCAAAATATGGCC
 CATCATTTGGGGAAGCTATGGAATCGCATAAATGGGCGGAACTTTGATTACTCGGATTATTTGCCAA
 CTTATTTATTTACAATTTTAAATATTTCTGATTCCGTTTTTTTATCTATGGATTCTCGAAAAGCAAG
 GTTATTTATCTCATAGTGTGATGAAGAGTTGTCATCGGTATCCAAGAACTTTTCTATATATTTGTGA
 ACTTATTTTGGTGTTCACAACTTTGGGTACCGCCTCTTTGTGTGATACGACCAAAATGCAATTGT
 ATTTAGCAAGATCAGCTCAGAGATTGTCATATGTTCTATGTTGACTTAATAATTCTACAAGGATTGG
 GTATATTTCCCATTTCAAATTTATTTGGTGGGGAACCTTACTTCGCTTTTATGTAATTCATATTTTA
 GGTGCAAGACCCCAAGAGATTACTTGAATTTGTACAAACCGCAGTTTTCATTTTGTGATTCACAAT
 TACCACAAACCAATATTTGATATTTATTTATTTACGTTGGTATATCGGTAATGTCCTCGAAGATATTTAA
 CTGCAAGGTTACTATATTTATTTATTTGTTTATTTGTTGAGCAAAATCAAAATGCTTTATGCTTTGTG
 TTCATCTCCACACTCAACCGGCAAGTTTGGCCAAATATTTCCGAAAGGATCATATTTAGGGTTAT
 TCTTTTTCAAATCAATGTTTGGCACATTAGCAATTACAAGATGCAATTCACATGTCGCTACTTTCT
 TGGCACCATTCGCGTTTTTGGACACTTTACTTTTGGTGGAGTTTCCATAAACCAATATTTTCCCTTTGT
 CAACATTCATTGCTTTGAGAGCAATGAAAGCAATGAAATATCAACCCCTACTGATTGAGAGCAAA
 TCATTGAAACCAACAATAATAAACTCTTGAAGAAAGAGGGAATTGAACACTAAATACGAATAC
 CCAATCTAGTTAATGATTAGACGGGCCAATGATTGCAATTGGATGGTGAAGATGATTGATGATGTA
 ATCGAGATGGTACAACTGTACGGAACCACTCAATATTTCAAGTTCAGATGGGACTATTAA

YLR241W_homolog 865aa (SEQ ID NO 404)

MIDNIINNLIQIILQONDDNFTSPHDDVIYRPHSARVARYQVIIASTLGLTALLFLSILRLKYPKIY
 VANFNHNLNLSLHSTSRRLPELPSNLSFGWIPTVYKITEQEILEHAGLDVAVFLEFFMKCIRIISI
 CLVFAIIIIISPIRYKFTGRVDEYDPPDDSDNDDDDGSSNNNGTTIIKIHVSAGISVASKNNDGBOYQ
 QFLNLYTIPTVYFTVTGYVFLFKQTNRIISMRQKYLGSNSVTDRTVKISGIPGSLRDEVALARHI
 DRLNIGEVDSVLIKVEQNKLKFKRRRIVRKLEESWVEYFEKNGITNKSOLDLISHPQVGESYRF
 SNRYTDDAESPDWGSQNSAQASIIDQDESVEGDSSTLNRLLNDESTRPSLRKGFWFLFGP
 KVDISINYDDKLEVIDIKETIRARTREYPATSTAFITMKTVAAEQMLAQAVLPDKVNHLITNLAPAP
 HDIRONWLTQRDNRLKILAVTTIFIGIMSLLVVVPFRFMAFLNFKSISKWPLSGKAIESHKWA
 ETLTIGLLPTYLFTILNIVIFFYVYVWISSEKGYLSHSDDEELSSVSXNFFYIPVNLFLVFTTPTGAS
 PVDTTKIAPDLARSLRDLISFYVDLIILOGLGIFPFKLLVGNLLRFLVNSLFRCKTPRDYLNLYK
 PFVNFQGLQFQPILFIITLVVSVMSKILLTAGLLYFIIGYFVSKYQLLYACQVHPHSTGKWPI
 IFRRIILGLFLQPIITWGTALQDAITCATFLAPLFLTLTYFWMSFHQYIPLSTFIALRAIESNE
 NINPTDLEQIENNNGKTLDERRELNTKYEYNLVNDLDGFMIALDGEDVLVNRDGTTVRKPPQY
 FSSEWDY

YLR321C_homolog 1559bp public: 1.947/1189..1559, PathoSeq:
 948..1188; CDS: 501..1556 (SEQ ID NO 405)

TTCCAGAATTAGTAGATATTTCTGATATCAAGTTGGAGATAGGGATATCGAACTGGGATTCTATAT
 TTTGTTTATCTTGGAGAACTGTGTGTGTGTGGCGTTCTATCTCTTTATATATTTTCTCATTA
 ATTCAATGAAACATTTGAAGGAAATCTTCTTAAAAGCACTAGTGACACATGATCTCTAATCT
 CCAGTCTTTGATTAATATATCTTTTGAATATCAGGTGAAGAAGTGTGGTAGTCATGACTAGTA
 GATACGTGTGTGTGTCTGGGATAATAATATATAATGATAAACAAACAAAGTCGTGTGAGTGTATATT
 TTTCTTTTGTCAATTCATCTTTTCTTTTCTCTTGAAGAAATGATAACAGAGGATCCATGATATT
 TGCTTGACAGAGAAATACAGAACTAAACAAACATTTTTCATCTCTTCTTTGTTTGTGTTGTT
 ATACCCCAAGGTTTGAATAAGTCTTCAGATATCTAGCATGGGCACTCTCAAGAATTTGACAGCAG
 ACATACAAGCTCTTGCACATAGTTTCCCAAGCGATTAGCTAATGATAGTACAACTCATTTACTTA

FIG. 2 - 44

TTAATGTTGCACCAACTGGTCGACAAGCCAAAAGACATATTCAACAGATTAATTACTCCGAAGAGT
TTGGAGATGACCTTGATTTTGTATGAATTCCTCATCTCGACACCCGGTACTAGAAAGCTTAAATGAAA
ATAAGGGCCCTTACAATGTTTACCATTTATCTTCGCAAAAACACACCAACGCCCAAGAGATCT
TAGAAAAACCGGTGTATCTGAGTTGGTTGAAAAACAGTGGTGTCTTATCTCATCAAAATTAATGA
TTGCAAAATTTGAACACAAAACCAAAAGTTGATTTGATTCCTTTATGTGGAACCTTGAATGAAAGCTTGA
TTACACCAACTGAGTTTTCGGGAAATTTGTTGCAAGTATTAGATTTACCATTCAGTATGGCTGCAC
AAATAGCAGACTCCATTAATCAACAGATTGAAGAGTATTCCTATGCATCTAATTTTACAACCTACCAA
ATAAGGGCCCTTACAATGTTTACCATTTATCTTCGCAAAAACCAAACTTAATCAACGAGATA
GATTTGAATGGGATATGAATCAAAATGAAGTTACACCGAAGATTTTTCGTGAAATAGTTGTTGCTG
ATTTCGGGTATCTGTTAGAATTTAAGAAATGCCATATCAATGCAATGGCAGAAATTAATTCAGAG
TGAAAAAGAAAGTATAGATGGTACTTTTGACAAATGAAATGCAACAATTCGATCTAGTAAAGAGTA
TAATATTGTTGAACAAAGGAATAGAATTTTCACTGAAACAGTGTTCAAAATGGAATGAAAGCTGGG
AACCTTTTGGTCGAAGTATTGACTTCTAGTGAATCGAAAGAGAGAAATGAAAGGGTTAGAAACT
TGAGAAGATTAAGAGAGAGAAATATGAGAAGAGATTACGATGATCATAGTAGGAGAGGCAAGCAG
GAAAAAGAGGTATGATGAGTTAGAAGGAGCTCGGTATAG

YLR321C_homolog 352aa (SEQ ID NO 406)

MATSQELTADIQALATSFPPKRLANDSDNSLLINVAPTGRQAKRHIIQIYNEEFDDDLDFEFPSS
TPGTSLINENKQIEAQRYSKANTPTPKRILEKPVLSSELVEKPVVLIPIKIMINENLNTNKLIDS
FMNINLESILPTFEFAIIVCSDDLDPFSMAAQIADSNQIIEYSYASNLQLFNKGPYNTVIDLSV
NLAKQLYQDRFEWDMNQNEVTEPELFAEIVVADLGLSLEFNKAIASHALHEIIRVKEVIDGTFDNE
MHNHLVKGIMFEQIRIFTENSVDQNGNDRWEPLVEVLTSSSEIERRENERVRNRLRLKRENMRDY
DDHSRRRQAGKRRRDELEGAW

YLR325C_homolog 737bp PathoSeq: 1..737; CDS: 501..734 (SEQ ID NO 407)

AAGAAAAGTATAGTCAAAATGTTATACAAGCTAAGGAGCCATAAACTTTCTTTGGACATGCTAATA
TCGCTCCTGACCATTTGTTTACTATATTCAACAAAACGAATTCACAAAGGCCAAACGAAAGCTACATG
AAACTTAAGTTATCGGCAACGCTGTTGGCCAATTTGGGGTGGTCAATGTAGGTATTCATGCAAGAAGT
GCAGCACTGAAAAAACCAGGTCCTTAACGTCAGTAACATAATGCTAAGCGAGTCTACACGAAGA
TGGATTATAAGTATAAAGAGGTTGATTAGTTTAAAGAGAGAGTATATAATTAATGCACGTGATTAG
TTTAGTAATTTTTTTCGCGAGTTAGGGCTATAGCCCTAAGACATTCACACAACCTAACAAAAAGGAAGT
TCTCACGCACATAACGTTAAACCCACATAAAGAAAGAAAAAAATTTCTTTTGAAAAAATTCACA
TCACCGCTTTAAACCTTCAACCTATAACAACTCCAACCATGGCTAGAGAAATCAAGGATATCAAAG
AATTCGTGCAATTTGGCTAGAAGATCAGACATCAAACTGCTATTTGTCAAAGTTAACGCCAAGGTCA
ATGCTAACCGGTAAAAAATTCAAACAAACCAAAATTCAGGTCAGAGGTTCAAGATACCAATACACAT
TAGTTGTCAACGATGCTTCTAAAGCTAAAAAATTAACAACATCTTTACCAACCACTTAAAAATCA
CCAACCTGTAA

YLR325C_homolog 78aa (SEQ ID NO 408)

MAREIKDKIEFVELARRSDIKSAIVKVNKVNANGKFKTKFKVRSRYQYTLVVNDASKAKKLQ
QSLPPTLKITNL

YLR344W_homolog 1348bp PathoSeq: 1..1348, exon 1: 501..515, intron 1: 516..979, exon 2: 980..1345 (SEQ ID NO 409)

ATACCATTGACAAAGCAAGCTCAGGGTCGCGGGTTCGAGTCCCGCGGGAGCTAATTAACCCCTATT
TTTGAACCCACCAATTTTCTTTCACATTAATGAATGAAGAGTATTCCTTCGGCTCTCTTTTCTTT
TTTTTTTGGGCAATATAGAGAAAGCTGTAATAGTATAGCTCACTAAAAGTCTTTTTTTTCTATT
CGTTTTATATTTTTTAAAGAAATTTGATGTTGATTTGGTAAATGCCAAATTTTAAATGTGTGTAG
GGCTATAGGCCCTAATGTACTGTATATGTCAGTATCAGAAATCACTTTTGTGTACGCACAGTTTGCTTA
CCAAATACATATATATATATATTTTTTTTTTTTGGAGTAGAGGAGCTACACTAGACACAGTGGC
AAAAATCATCTCTCTATACACTTACTCAATTTGAAGATATCAAAATTTTTTTTCAAAAAAAATTC
CTTTTGGATCGATACTAGATAGCATATATCATCAAAATGGCCAAGTACAGTCAAGGTATGAAAT
AGATATTCAATTAGATATGGAGAAAGGAAGATAAAAGGAAAAAGAAAAAGAAAGAAATAA

FIG. 2 - 45

AGGAATATATACATTGAAAAGGAGATAGAACATCAAACAACAACCATTAAGAATTTAAGTTTAATAC
AGTTTCAATAAGAGGGTTTTTTTCTCAGAACCAACCATTTGACTGAAGTACTACACCAAGAAGGTA
TAATGATTTCACGATTTTACCTGGAATATAAAGAACATCCCTTAATATTGAATTTCAATATTAAAAATA
CAATTTGGGGATATTGATGAATATTATGTATAGGAGATTCCATTTTCAAACCTTTGTAATGGAAAA
CTTGAAAAATCAAATCAAATCAAATCATAACCCCTTCAATATATTCCCTTCCTTATCTTACTTTTCCT
ATTAAAAACAAGACTAAGAACATTCAGTAAAACTAACAAAAATTCATTTATATAGACGTTTC
TTCATCTCGTTCTAAGCTAGAAAAGCTTATTTCTAGTCTTCATCAGTTGAAAGACAGATCTTTT
ATCTGCTCCATTTATCCAAAGAAATTAAGACAAACATACAATGTCAAATCTTTGCGCAATTAGACAAA
TGATGAAGTTTTAGTTGTTAGAGGTTCTAAAAAGGTTCTGAAGGTAAAGTTAATTTCTGTTTATAG
ATTGAAATTTGCTATTCTAAGTTGATAAATTACAAAAAGAAAAATCAAATGGTGCTTCTGTTCCAAT
CAACATTCACTCATCTAAAGTTGTCTATTCTAAATTACATTTGGACAAAGATAGAAAAAGCTTTGAT
TCAAAGAAAAGGTGTTAAAGCTGAATAA

YLR344W_homolog 127aa (SEQ ID NO 410)

MAKISIDVSSSRKARKAYFTASSVERRVLLSAPLSKELRQYVNVKSLPIRONDEVLVVRGSKKGS
EGKVNSVYRLKFAIQVDKLQKEKSNASVPIINHPSKVITKLHLDKRKALIQKGGKAE

YLR393W_homolog 1631bp public: 1..1207/1209..1631, PathoSeq: 1208;
CDS: 501..1628 (SEQ ID NO 411)

TTTCATCTTTTGGAAATCTTCCCTCTTGGAAACGACCAAGAGTTGGATTTCGGTGCCCTTGACTAGCAG
AACTTTTCTCAAATCTTTATTGAATAATGCAACACCACCGGATGCGTCAATTTATTTATTTTCC
GAATTTAGATAAATGCTTCTCTGGGTCAACCCCTTTTCCAAATAAGCGGGCATTTCTCTAAAATCTTT
TGTAAGTGAACGCTTCTCATCTCATGCTTTTGGAAATCGGGATTCACATGACGAACAAAGTCAGCATA
AAACCATTTGCTGCTCTCAATCTGAAACATTATTTCTTCAATGGAAGATAAATCCCTCTCGGGAAC
ATTCAACCAAAATCTTAACATAAAATCTTCCAAACCCGATCTAGAGTTTGATAGCTAAACCAT
CGGTAATTTGGATCGACATCTTGTATTCTTATGATTAAATCTTTCTTTCTTTCTTTCTTTCTAC
TGAATATTCGTAATTAATAATTGATTCAAATTTGATTGATGTTTGTATATCTGGATAAAACAACTTGT
GTGAGATCATTTCAATGTAATTTGCTGGCGGAGAAGGAGGCAAGGACGAACCTTTTCTCTTCATACT
TTTTTTTTCTCTCTCTTTCTTTCTTCTCAGTCACATTTGCTGAGTGTTAAAGGCTGGCTTTCTCTGTG
CTGAACCTTGTGGACTGGTAAACGCACGACATAGAGTAATATTTGGAGAAACCAAAAGAATTTGA
AAAACCGTGGTTTGAATTTCGACACAGATTGGTTGGACGACAAAATGCAAGGTGATTTATCCCGGA
CTTTTGTCTACCTCAAGAAATAGAGTTCCAGCGGTACCAGCCGCTTTTGTAAATACCATTAAGAAAA
CGGTCAAATCGGCACAAGAAAGTCTGACAGTATTACTAGACCATTTGGGGTTGTCAAAACCATGTTT
TGTAAATCATAAATTTGTCAGACACATACACTATTGTCCTCAATATATACGAGGAGTTGTTTGGTCAAA
AATCCAAAGAAAGAGACAGAAACAACTAGACTACGATTGTAACACCTCGCCAAATTTATGAAGTCA
AGTCAATTTGAGAATCAAAAGGGGAAAAATATTTACTCTCTCTGTTTCGTACTTTTCGACAAGACAAAT
CTTTGTATTTCCTCGGATTTTATAGCGAAAACATTTGGCAGGTAAATCAGAGAAGTTTGTACGACTCAT
TAGACAATAGATTAAAGCATAGTCAAATTTGTTTCTTCTGTTGCTGGTGAGCAGTGTACCCGTTCTGT
ACTTTAAGGTTGAAACAAAGATTACTATTCCAGGATTATGATACCTTTTGTGGAGGAATATCCCC
ATACCCAGATACTTTGATGTGAATATGCGCGCAAGGTTTGGATCAAGGGGTTTGTGACAAAATTTGACGA
CAGGAAATTTAAGAAAGACTTTGAAGCCAGCTCTGAGATACGAGAAATTTATTTCTATCTTGTCCCTGGCC
ACATAATGTCAAGCGGAAATTAGAGAACAGTTGATCTGTGATAATCAATGTATTCGGGTATTTATATA
TTGTTGATTTCGATGGGGAAGATAAGATGGGCGCAAGTGGGTATGCAACTCTGAGGATTTGAAAT
TGATGTGAAGGTTTGTAAAGGGGTGCAAAAGAGAAATGACCAAGTAA

YLR393W_homolog 376aa (SEQ ID NO 412)

MFVYWINNLCELLQICNRRRRQRGRTFFPSYFFFLSLSLFFQSHCSSVKGWLFCAEPCGSVNAHRV
IFGETKRILKNRGLNSTTDWLDKMQSVFIRTFATSRIFQRQYRFRVNTIKETVKSQAQKSYSIT
RPLGLSKPVLLNHKLSDTYSLSNIYEELFGQSKERRQQLDYDLKHSPIYEVKSFENTGKGFPP
PVSYFRQDKSLYFPDFIAKTLAGNQRSLYDSLNDRLSIVKLFSSVAGEQCTRSYFKVENKDYSSQ
YDTFVEEYPTHQILDDNMPQSWIKGFVNLSTGLNRKTLKPSRYENYFLPGHIMSAREIQLYC
DNQCSGYIYIVDSMGKIRWATSGYATPEDLKLMLKVVGVQREMTK

FIG. 2 - 46

YML063W_homolog 1271bp PathoSeq: 1..773, public: 774..1271; CDS: 501..1268 (SEQ ID NO 413)

CCAGTGCCTTTTGGTTTGTTCACATCATACACTTCACTGAACTAAATAGTTTGTTCATTTT
 GAGACTTCAGGTACGACCCAGGTTGCGACAAAGTTTAGGTAGTTTGTGCTCGAATGTCGCAACA
 AAATAGGGCTGTAGCCCTAGTGCATGTGATGTGAATTAACTAACAAGAAGAATTGCTGTGGCGCA
 AAGATTATGTGTATTTTATGTGCGTTGTATCTCTGCACACTAAAATTGAGCAGTGTACACACACA
 CATATTGGCGTGTATTTTATTCTGTGTTTCTGCTGTTCTCTCACTGTTAAGCTCTAAGTGGAATT
 TGTGTGCTGTGAATAGTGTGTGTGTTCAGTCCAGCTCTCACAGATCTCACGACGCCCATTA
 CTACTGAAAAATTTCTGACTTTCTGTATCTAAAAATTTTCTACTAGGAATTTTTTCTTTTACGTT
 TTTCTGTTTCTATATAATTCACCAACTCAAGTACAACATGGCTGTGCGTAAAAACAAGAGATTGT
 CCAAAGGAAAGAAAGGATTAAAAAGAAAGGTGTTGACCCATTCCACGAAAGAAATGGTTTGACA
 TAAAGACTTCCAACTCTTTGAAAAACAGAAATGTTGGTAAAACTTTGATCAACAGATCTACCGGTT
 TAAAGAAATGCCCTGATGGCTGAAAGGTAGAGTTTTCGAAGTTTGTGTGGCGACTTACAAGTT
 CGGAAGACCACTCTTACAGAAAAATCAAATTGAGAGTTGATGAAGTTCAAGGTAAAACTCTGTGA
 CCAACTTCCATGGTTTGGATTTCACCTCTGACAAAATTAAGATCATTTGGTCAGAAAATGCGAATCAT
 TAGTTGAAGCTTAATGTCATGTTAAAACTTCCGACGATTACGTTTGGAGAGTTTGTGCCATTCGCTT
 TCCAAAAAGAACCAACCAAACTCAAGAAAACTACTACGCTCAATCTTAATTTGAGAGAAG
 TCAGAAAGAAAGATGATTGAAATATGCAAGAGAGAAGTTTCCAACGTACTTTAGCTCAATTAACCT
 CCAAAATGATTTCAGAAAGTATTGGCCGTGAAATTTGAAAAATCCACCACAACCTTTTCCCATATC
 AAAATGTCCACATCAGAAAAAGTCAAATTGTTGAAACAAACAAAATTCGACTTGGGTTTCATTATTGG
 CTTTGCACGGTGAAGGTTTCAACCGAAGAAAAAGGTAAGAAAGTTTCTTGTGTTTCAAGATGTGTTG
 TTTTGAATCTGTTTAA

YML063W_homolog 256aa (SEQ ID NO 414)

MAVGNNKRLSKGKGLKKVVDFFTRKWDFFDKAPTTFENRVNKGTLINRSTGLKNAADGLKGRVF
 EVCLADLGSEDSYRRIKLRVDEVQGNLLTNFHGLDFTSDKLRLSVRKWQSLVEANVTVTSSD
 YVLRVFAIAFTKRPQNIKTTYAQSSKLRVVRKMIEMQREVSNCIAQLTSLKLPVIGIREIE
 KSTQTFIFPLQNVHRHKVLLKQPKFIDLGLSLALHGEGSTEEKKKVSSGKDVVLESV

YML128C_homolog 1517bp public: 1..1499, PathoSeq: 1500..1517; CDS: 501..1514 (SEQ ID NO 415)

TGATATGGATTTTCAAACATAAGAAACAATACCACTACAACAACAAGAAACATAAGTGTGTGCT
 TAATTCAATGACCTTCGAGTCATATTCCCAGTTTAAAGTATGAGTGTGTTACGAAGTTGTGGATCC
 TATTTTAAATAAACAATAATAGTAATAAAAAAAAACCTCTTTGCTTTTCGAGAAATTTCTTAAC
 ACATTTGTTCTCTTCTCCCAACGCAACCAAATTTTATTTTATTTTCTTTTGGGACTTACCACACA
 GTTGCTCAATATGTATAACAAGGTTAGAACTCTGTGGGATTCCTTCTTAAAAATATAGCAATC
 CTTTTTCTTCAACAGATTTGCTATATGACCCCCCCCTTAAGCATTTCATTCGCTTTTATATATATT
 ATAAGTATTTCTCTGTTTTCAGGATAATTATCACTAATTGTGACGTTTAATTTTATCACTTCTCTCT
 TCTTCTCTCTCCTATTTCAACATTAAGAAACATTTAATATGTATTTCCCAATCATTTGATGTGTTAT
 ATGATCTTCACTTTTGTGGTTGCCAATTATGGTTTGTATCAATGGACAAATGATGATTTAAAAAC
 AATTTTAAAAAGAACGTAAGATTGCAATCAATGATGCCTTGGAGAATCCAAAAATTAATAGTTTGG
 CTAATGAAGAAGCTTAAGAAATAGAAAAAGGTTTACAAGAAAGTTACTGAAGAATTAATTAAGCAAT
 TGAATTCCTCCAGATGATTCAATTAATGATTATTTGAATTTTGAATTTACTATTTTGGGAAAAAGAAAG
 AAAATTAATTTCAATTAAGTAATGGATTTTTGAAGTTGGCCAGTAACACAGTTTGCACAACTTTTAA
 CTCAAAAATAATCAATATAGTGCAAGGATACCAAAAGATGATTTAATCAATAAGGTTAAAGATC
 AATTGTGATTTCTATTCTTCAAGAAAAATCAATGGGCTAGTTTATCTCTGGCAATTTGGTATATAGAAT
 CTGTGTGAGAAAAATGATTTGAAAGATTGGTTGAAATCTTATGGCATTGAAATTTAATCTTAGTTCAA
 CAAAGGATCAATTTGGTTGAAAAATTAAGAATTTGATTATCAAGCCACTATTCAATATAGAGATT
 CCAAGAATCTTTTATTTGATTTCATTTGGAATTTATTTGATAAAACCATTTTGTATAAAAAGGTCAAA
 TTGAAGATGAATTTTTCGAATCTTGGTCATATTCTCAATTACGTGAATGGCTTTATTTACATGGAT
 TTATTGACACTAAACAGGAAATTAACGTTGAAGATTGGATTAAGGAAAAATTAAGTCAAGATTGCC
 AAGTTATTAAGAAATGTTTGGTTGAGTGACATTCATCTTGGTTAGGAAAACTGAAAAAGAGTCTC
 AACCTTGGATCACAAGGGGAGAACAAAGCTCTCAGAAAAAGAGGGTAGTAATTTGATTTAATGATA
 CATCTCTTTGTGTTGATTAAATAATTGGTCCAAGGATAAATTCGCTGAATTTGGGCAATCTTGACTAA

FIG. 2 - 47

YML128C_homolog 338aa (SEQ ID NO 416)

MYFFPIIIVWLYVSIITFVVVANYGFDQWTDNDLQKFLKERVAFNDALENPKLISLANEEAKKLEKGYK
KVTEELNNNNLPDDSLNDYLNFDYLFGRKKENYSIKEWIFESWPVTSLQTLTQNNIQYSAKDTK
DDLINVKVDQFDSISKKNHSGSYFPGNWLYESWSWENLDKDWLKSYSIEFNPSSSTKDQLVEKLKFS
YQATHSIRDSKESLFDSDLDFDKTIFDKKGQIEDEFFQTNWSYSLREWLWYLGHFIDTKPGIYVEDL
DKELVKVIAQSYKKCLLSDIHTWLANTEKKSQFWITKGEQKSQKKGKSNLINDTFFVGINNWSKDK
LRELGNLD

YML130C_homolog 2243bp public: 1..829, PathoSeq: 830..2243; CDS:
501..2240 (SEQ ID NO 417)

ATGAGTTCATAGATGATCTGTTTCACATTTTCAAAATAACGTGTCAACAAAAATAAGTTAGAGCATAG
ATTTTGCCGCCCACTTGTACAGATGGATAGAATTGAATGCAAAATTCGCATATAAGATTAAAGTGA
AACAAATTCGCAAAAAAGAGAAAAATCGAACACATTAGAAAAAGAAACGAACAAAAAGAAAAAAAT
TTCAAATTTGATGTGCATGTATATAAAATAATATAAAAGATATATCACCAGCACAACTGATTACTT
TTTATTTATATCACCCTGTCAACAAACAAATTTCCAAATAAATAACAACCTCAGAAAAAACACTTACTAT
CTTTCTTAGTTTGGTTTCTATAATCTTATTAACATCTTGCCCTTCATCCTTGA/TATCATATATT
AGATCTTATCTTTAATTTGTTGAAAAATAATACCAATAATCTTCCCATAGAACTTACAAACACA
ACAAACAAAAAACCCATTCTAAATCCTATTCTCCATTATGAAAAATTTTCAGATTATTTTCACTAC
TAATCGTACAAATTTATCATAAATACCACCTGTTGCAAGTATCACCCTGTGTCAGCAGTTTATCCAAAC
TGATTTTCAGTGCCATTGATTACCCAGAAATTTGTTACAGATCAATACTCCCACTTGTAAATACAA
CTTTTCACCTACATGTAGTAATTGAAATAAGATATTCGTCCTACTTGTGCGAATTAGTCAAGACCC
TGATTTTCGCTTATTTAAAGTCAATTTAGATAAACATGTCGT-TTTGGAAATGCTCAACATTTTGT
GTGCTAGTGAACACTGTGCTGTGAAATATTGGAAGATTTCATTTGGAGTCAAGTCACCAATGAAA
GTTTGAACCTTCAGGATTAGGTAAGATTTCATTAACCTGACAAATCATCAATTTGATAATTCATGT
AAACCGAAGAGTTCAAACCTTGTGAAGATTAGATTATAGTGAATAGATGATGACCATCATTTGTG
TTTATGTCAACTTTGTAATAAACCCAGAAAGATTACTGGGTATGGTGGTAATCAAAGTTTGTATG
TTTGGAAAGCTTATTACCTGGAATAATTTGTTCCCTAATCTAATCTCAAATGTGAGTGAACAAATGATG
CCGACAAATGGTGGTGAACAATGTATCGAAAAGAACTTGTTTATCGTGTGTTAGTGGTATGATG
CTTCAATTTGCAGTACATTTATCAAGAAATATTGAAATCTGAACTGGTGAATTTTATCTCAAT
TAAAGGTGTTTATGGAAGAGTAGGTATGCATAATGACAGATTCTAATATTTATTTCAATTATG
CCTTAGTGTCACCAAGCTATAGTTAAATGAGTGAATTTTACCATTGAGAGAGTTCAATTCACCTG
GGTATGATGACATTCTCCAGCTCAAAAGCAACATTTATGGCTAATATGATGTGCAATCACTGCG
AAGTTTATGATCGTTTGTGTTAGATGACATTATTCCTAGTTTGGAAAGCAATGTGTTGTTAATA
CTTCCAACCTTGTGATAATAAGCAATTTGAGGATGAATTTAGATCAAGATTAGAAACATTTCTG
CCATTTATGGAATTGTTGTTGGTTGTGATAGATGAGAAATGTTGGGGGAAAAATCCAAACCATTTGGTTATG
GTACCGCTCTCAAGATTTTATTTGAAGATGACCACTATGATAATCAAAATTTGAAATTTAGAAGAA
TTGAAATTTGTCCTTGAATTAATACCTTTGATCGTTTATCTAAATCTATTGAAAGTATTAATATGT
TTAAAGAAATGTATTTCGACACCTTAAAGATATTGCTGAAGAGATTAAACCAACCTCGTGTGTTTACG
ACAAATACAAACACAAACACAGGTAAACGGATTGCTCTCCCAATTTGTTAGTCCATTAACCTCAGA
AAAAACCTTGACCAAAACCAACCCCAAAAAATCAACAACAAAAACAACCTCAAGAAATCTGACAAAA
AAGACTTCAGATTAGAAGAAATTGCCACACAAACCTGAAGATCGAACTTTTGTATTGAAGACTTCA
GATTATCTCTTTGATGAAGTTTGGCAAGCATTAAGATTTGTTTAACTAGTTATCAAGAGATTCCCG
CCGATTTGAGTAGATTTCATTTGGTTCAATTGAATGAATGGTGAATAAATTTGCTTGGTAACCA
CAGTTTATGATTACCAAGTCTTTTGATGTTGATGCCCTACAAATACAGTCAAGTCCTTGGATAA

YML130C_homolog 580aa (SEQ ID NO 418)

MKIFRLFSLLIVQPIINTTAVSPVSAVLPKSSFSPEFCSQIITPTCNTTFTYIDELNKDIR
PYLSELVKSITYFRYKVNLDKQCRFWNAQHFCASENCVEILEDNFWSQVNTESLKPSSGLGKISLP
DKSSINDNSTEETEVQCTEDLDYSEIDDDHCHVYVNLVNNPERFTGYGNGSFDVWKAISENCFPN
TNMPSVTNDADNGEQCEIKNLFYRVVSGMHASIAVHLSREYLNSETGEFFYNLKVFMERVMGHN
RLNSIYFNALVSQAIVKLSEILPLREFIQSGYDDITPAQKQHLLANNDESVEYDRLLDDIIP
SLEANNVFNNTSNLFDNSNLREDFRSRFRNISAIMDCVGCDCRCRMWGKQTTIGYGTALKILFEEDNY
DNHNLKFRRIEIVALINTFDRLSKSIESINMFKEMYLQHLKDIAEGLTQPGVYDKIQNNKPGNGFA

FIG. 2 - 48

FPPVSLPQKKKPDQNTNPKNQKKQKQPDQETDKKRLTLEEIAHTKPEDRTFIEDFRLSFDEVWQALRF
VLTSYQRFPVLSRFTLVQLNEWWNKKLGKPTVYDYQSSFDVALQYSQVLG

YMR022W_homolog 1004bp public: 1..507/668..1004, PathoSeq:
508..667; CDS: 501..1001 (SEQ ID NO 419)

TGTGAAAAAATTTGGTGTGGATGTTGTTGTCGTTGTTGCGCTGTCCACAACAAAAACAAGT
AACAAATTCAGAGTTGGGCTTGGAGATCGATTTTTTTCGCCGCTCTGTGTGGCAGGAGACAAATG
AGTCGACCAAGTACGTTTAAATTGAATACGAGAGTCGACGCAATTACATCAATCCAACTTCCACTT
ATTCTATATCAATGTAAAGTCATTTTTTGATAATATCGTAATTTACACATTTTCGTATATCTCGGCA
ATAGGGGGGATAAAAAATAGTATTGACTAATTAATATATCTTGTTTATCAAATCAGGAGTATAGAA
TTCACCCCAACAACTAGATTTTCCGAATCGGAAACGACGAGGACGACACAAACAGCAGTAAAGAGT
AAGAAGAAAAAATTAATAATTAATTTGATCAGGCACACATTAGAAACAAATTTGGATCTACTTTT
TTCGATAATACACCACACAGCTCATTACCACCTCATGCCCGAAGTTCTACTGCTCAAAAGC
GTTTACTAACAGAGTATCACAATTAATCGAGGGACCCACCCTGGGATAATCGCAGGACCCAGTGA
GTGAAGATAATTTTACAAATGGGAATGTTTATAGAAGGACCATCCGATCTCCATATGCAAAATG
GAGTATCCCCAGCAGATTTGACTTTCCCTAAAGATTACCCATTATCACCACCTACATTAAAGTTTG
ATCCACCAATTTTATCATCCAAATATTATGCTGATGGAACCGTTTGTATTTTCGATTTTACATCTCT
CTGGTGAAGATCCAAATCAATATGAACGACGAGGAAAGATGGTCACCTGTGCAAAAGATTGTAA
AGATCTTGTGTAGTCTATGCTCTATGCTTGCAGAACCTAATCTCTGAAAGTGGGGCTAATATCGAAT
CTTGTAAATTTAGGAGAGATAATCGTGTGTAATATGACCGACAAATAGACAACATGTCAAGGAGT
CATTAGGATTATGA

YMR022W_homolog 167aa (SEQ ID NO 420)

MPRSSTAQKRLLTLEYQQLSRDPPPGIIAGFVSEDNLYKWECLLEGPSDTPYANGVSPAVLTFPKDY
PLSPPLKFDPLPLHNPYADGTVCISILHPPGDPNQYPERPERWSPVQSEIKILLSVMSMLAEP
NPESGANIDACKLWRDNRADYDRQIRQHVKESLGL

YMR118C_homolog 1031bp PathoSeq: 1..1031; CDS: 501..1028 (SEQ ID
NO 421)

CTACACAAAGCTTCGAGAGTTTCTTTTCGTTGTCAGGGGTGGGACAGGTGAGTAACGAATAAAACGT
CGATTGCTCTTCTCTTTATGATTTGTTCTTTAACGGAAATGTGTTCTTTAAAAAATAATCAGTTCTGCG
ACGTGATATAAATCTCCTTATCGCTAGTAGTAAGTTTAAATTTTGTATCAAAAGTACACTCATCAG
TCTATTGTGCTAGATTTCGCATACTTGTGATATAATCTGGTGTGTACACTACTTTTTTGGTTGTGA
TTGTAATAATACAAATTTTCTATTGGTTAAATGATAATTGTTAAACAGCTTTTCTTTCCCGGGGA
TTGAATCCGGGAACTACCATTAAATCTCACTCATTCTCACTCACCTCACCTTCACTCACTCAAT
ACAATTTATATCAACCAAAAAAATAATCTTCACTACACCAATAACAAAGAACCAATAGTTCTCAAT
CTAATAAACCACTCTTCCCTTACCTTGCACACCAACATGATTTCTCGTATTGATATTGAA
GACCTACCGTGTCCACTTTAAACAACTATGTCATTAATACCAATCGACATTAGCCCTTAAAGATACA
CATCAACCGTACCAAGCACTTCAAAATCAAGAACAGAAATATTGGTTGCCCAACGTAAAAATAGAC
CTACATCACCTCATTTACAAATTTATGAACCAATTAACCTGGATCATGTCATTTCCATAGAA
TCACTGGTGTGCTATGGCCGGTGCCTTTTATGCTTTAACTTGTGGATTGTCTGCTACTTCAATTT
TAAATTTTCCATTTGCTACTACTTACTTTAGTATCTGCAATCACCACATTTACCAACATTTGCTCAAT
ATGGTATCAAAAGCTATTGTGCTTATCCATTGTTTATCATATTGGTAATGGGATAGACATTTGG
TTTGGGATTTTGGTAAAGAAATTAACCATCCCTGGTGTATTAGAACTGGGTATGCTGTTTTGGCTG
CTACTGCTGTCATTGGAAGTATTATTAGCTTTCTTATGGTAA

YMR118C_homolog 176aa (SEQ ID NO 422)

MISRIGLKRPVSTLNNYVKLQSTLALKRYTSTVPATSNQEQLVAQRKNRPTSPHLQIYEPQL
TWIMSGFHRITGVAMAGAFALTCGFAATSIILNIPFDTTLVSAFTTLPTFAQYQIKAIYAPFVY
HTGNGIRHLVMDFGKELTIPGVYRTGYAVLAATAVIGSYLAFWL

YMR230W_homolog 1176bp public: 1..1176; exon 1: 501..551, intron

1: 552..870, exon 2: 871..1173 (SEQ ID NO 423)

AAAAGCAAGAAGAGAAGGACTCGTTGGCCAAATTTCTTCGGCAATTTCAAGAAGAAAAGAGTAGCTG

FIG. 2 - 49

TTTAGAACTATATATATGTACTCGCGCTTTAATGTTTATAGCAAATAAGAAATGTTTAAATAAT
TATTTAATCAAACCTGGTGTGAACCTATGATTATGGTAGTGATCTAAGAACACAACTTGCAAAAGCA
ATGGTAGTGTTCCTTTGATTGTTGTTCTTATTAGATTCCGTGTTCTATTAGATTCCCGCTTTCTTTT
TTTTTGCAGACATTAAACCTCAGGGCTATAGCCCTAATGCGAAACATGCAAGTGTATGTTTCTTG
ATTTTTCTACACTACTAGTAAAAAAATTTCTTTCCGCTCACTATTCCACATACACTCTTTTTCG
CACAATTACAGTCTACCAACAGGAAAAAGAAAAAAGGAATCTGGTAAATTGAAAAATTTGAAGTT
TGGTTCTTTTAATCTATTCAATCAACTAGAGTCACAGCATGTTAATTCGAAAAGAACAGAAAGA
AGATCCACCAATACCTCTTCCAAGGTATGTAATATGAATATATAACTGGAAACAGAAATATGGCATT
TCAAGGATGTCAGATAAGCTCAAGAGTTCATGAAAAAGCAGAGTTATAACAGTCTGTAAGCAAAAA
TTTCACTACCAACAACAATAAGAAGATATCAAGAGATTGAGTAATCACTACTTCAAGAAGACATA
TAACATCATGGAGAGTTTAAATTGAAATACGAATGAATATACAATGAACATATACCCTTTTATGG
CCATATACAGTTTCAAGAAATATTAAACAAAAATAAATGAAGAAATAAACTTGGATATATCAAC
ACATGTATTATAGAGGGTGTCTGTTGTCTAAGAAAGACTTCAACCAACCAAGCAGATGAAAT
GATACTAGAACTTGTTCGTATCAAGCTTTACAATCTTTGACTCTTAAAGGTTACGTCAAGACT
CAATTCTCATGGCAATACTACTACTACACCTTGACTGATGAAGGTGTTGAATCTTGAGAACCAG
TTGAACATTCCGAAGGTATCTTGCCTATTGACCAGATTGAAGAAATGCTCCAGCTGAAAGACCAAGA
CCATCAAGAGCGGTCGAAGAAGAGGTGGTTACAGAGGTAGAGCTAGAGACTAA

YMR230W_homolog 118aa (SEQ ID NO 424)

MLIPKEDRKIKHYOLEFOEGVVVAKKDFNPQKHDEIDTRNLNFKALQSLTSKGYVKTQFSWQYYY
TLTDEGVFLRLTELNIPEGILPLTRLKNAPERPSPRSGGPRRGYGRGRAD

YNL054W_homolog 2840bp public: 1..2197/2199..2840, PathoSeq: 2198;
CDS: 501..2197 (SEQ ID NO 425)

TGTTGGGAGTATCTGCGCAACAATACTTACTTTTAGTTACTAACATTATTTTCTTCAGCTA
ACTAATTATCTAGTTTATATCTATATCCATTATGTTGAAATCACTATCGTGAGGTAAATAACAA
TACAGAGTTGTGCAGATATCCAAAAAACTTTGTACCTATCAATACATTTAAGCAATAGGTCAAT
TTATTGCTGTAATCAAGTGTACCAGTATCTCTAGTTAATGTTGAGTTTATACCTAAAACTGAAC
TATATCAACTTTAAATGCCCCTAATCACGTGATACAGCACATGGGAATTTGCTGATCTTGCTCTCT
TGCACGTACACGGCACATGTACACGACTTTTTTCTAAATATTTTTTTTTTTGTTGTTGTTGTTA
TTAAACAATATTATTTTCATATATATAATTGCTTAGTTTACTTGCTTCTTACACCCCTTTGCATATT
TTTTTTTTTCTCTTTTCTGCCAATCTTGATCAAATTCGATGCTACATCCTTAATTAATTCAGTAGTCG
ATATGCTCTAGCACTGGAAACATGAATGAAATACAGATGCTCCACCGAAACAGCAGACGAAAAAGA
AAATATCAAAACAGAATTCAACCAAAACCGATTTTTTTGTGTCACGATTTGGCTAGTGGCGTTGAGC
ATATAGAAAGCAGTGATAGTGATGAAACGTTTATATATAGAGAAATAATGATCTGAACTTGATGATA
ATGCTAGTAAATATTAACAATAACAACAATAACAGCAACCAATAACATTATCAATTTAGATAATGCTA
GTGTTAACGGAAGTATGATTGCTTCAATCCAAATGCAATGGTGAATGGTCTTCCCGGAACATCGATAG
CGTTAGGATCGGGCTTCGATCGCCATCCATCTAGAGGGGAACAGCTTCAATATTTTTCATGACC
CAGTGAGGCAACAACAGTTTCAAACTTCTTCTACCAAGGCTCCGTCATTTTCAACTCCATCAGCA
GTTCAAATAATATAGATTCAATACTTAAACGACCTGTACATCTACGTGAGGCATCAACGATTTTCAG
TGAATGATAATGACCAACCGAAATCTTGTGCTACCAAACTCAACTGAAAGGTTTACTGCTTCACTT
CGAACAATATTGGTAAATGAAATATACCTCAATCAACGAAAACTAGTAGTGTGCGCCACTCAATCA
ATGAAGGATACAAATGATGATACATTTCATATAATGAAGTTGAGGATAATTTAATTTGATGAAGATT
CCACGACGATGGGGATTGTGCAAAAAATACCACTTACTTAATAACAACAACCAACACGCTCGA
GCCACAGCAACCAACCGCAACCAACAGCCGCAACCAACCAACCACTACATCATCTGCTCTCT
CTCTAAATCAGATACAGCAGCGACATCAGCAACACCTCTGTGTCTCAATAAAGCGCTCTTAA
GAAATTACAAAACTCATCCACTTCTCTAAAATTAAGATCAACTACATCAAACTTTTCGATAAAA
AAGGCTCAACAACCAAGAGATACAGTACCATTCCTGATGATATTGACATTGAAGATTTCGATGATG
AGCTTTATATCTATGACACACAGCTAGGTTCCAGCGAAGCAATCAACTCTTACTTAATTAACAA
ACCAAGAAATCCCCCAATTATAGATCACTTAATTTGAAATTTCCCTCAGGTGAAGCGCCAAAGCAAGC
GTTATTGTTGCACTGGCCAACTTTAGAGAGTTCTGATCGGGCTCTAACAACAAAGATGTTGATGATA
ATGGAACAAACAGTGATCACAATATTAATTTCTCCTTTGACTGCTTAATAATAATTAATAACGTGATA
ATCAACAGCATCTGGTGATAACAAAAAGAGTAATACCAACAACAACCAACTGCTTAATAATGAG
CATTTCCATTTCCTTATCAAGATCAACAACATCATTTATTACTACGACTACGATGATTTTGACCAAG

FIG. 2 - 50

AATCACAAATCAATGGACCAATTTTGATTGGCCAGACCTCCCTATAAACAGATCAGCTTCACGGA
ATTTTAAACAACAACAATACCCCAAAGATTGGCGCAGCATCTTTTTTCTACCAAGAAAGACAG
ATCAGTATAGTCAAAAGAACAGCTTTC TAAAGTCATGCATTTATACCTTGTGTTATATTAATGT
TGCTTTACCATAGGGTTTGATTTGGGGTTTGCTTTGGCCACAACAAAAGATTTAACTGATGTAGGTA
TCACATCCATTGAGAAGCCCATTTGTTAGTAAAGATGAGTTAGTTTTCATGTTGTTTATTGAAGCAT
TTAATCCAGGGTGGTTTTCGGTTGACATCAATGAAGTAGAGTTGGATTTATTTCGAAGAAAGTGGCT
ATCTACCTGATACAGATAATCTGAAAAATATCTAACATGGGAGGGTCACAAAAGTAGAGAACGGTTA
AATTAGGAACGATTTTGAATTTTGAATCGGTTCTCAATTTCAAAGGTGGGTTCTCTCTCGAGAAC
CGACAAATCAAAGGGAGGAATCCGATTATTATATCTGGCAAAAATGTTACTGCCGAGGCTAAAT
TGGTTGTAATATGGCTGATATTAATAAGTCTGCTTCCAATAGCATTTGCTAAAGAAAGACATCTACTA
GTAATGACACCAACGATAATGACAACTCCAAGAAAGTGGGAAATCATATCAAGCAATCCATTGATT
TGATTATAACTGGAGTATTGAAGTATGATTTACCAATTTCAAAGAACTCAAGATCAGTCGGTGGTTA
GAAAAACTGGGTATATTGATCTACCTTATTTCGTAATACCACAAGGAGAGATAATATTTCAAATTT
AG

YNL054W_homolog 779aa (SEQ ID NO 426)

MLHPNNSVVDMSSTGNNMNTDAPPKQTKKKISKQNSTKTDFFAARLASAVDDIESSDSDETFPIY
ENNDETLEDNASNINNNNNNSNNIINLDNASVNGSMIASSNAVVTGPPGTSIALGSGLRSPSILE
GEOLQYFHPDVRQQQFKLPSTKAPSISSNISISSNNIDSILKRVLHREASTYSVNDNHRNLVLPN
STERFASPSSNNIGNENIPYQKTSVVAHSINEGYNDFTSYNEVEDNLIDEEDTDDGDLTKNITL
NNNNPPTTSSQQQFPQQPQQPQQPQLHTSSPLNQIQAATSPSPKTNASKRNYKTSSTSSKLK
STTSKLPDKKGSQPRYSTIPDDIDIEDFDELIIYDNTARFPANESTSLLNQNRIPHYRSLNIN
FPQVRQSKRYLSTGQPLESSDRGSKNDGTDNGNNSDHNINSPLTANNNNNNVNDHGDNRKNSNT
NNNNIANNRAFPFPYDQDQHHYYDYDDFDQESQINGPNFDPDLPINRSASRNFNNNNNPKRPGD
SHFFLPKRKTQYSQRTSFLKSCIYTFVCILIVLTIGFVLGFVLATTKDLTDVGITSIENPIVSKDE
LVFNVVIEAFNPWGWSVDINEVELDLFARSGYLPDPTDNSKI SNMGGSQKVETVKLGTLINPESVILN
FKGGFLSREPTIQKGGIRLLYPGKNVTAELVNMADIKIAASNSIAKESTTTSNDTNDNDNSKKW
ELISSNPFDDLIITGVLYLDPFSRTSRSVVVRKTYIDPTLFVIPGGENNISI

YNL075W_homolog 1352bp public: 1..136/138..1352, PathoSeq: 137;
CDS: 501..1349 (SEQ ID NO 427)

CCCACAGACCAATAACGTTTACCACCAAAACCTCTGATATCAATGATTCGAAAAGATTCAATCA
ACCCCGGTAGCTGTTTGGATATTGGATAGCAACAACATTTCAATTAGTGAACAACAATCAAATTACC
AATACTGTTTACCTTTTACATCTGATTTCAATTTGGTTCATAGCAATATAGTCTCTCTGTTGTTGA
TATTAATATAAATAAAACATTTATATCACGTTGTTTAGTAGCTCTCGCAAAATTTGAAACCATGGATG
AGTAAACTGTTGTGTAGATGAGCTCAAAATATCTGGTGGAAACAATTTGTGTAGTAGTCTTTGATA
AATATCCAAGAACAGTCGGTCAAGTTTCAAATACCATCCGAAAAATCTCATAGCACTTCCCAAGTAA
TAATAAGAAAAAGAAATAATTTCTATAATAGCTCATCAACAACATTCGTCTACACTTCCCACTGAT
TTGTTGGTTTAAATATAATAAGACAAACCTCAGAAGCTATGATAAGAAACAGGCTAGAGAAAGAA
GAGACTATCTTTATAGAAAGGCTTTACAGCTTCAGGAATCTTCTCTTAACAGAAAAAGACAAACAT
TCAAAGCAGCTCTAGCAAAGTGGAAATCATTTATCAAAGGAGCTTGCAGAGATGAAAAATTACAAAC
GTGATTTTATTTACGATGAAGTGAACAAATAGAAATTTGATGACCAATACAGTCCGGTTGTCCGGAA
TATCTGATCCAAAGTTGTTATATACCACATCCCGTGATCCATCTGTCAAGTTGTCTACAAATCTCGTA
AAGAAATCAAGTTAAGTTTCCAAATAGCTTGAAGTTGAATCGAGGAACTATATAATCTTCAAGT
TGGTAAGTACCTGTAATAGAGTGAAGTTTCCGATATGATTTTATTTGCACGAGCATCGTGTGTGCC
CATCAAGTTTAACTGTGAAGCCACTTTCCTCATGGCCCAACTGCGATTTTTCAGTTTACATAATGTCA
AACTAAGACACGATTTGGCAAACTTTGGGAAACGCTCTCAGAGTCTTCTCTACTTAAATATTGAGA
ATTTCCAATCCGACTTGGGTAAGCGTGTGGTTAAAAATTTGCAACATTTGTTTCTCCAGGTGTCA
AGAAAGTACGCTCCAGAGTAATAACATTTGTCAATAACGATGACTACATATCGGTGAGACACCATGT
TTTACGTCAAAACTAAGGATTCAGTGGAGTTGAGTGAGATTTGGCCACAGTTTTCGAAATGAGATGTG
ATGAAATCAGACTAGGATTAACCTGACAAACAAGATGCTGATGTGCGAGTGGCAGATGAGAAAGATTCA
TAAGAACAGCTAATAGAAAGAAATTTACTGTAA

FIG. 2 - 51

YNL075W_homolog 283aa (SEQ ID NO 428)
 MRRQARERREYLYRKALQLQESSLTEKRQQLKAAALASGKLSKELAEDKLQRFIDYDESEQIEI
 DDEYSRLSGISDPKVVIITSRDPVSKLLQFSKEIKLMFPNSLKLNRNGYIIISDLVSTCNRVQVSDM
 ILLHEHRGVPSSSLTVSHFPHGPTAIFTLHNVKLRHDLPLNLMNVSESYPHLIPENFQSDLGKRVVKI
 LQHLFPFPGVKDSSRVITFVGNDDYISVRHHVYVVKTKDSVELSEIGPRFEMRLYEIRLGLPDNKDA
 DVEWQMRFRITRTANRKNYL

YNL096C_YOR096W_homolog 1061bp public: 1..1061; CDS: 501..1058
 (SEQ ID NO 429)

TCCTTTTGTGTTTATTTTGTGCTGTGTTACTCCAGAAATGTGCATAATAATGATAATAGTAATTTGT
 GACTAATATAGATGATGCTATGTGGGTGGGTGGGAGGAAGGACCCGGAATCTTAGGAACAGGA
 AAAATAAAAAACGAATAAACAACAAACCCCAATCGGCATGCATCGGAATCTTTCAGCCCAATTAC
 TTTATTTTCCCCACTTCTTTTGGATTAGGGCAATAGCCCTAAAGCTCGTGTTTTAGCCCTTTATA
 TGCAGTCTATTTTATTTTCTCTTTTCTTTTGGCTGTGGTAAACCTTTTCTTTTCGACGGTG
 TGTAAAAAATTTTATTTTACAGTTTACATTTCTCTAACCTGCAAAAAGCTCTCGTCTTTTGTGA
 GTGAGAGTTACTCGTTCACAATAGTATACCTTTACAGGGGAGTCTTTCTTTTGGGAATAGTCAACC
 AACAGCAAAATAGCCAAGGATCAAGCTTCATCATTAATCATGTCTCTTAAGATCTTATCAGAAAAAC
 CAACCTGAATTAGAATTAAGAGTTGCTCAAGCTTTCGTGTGATTGGAATCTCAAGCTGATTTAAGAC
 CTGAATTTGAGACCATACAAATCAAACTATCAAGAAATGTAGTGTAAATGGAGGTAAAAAGCTT
 TAGCTGTGTTTTCGTTCCACCACCAAGTTTACAAGCTTACAGAAAAGTTCAAACTAGATTAACCTAGAG
 AATTAGAAAAAATTTCCAGATAGACATGTGTCTTTTGTAGCTGAAAGAGAATCTTACCAAAAC
 CAGCTAGAAAAGCTAGAAAAACAACAAAAAAGACCAAGATCAAGAACTTTGACTGCTGTTTCAATGATA
 AAAATTTGGAAGATTAGTTTTCCTCAACTGAAATCATTTGGTAAAAGAGTTAGATACCTGGTGTGGTG
 GTAAACAAAATCCAAAAGCTCTGTGTGGATTCTAAAGATTCAACTGCTGTGATTACAAATGGATT
 CTTTCCACAATTTGTACTCAAAATTGACTGGTAAACAAGTGTGTTTGTAAATCCCAGGTGAATCTC
 ATTAG

YNL096C_YOR096W_homolog 186aa (SEQ ID NO 430)
 MSSKLTSENTELEKVAQAFVLDSEQADLKAEIRLPQFSIKEIDVNGGKKALAVFVPPPSLQAY
 RKVQTRLTRELEKKFPDRHVFLAERRILPKPARKKQKRPSPRSLTAVHDKILEDLVFPTTEII
 GKRVRVYLVGNKIQKVLDSKSDSTAVDYKLSDFQQLYSKLTCKQVVFEPGESH

YNL178W_homolog 1256bp public: 1..1024, PathoSeq: 1025..1256; CDS:
 501..1253 (SEQ ID NO 431)

TGTTTGTGTTTTCGAATCAACATAATAGAAGACCAACAAATAATTTCTATTTTGTGACTCTCC
 CGTAGTTTACAGTCTAGCCTCTCTGTGAATATACACCTTAATGACAGTACCATAGGACCCCA
 TCTTATGTTAAGGATAATACTTCTTCTTCTTCTTCTTGTGTTAATCAAATTTGCAATAAATA
 AAAAAAATAAAAAACAAGCCGACCAAGTTTCTCAAAATGACTATTTTGTGTAAACGATCTAC
 GTGATCATTAATTTTTTAAATTCAAAACTGAACCAAATCTCTGCATATTGAGGTTAAAAAATA
 AGAAAAAGAAAAATTTTTCAATCTGTGTTGAGGAGAGAGAGGTGAAAAATTTTCTCTCTCTCTT
 CTTTCTTTCATCTCATATACCAATAAACTTAAACAACTCTTTTACTTTTCTCTTCTTCTTCTT
 CAAACCTCTACACAGATCCAATTAATTAACAAAAAATGGTTAAGCGCTATCTTATCTAAGAAAA
 AGAAATTAGTAGCTGACGGTGTCTTCTACGCTGAATGAACGAATCTTCAACAGAGAATTAGCTG
 AACAAAGGTATATGCTGGTGTGAAGTTAGAAAACTCCATCTAAATTTGGAAGTTATTTGTTAAAGCTT
 CTAACACTCAAGGTGTTTTAGGTGAACAAGGTAGAAGATCCATGAATTAACCTATTGATTGTTA
 AAAGATTCAAAATATCTCCAGAAAGGTATGCCATTTATGCTGAAAGAGTTGGAAGAAAGAGGTTAT
 CTGCTGCTGTTCAAGCTGAAGCTTTGAAAGCCAAATTTATGTGCTGTTTACAAATTTAGAAGAGCTG
 CTTATGGTGTTTTAAGATTGTCTATGGGTGCCGGTGCTAAAGGTGTTGAAGTTGTTATCTCTGGTA
 AATTAAAGAGCTGCTAGAGCTAAATCTCAAAAAATGCTGATGGTTTATAGATTCAATCTGGTCAAC
 CAACCTAGAGATTTCATGTGATATTGCCATAGACATGTTTAAATGAGACAAGGTGTTTGGGTATCA
 AAGTTAAATTTATGAAGATCCAGCTGCTAATAGATTGGTCCAAAGAGCTTTACAGATGCTGTGTA
 AAATTTGCTGAAGCTAAAGATGAAGATGAAGTTATTTCCAGCTCCAACTGTTAAATCTTATAACAAA
 CTGCTGAAGATGAACTGAACTGATGCTCCAGTTGAAGCTGAAGCTGAAGTTGAAGCTACTGCTT
 AA

FIG. 2 - 52

YNL178W_homolog 251aa (SEQ ID NO 432)

MVNAILSKKKLVADGVFYAELNEFFTRELAEQGYAGVEVRKTPSKLEIVKASNTQGVLEGEQGR
IHELTSLIVKRFKLSPEGIIAYERVEERGLSAAVQAEALKKLLSGLPIRRAAYGVLRFMAGAGA
KGFVVLVSGKLRAARAKRSQYADGFMHSGQPTRDFIDIAIRHVLMRQGVGLGKVKIMKDPAANRF
PGRELFDVAKIAEAKDEDEVIPTPTVKSYKQTAEDETETDAPVEAEAEVEATA

YNL182C_homolog 2105bp public: 1..728, PathoSeq: 729..2105; CDS:
501..2102 (SEQ ID NO 433)

AAACTTTCGTGATTGAATAAGTGAACCTCAATCACAATCTCTTCGGCATATATCAAACCATTTAGT
TTTATTCACGTAAAATCTCAATATATCTACGCCACCCATGTATCTGGTCTCTCTAGTAGTAATAT
TAGTTGTGCTCTCTCGTTGTGCCAATTCATATGCTATTGTAGCTCAATACCACCTGGTCCCAACAGT
AATCATAAACACTTTCCATCGATGCTCTCGCTCCACGTATTGGTGGCACCATTGGAATAATACCT
GGCTCCAGCAAGAGCTTAATAGAAATGGGAAGAACGGTAGGTCATATTTCTTTAATTTGGTCCCAATA
TGGAAATCACTCTGGCCCATCAAACACAACACTAGTTAAAAAATTCAGTGGCATAATTTGGTATATC
AAGAGTGAAGAAAAATGCTGATTGGAGGTTGGAATTTGTTCACAAATTTGGTTGGCTTTTATTTCT
TCTTGTCTCTTTTCTTTCAGTGCTAACATAATTTGGGATGTATGTATTGAAAAAATAAATTTTG
TACAATTTCTTGTCTTGTCTCTCCACTCATCTCATCGCTCTCTTATAAATTCACAAACATGGATG
AAGTAGATTATTACATAGCTCAAGGTGATCCAGCTGATAAACAAGTCAAGAATCATATGGATATG
TTACATCAATCCATCTCTTCCAAACAATATGCATCTTATCGACAAGCAGACTCGCATATAAACGGTA
CTGCCATAACTGGTATTGGCCCAAGGAGAAAGAAATTTTCACTGCTTTCTTCAACAAGGCATTAATCA
ATGTATATTCTATGGGAAAAAGAAAGTGTGATCAACGCTATACCGATACACAGAAGCATTGACTTGTA
TCACGTTGATAAAACCATCCAAATGGCAGTAACAACAACAGCGACAATGATGACAACCAAGTTATACA
AATTACCAAATTAACCGAGTTCTTGGTTGTAGCAGGTGGATCAAAGAGTGGGAAATTTGATACATTT
GGGAATTAAGTTACGGCAATTTTATTATGTGTGTCAGAGACGCCCATTTATCAGGGGATCACTACCATCA
AGGGTTCAAGCTGTGGAACATTTTAAATACCTGGAGGAGAGGATGCCAGATGCTCTGTATGGAATTT
TAGCAGAATTAATTAGTATTATGACAAATCAGACCATCAAGTGAAACCATATTGGCAAATCACTG
ATAACACATTACCACTCACTGATCTTTGTTTAAATGATACATCAATCAATTAATGATCTAAAATAT
ATACAACTTCAAGAAGACAGCAGGTCAGGATTTATGATATAGTCAACAAGAGTTTGTGTAACCAAT
TTATTTTACCCAGTTCTCGCTGAATGTATCACCAGGATCCAGCTAATAGAGCGTTATATGTCGGGT
TGAATAACGGTCTGTGAAGATCAATTCCTTTATATTCTATAAATAGCCATACATCAGTGTGGAAA
GATTGGCGGATGAATAAGATAATCAGCGTTGATGCTGATCAAAATTTTAAAGAGACATTTGTTG
CACATCAACAAGAAACGAAAAACAGGAGACGATAAGCCTGTGTGTTTACGAAATTGACAATTTCTT
TTGATGGTACAAGATTAATATCTGGTGATCTGAAGGCAGAGTGTGTTGTCTGCATCATTTGAACAA
AACAAAGTTGTGAATATCTTACACCTTGTAACTCTCAATAGCTTATATTGCTGTGGAACATCC
CTGATGACTTTGTCAATTAATCTAGCTACTAGTACTTACCCTAATAAAGCTGACAAGAAACATAGA
TGATACCTCAATTTAAACAGGACTAGCAGACCAATTCGAAGAAGACATACAGATATTCTGGACA
TTCCTGGTAAACACCGCAACCAACCGCAACCGCAATATTGACTTTGCAACTTTGGTTACAAG
GCAACAACTTGAAGAATTACATTTCAAAACCTTTCTGGAATAAACTCTATTGTCAACAAAGTTG
GCAACGAGAATGTATCGGATCTCGAAGAGAGATTACAAGAGTTCTCAGCATACATCACTGAATTA
GAAACAAATCAAGAATTAAATTAAAGAACATGCCAAATTTATTAGATAAATTAGAATAG

YNL182C_homolog 534aa (SEQ ID NO 434)

MYVLKKNFVQFLVLVPLISSLSYKFTNMDVEVFYIAQGDPAKDKHSQESYGYVTSIHSSKQYASY
RQADSHINGTATIGIPGERIFTAVPNKALINVYSWGKESVDQRIPIPEALCTCLINHPNGSNNN
SDNNDNQLYKLPNRYVFWLLAGGSKSGKLYIWEISSGNLCLVRDAHYQGIIITTKGSSCFTPLITGG
EDARCLVNNLAELSIYDKSDHQVQKPYWQITDNTLPLTDCLNDTHNINDLKLYTTSSEDSVRIYD
VINTSHTSPVLESIGMMKIITVDA
DQNLKETFVAHQQTTKGDDKPVVVKLTISFDGTSIIISGDSSEGRVFSVDIVTKQVVKSFTEPCNSP
IAYIAVETIPDDFVNNLATSTTNKADKKHRMIPOFKRVLASTNSEHQIFLDIPGKTATTATNATG
NIDFATWLQGGQSEELQFKNLSGINSIVKQVQNVNVDLEERLQVRVQAYTELNRNKEELIKEAH
LLDKLE

FIG. 2 - 53

YNL190W_homolog 896bp public: 1..896; CDS: 501..893 (SEQ ID NO 435)
 TTTCTGCAAGTATTGCGGTGCTGCACAACTTTTATATCCGAAAATTTTGGCCGGGAACGAAA
 CGGCAGAGAAAAACGAAACAATACCCACGACCGGACAAAAGATTATAGCTTTGTGTAATAAG
 GTTATGTCACTCGGTATTACAGATTGACGGGCCATCTTGCTTCATCAGTTATAGCATTTCAATAA
 AAATAAGCCACATATTGTGTACAGCGCTGAGTCTACTCAACATGTGTAAATAGAATAAATCAATTGA
 CACAGTCTTTTGTAGATCTGTTATTCTGGCCTATAGCGTTTGTAGGAAATTCGCGGTATTCTTGTGCT
 GTTTTCTTTTATCTATTTTCGCACGAGCTTGGGGTGGTTTGTGTGACTTTTTTAGCAAAATAAATTT
 TGTGCGTCTTCGCAGTAAAAATAAAAAATTCAAAAAAACAATAATTGACTTTTATTTTAACTTT
 CTTTCTTTTCTTCAACAATACTAATCAACAGCCAAACCATGAAATTCCTACTCTGTTGCCACTGTTT
 TTGCTATTTTCTCATTTAGCTGCCCTAAAGGTGGTGAAAGATCAACGGTAAAGCTTCTACTGTCA
 CCAAAATATGTCTACTGAACTACCCACAGATACGGTCGTTTGTACAAAACAGTAGATCTAAAAAGC
 CAAAGGAACTGGTACTCACAGATACGGTAAATTCACAGACTCCACGTCCAGTTACCAACACTG
 TCTTGGTCAAAGAAAGCGACCTTCCAAAGAAAGAGATGCTGTTGTTGCTAGAGATTCTAAAAACG
 CTCTTCCAACTTACCACCTCTAGTGGTAAACAATGGTGCCTCCACTGGTGTGAGCTTGGGTCTTG
 CTGGTGTCTTAGCTGTTGGTGTGCTTTTGGTCACTAA

YNL190W_homolog 131aa (SEQ ID NO 436)
 MKFTTIVATVFAISSLAAGGKEDHGKASTVTKYVTEETHRYGRFDKTSRSKKPKETGTHRYGKFN
 KTFREVTITVLVRESLDPKKRDAVVARDSKNASNSNTSSGNGNVATGVSGLGLAVLAVGAALVI

YNL208W_homolog 1076bp PathoSeq: 1..1076; CDS: 501..1073 (SEQ ID NO 437)
 TTTTGTATCAGCGCTTTTGTTTTTTTTTTGGGTGGTGCCTGGTTCGTTGGGTAGTTGGCTCTTG
 TTTCCGTTCTACTGTGTTCTTTTATTTCTCTCTCGTTAACTCCTAAATTTTGTGTAAACAAATTAAT
 TATAGGGAGTTGGAATAATTAAGAGCTTGAAGAGAAAGAAAGAAATACCAACGTGGAATTTCT
 ATTACGTAACTACTATACTTGCATAGAAATTTTCAAGTTTCAATTTTAAAGAAAGTATTAATCAAC
 TGAATTAAGCAATTGAACGAATTTGAACAGCTCAGCATTTATTTTTTCGTTTCTTTTTTTTTCAA
 GGGGTGGGTGAAAGAAAAATCTAAAAATATATAAATCTCCACTTATCTCTCTCTCTCTCTCTCT
 TCTCTCTCTAACTCAATTTCAATTTTCCCAAAACCAAAATTTCTTTCTTTCTTTCTTTTATT
 TTTTACTCAATTGAATCAATATTAACCAATTAAGCCATGTCACTAACGATTTTTATTCATCTG
 GTGATCAATCCAATTATGATCCAAAAAGATCTCGAATCAAGGATCATCATCAATGATGAAC
 AACAGACAGAGGGTTATTATCTACTGTGCGCGGTGGTGTGCTGGTGGTTATGGTGGTCACAAAT
 TAGGTGAAAGGCAACACATGGTACTTTGGGTACTGTATTAGGTGCCATTGGGGGTGCCATTGGGT
 CCAATTAACATAGAGATGCTTATGAAGACCGTAAAGAACATAAAAAACACGAGCAACAAATATGGT
 GTAGTGGTTAAACAGAAAGCGGAAGACATGAAGGTGGTTTGGTGGTGGTAGACAGATGATCGTT
 ATGAAGGCGATAGAAGAAATGATAATTACGGTGGTGGTTACAATGATAGAAGAGATGACGGTTATG
 GTGGTGGTTACGGTGGTGGCAGACGACGATAGAAGACAGAAAGTGGTTTTCGGCGGTGGCAGAC
 CAGATGACCGTTTGGTGGCGGTAGACAGATGACCGTTTGGAGGTGACAGAAGAGATGATAGAA
 GAGATGACCGTAGATGGTAA

YNL208W_homolog 191aa (SEQ ID NO 438)
 MSANDFYSSGDQSNYDFPKRSSNQSSSSNDEQDRGLLSTVAGGVAGGYGGHKLGEQAQHDHNTLGTV
 LGAIGGATGKNGLEDYEDRKEHKKHEQYQYGGSGKHGEGRHGEGFGGGRPDRTDREYGRNDYGGG
 YNDRDDGYGGYGGGRDRTDREHGGFGGGRPDRTDREYGRNDYGGG

YOL031C_homolog 1745bp public: 1..1342, PathoSeq: 1343..1745; CDS: 501..1742 (SEQ ID NO 439)
 TTGGTATTGAAGACACCGAAGACTTGTGAAGATATTGAACAAGCTTTACAAAAGGCTGCTTCTG
 TTTGAGGGGATGTTCAATTAGCAATGTATATAATTATTTGATATATTGACAAAGAAAGAAAAAGAA
 AACAGAAAGATGCTGTTTATACAGGAATATTTTAATAGAAATATCGCTTATATTTGTGATAAAAGAT
 TGAAGACAACTCCGAATGTAGTGTCTTGTCTTATTCGTCTGGGAATCACTGTAGTATTAGCATCAAT
 TGAGGAAATTTCCAGATAGCTAACGGTTTTCGCAATTACGAATTTCCAAACAAATAAATATGTGACA
 AGGAATACACTACTGATCAAGTTATTCTTAGTACAATGGAAAAAAGAAAGCAACAAAA

FIG. 2 - 54

AAACGAGAAATTAATGAACACGACTTCACTTCTACAACCTACTGGGAAAAAAGGCCAGAGAGTTA
 TTGAAAAAGGATCATATCAAGTTCTTATTGTATATTAATATGAAGTTTCTGTTTTAGTATTACTTG
 CCAAGTTACTTAGTTGGTGTGAATTCCTCTGATTGTGTGACTCTCAGAGGAATTAATTTTGTCCAGATC
 CAGAAAAACCCCTTAGATTGTGTATCCAAAATGTTTGTTCACAAACAGAGTGGCAAAACCATTAAC
 CAGGTCAGAGTATACCACTGGGTTACACGTTAGATTAAATATAGATACGTTGGAAAAAGAGGCCA
 AGCTAATGAGTGTGACGAAAAAGACGAGCCAGTTCAAGAAAGTAGTTCTTGGTGGCGAATTCGAGG
 ATCATCTCAGAGGAAGCCATCACTGAGAACTACAAAAAGTTGATGAGCTGAAACATCTCTGAAGTAA
 AACAGGAGCAGCTCATCGTACAAAGGTTAGCCAGGGAGATTTGAGTAATTTTGTACGCGAGCTGTCT
 TGGAAATTGAGAGTTTCAAGCCACATGAGAGTGTGTTGGAAGGTTGCACTTTGGCACATAGATACCT
 TAGAGAAATTAGTCAATGATTCGAATTTGGGGTGAATTTGACCTCAGACAAAGCCATATTTCGA
 GTTTTGTCAACATTGCCAAATGGTGTCTTGATCCAAAAATAACCGAAAGGATATATCGGTGAATGG
 GGCTCTAGTTTGGAGAAATAATCCTGAAGCGATTAGTAATATCTTGACCAACTCGACAGAGCATATG
 TGGATAATTTGTTTGTAGCAATTAGCGAATGAAATGATGTTCTACAAAAAGAGGATTTTGGGTATATA
 TTCAAGCTTTAGTCCAAAGTAGCCATTTTGCAGACAAATATTTTCATTGTACCAAGTCTCCGGT
 TAAATGATTAAATAGCAATTTTTCCTCAAACTGGTCCAAACTCAAAGTCCAGGCGAAGTAAACATT
 TAGAGGATTTTCAAAATTTTCTCCAGTAACAAACGATAGAAAGATCACTTGAGAGATCAAGATCTCGAAT
 CACAGGTTTCAAAATTTTATCAGAATTCCTTTGTGGAATAAACTTGACGAGAAGAAATTTCAAGT
 CTTATTTTGTATCAACTAGTAAATTTGCATCAGCTGAATAAGATTGTGGCAGCAAGTGGTGACTTTTC
 TCAATTTGGTTAGCTGAGATGGAGTGCCTGAAGAGAAATAAAAAAGAGACGATTATTCACAAG
 AAGACAAAGACTTTGATGAGTACATGTTGCGAGCACGTCATGAAGTATTGGCAATCCAATGGGAT
 TAAGAAAGCCAAATGGCCAGCGAGTTGTAG

YOL031C_homolog 414aa (SEQ ID NO 440)

MKFSVLVLLASLYLVGVNSSIIVDTSEELICPDFNPENPLDCYPKLFVPTNEWQTIKPGQDIPPLHVR
 NIDTLEKEAKLMSADEKDEPVQEVVVGELQDHSREAITENLQKLHESKHPEVKQEHARHTKVSQG
 DLSNFDAAECSEIESFKPHESDVERLHLALDITLLELSDHIDIEFGVKLTSDKALIQFSFVNIAANGSDFK
 ITEKVVYVMGSSLRNPEAISNLTNFDKSYVDNLFEQLANENDVLQKRLGLIQALVQNSHFARQ
 YFSFDHSSGLNDLIAIFPKLGPNSKSRASNLLEDLQLFPVTNDRRSLEDQDPESQVSKFIQNSFVG
 NKLDEKNFKSYFDQLVNLHQSNKSLRPSGDFLNLWLAEEVESRKENKRRDDYSQEDKDFEYMLRAR
 HEVFGNPMGLRKAIADEL

YOL048C_homolog 1244bp PathoSeq: 1..27/985..993, public: 28..984/994..1244; CDS: 501..1241 (SEQ ID NO 441)

ATGATTTTTCTCTTGATTTTTAGAGCTGTTAATTATACCTTTTCTGTTCCCAAATAAGCGCTAAAAA
 TGATTGAAATFAAAATATCACTAATTTCCAGGTCAAAGTAAACACTATAAAACAAATATATTTCAAT
 ACAGGAGCAGTAAATTAGCTTCAACATCAAGGTACTCTTTATTTTCTACCAAATAACATCTGA
 AGTAGCTCTTATCCATAGATCCAAATATTTTAACTCTTTTCTTCTACTCTCACTACTTTTCTT
 TTCAACACTCTACGCTCACAAAGCGCAATGACCATACCATTAATTTCAATAATCACTCAAGAGCT
 TATTGTATCTCTCAAGGTATGTTAATGATTAAACACACCGATTCTATTTCCACCAACTAACAGC
 ACAGAAAGGGGTGTGATATTGTTGTAACACATCCGACCGTTTGGCCCTTTACATAACCATATATGA
 TACCTCAATTTGGTCTTACACTAGTCATTACCTGATATGTTTTCATTGTTCTTCCCACTCAAG
 CTATTGTATGATGATCTGTTAATGGGACCATTAGGGGTGATGTTGTCGCTGGTATAGTTGTGATCTGC
 AAGCAGACACATGTTCTATTTTGTGTCACAATATCTTAAATGCTTCACATACAACGAGTGGCAT
 ATGATGCAATATTGGAGTAGAGAGTGTGCAAAATGATGTTGTTACTAATGGGAAAACTTAGGAGGTATA
 GAAAACTACCATTAGAGTAAGGGCCAGAGAATACCTTAAAGGCCATTCAGATTCTTCGATCTTCT
 CCTCTCTTGTCTCAAGCTACTGTGTTTTCGGTATTACTTACCTTCTGAGGTCCTCAATCA
 TTGTTATGTTTTCCTAATCTTCAAGCGTGGACTAAAGGCACATGCAAGATACCTTTAAGTTGAAG
 GGTTTCTGCGTAGTGACATAAGAACCAATCCACAAGCTAAACAGACAGCATATGTTGGGTGAGGAG
 TGGTTGCGCTTTGGCTCGAGCTGTTTCCATTTATCAATATGTTTATGTTTACCAATATGTTTGG
 GAGCTGCTTGTGGGCAATTTGATATTGAACAAACAGAGAGGCGCTCAGAGAAATGTGGCGCAG
 CTACTACCAACGCGCACAGATACGAATAGCGTCAATCAACAGGCTCTAGTTATACCGTACACAATG
 AACCAGCACTAATATACCTGAGGCTACCCAAAACTGCTACAATAACCATCTAA

YOL048C_homolog 247aa (SEQ ID NO 442)
 MFSLFFPPQAIYVYLLMGLPVGIVGAWYSLISQASTLSIFVVTISLMPHIQRVAYDAILSRACANDV
 VLMGKLRRYRKLP.IRVRRAREYLKAI.PDFSIFPPSLKLLVFFGIYFIPFGVPII.VLFPQSSKRGKL
 AHARYFKLKGFSRSDIRTIHKLNRPAYMGVGVVALWLESFPFINMFMFTNTLGAALWAVDIEQQE
 KAVTENVAATTTTATDTSNVQQLVIPVHNEPATNIPEATPKTATNTI

YOR027W_homolog 2270bp PathoSeq: 1..947/1781..1828, public:
 948..1780/1829..2270; CDS: 501..2267 (SEQ ID NO 443)
 GCATTTTACTATTTAGATATTACTTCATATTGCTTTTATTAGATTGATTTTGTTTAAACAGTGAA
 AGTTTTTATTTTTTTTTTGTTTAAAGTTTTTATTTTTTTTTTTTAAAGTTTTTGTATTTATACAA
 TATTTAAATTTATAGTAATCATCCTATAAATTTCAAAGTCAAAGACAGATCTTTAAGGCTCAATTTAA
 TAACCTCTTATGGCCCTCTGTGTCAAATTTGTGCTGTTGATAACAAGTTTGGAAACGGTAATGGTT
 GAAATTAGAAAAGAAAAAATTACATAGTGTAGCAGCTGTAGTATAGAACTTTCTAGCAAAAAAAA
 AAAAGAAAGATTTTTTTTTTCTTCCATTTTCAAATTTGAGAGATCGAAAAATTTTTCTTGAATTTA
 TAAAAGGGGAACCCCTCTCCGAAAAATCCAAACCAAACCTTCCACCCAAATATCAAAATACTAAC
 TTTATCATTTCCACAGATAATATCCCACTTCAATAACAATGACAACAGCTGACGAATACAAAGCAG
 AAGGTAAACAAATTTTTGCTGCTAAAGATTTTGAAAAGGCGATTGAAGCATTCACATAAGCAATTG
 AAGCATCACTGAACCAACCATGTTCTTTATTCAAATCGTTCTGGATCTTATGGCTCTTTTAAAG
 ATTTTAAACAGCGATTTAAAGATGCTCAAGAAATGTGTCAAGATCAATCTAGTTGGGCCAAAGGGT
 ATAATAGAAATGCTGGGGCTGAATTTGGTTTGGTAAATTTTGATCAAGGCCAAATCCAATTTAGAA
 TATCTTTTGGAGTTGGATCCAAATTAATGCTATGGCTAAAGAGGTTTAAATCAGTTGAATTCGCTTT
 TATCATCTGGGTGGTGTGATGACAAAGGATTTAGGATTTGGTAAATTTTAAATGATCTCAATCTTT
 ATCTAAATTTGAAATAATATCCTAAACAAAGTGAATTTATGAATGATCTCAATTTTGTGTGCTAAAC
 TTGAAGCTCTTAAACATATCCCAATTTGGGTAATCTGATATGTTTATGATCCAGATTTATGA
 CGGCTTTTGTCTGCTTTAATGGGTATTTGACATGGATTTACCAAAATATGGGATTCACCTGCTCCAAAGC
 AATCACAATCCAATGCATCAGAACCAAACTGCAACCAAAATCAGTACCAGAAATCAAAACAGAAC
 CAAAAGCAGAACAAAGGAAGAAAGAAATCAACCTCAGCCAAAGATGAAGACACTCCAATGACTGATG
 CCCAAGCAGCAGCTAATGATGATGATGCCAAACCAAGCTGACAATGCTAAAGCTGAAGGTAATG
 CCTTATACAGAAAGCGTCAATTTGATGAAGCAATTTGCCGCTATTAATAAGGCTTTGGGAATTACATA
 AGGATATCACTTATTTAAACAATCGTCTGCTGCGCAATATGAAAAAGGGTATATGATGCTGCTA
 TTGCTACATGTGAAAAAGGCCATTGATGAAGGTAGAGACATGAGAGCTGATTATAAATTTGATGTCTA
 AATCATTTGCTAGATTAGGTAATATTTATTTGAAAAAAGATGAATTAACCGAGCAGTGGAAAAATT
 TTGAAAAATCTTTAAGTGAACATCGTACCCTGATGTTTAAATAAATTAAGATCAACTCAACGCTG
 AAATTTAAACTAGAGAAATTAATGCTTTATATAGATCCAGAAAAGGCTGAAGAAGCAGAAATTAACAAG
 GTAAGAATATTTTACCAGAGGATTTGGCCAAATGCGGTTAAAGGCTTATATGAAATGATTAAAAA
 GAGCACCAGAAAGTCTAGAGGATATTTCAATCGTCTGCTGCAATTTGGCAAAATTTGTTATCATTTTC
 CTGATGCTATACAAGATTGTAATAAAGCCATTGAAAAAGATCCAAATTTCTATAGAGCTTTATATTA
 GAAAGCTAATGCTCAATTTGGCAATGAAAGAAATATAGTCATGTCATGGATCTTTAACCAGAGGCAA
 GAACTAAAGATTTGAAATTTGGGTGGTAAATCAATTCATGAAATTTGATGAATTAATGAATAAAGCTA
 CTTATCAAGATTTTCAAGCCATTGAAGGTGAAACTCTTGAACAAACTATGGAAGAGGATTTCTAAAG
 ATCCAGAAATTTGTCAAATTTTACAAGATCCAGTATGCAAGGAATTTTAGCTCAAGCTTAGAGAAA
 ATCCTGCTGCTTTACAAGATCATGAAAAAATCCTGGAAGTTTATAAAAAAATTAATATGTTGATTG
 CTGCTGGTGTATTCTGCACAGATAA

YOR027W_homolog 589aa (SEQ ID NO 444)
 MTDAEYKAEENKRYFAARDFEKAI EAPTKAIEASPEPNHVLYSNRSGSYASLKDFNNALKDAQECV
 KINPSWAKYGNRIAGAEFLGNFDQAKSNYKCLELDPNNAMAKEGLKSVESALS5GGGDDKDLGF
 GKILLNDENLYTKLKNPNKTFSEFMNDPQFVAKLERLKTNPQLGNPDMFSDRPLMTAFALMLDMIDL
 PNMGFTAPNESQSNASEPKSEPKSVPEKPEPKAKQKEESTSAKDEPRLLTAQDDTNDNDAKTQ
 ADNAKEBGNALYKKRQFDEAIAAYNKAWELHKDIITLNNRAAAEYKGDVDAIAITCEKAIIDEGRD
 NRADYKLIAKSPARLGNLYLKKDELPEAVKNFEKSLTEHRTPDVLNKLRSSTQREIKTRELNAYIDP
 EKAEEARLQKEYFTKGDWPNNAVKAYTEMIKRAPEDARGYSNRAAALAKLLSPFDAIQCNKAIIEK
 DPNFIRAYIRKANAGLANKEYSHVMDTLTEARTKQVLEGGKSIHEIDELMNKATYQRQFAIEGETP
 EQTMERVSKDPEIVQILQDPMVGILAQARENPAALQDHMENPEVYKKINMLIAAGVIRTR

FIG. 2 - 56

YOR312C_homolog 1019bp public: 1..1019; CDS: 501..1016 (SEQ ID NO 445)
CCACATAACAACTTTTTTTTGGACTATACACCACTGAAAAAATAAATTTTTGTAAAAATCT
TAAGAATTTTCAGTTTAGAAGGTATTCACAACAACCGAAGAGTATGTTCAACATCGTTATATATAGA
ATAGAATTAAGAGCATGACAACAAGGGGATACAAGCTTGAAAAAAGAAAAAGGGTGGGATATCTTAA
AATTTATTAAGAGTTTTTTTTTATAACATGTCAATTGAGATTGAGATTGGGAATCTGAATTCCGATT
TAAAGTCATTTGGATTGGGAGAGTTAATTATTCGTTTTATTATTAGGATTACCAATGAATAGTAATGA
AGTGATGGAGAGATAGAATGAAAGTATTCAGAAGAGCATCAAGTCCTTATAAGTTTGTGAGACAT
AATATGCTCAACCCCTTGTCAACTTGTCATAAATTTATTGCTCGTCCTTTAAAAAGAAATGAATAA
AAAGATTTACTAACTTAATTTCAATTATTATAGAAAGATGCTAGATTAAACGAATATCAAGTTA
TTGGTCTGTAATTTACCAACTGAATCCGTTCCAGAACCAAGTTGTTTCAGAAATGAGAAATTTTGTCTC
CAAAACACCGTTGTTGCCAAATCAAGATATTGGTATTTCTTGCAAAAATGTCATAAGTTAAAAAAG
CTTCTGGTGAATTTGATCTGTGCAACATTATTCTGAAGCTAAACCACTAAAGTTAAAACTTTTG
GTATTGTGTTAAGATATGAATCCAGATCTGGTATTCTATAACATGTACAAAGAATACAGAGATTGA
CTAGAGTTGGTGCTGTTGAAACCATGTACCAAGATTAGCTGCTAGACACAGAGCTAGATTAGAA
GTATCCATATTTTGAAGTTGTTGAATTAGAAAAAAGCTGATGATGTTAAAAAGCAATACGTTAAAC
AATTTTGACTAAAGATTGAAATTTCCATTACCAACAGAGTCCAAAAATCTAAGAAATTTGTTCC
AAGCTACTGCTCAACCACTTTCTACTAA

YOR312C_homolog 172aa (SEQ ID NO 446)
MSRLNEYQVIGRNLPESVPEPLFRMRIFAPNTVVAKSRYWYFLQKLHKVKKASGEIVSVNIIE
AKPTKVKFTFGLWLYESRSGLHNMVKEYRDVTRVGAVETMYQDLAAHRHARFRSIIHLKVVELEKT
DDVKRQYVFKFLKDLKFLPHRVQKSKFLQATATFY

YOR369C_homolog 932bp PathoSeq: 1..228, public: 229..932; CDS:
501..929 (SEQ ID NO 447)
TGTTTTACTTTTTCTGTAGTTTTAAAGTTTCCTAAATTTAACTTCCAAAAAGTTTCATTAAACAATA
TTAACATACCTTTGTGCACAAGCAATATATTGAAGTTTTTTGATACAAGTGTGTTGTTTTTGTG
TACATGTGAGATATATAATTGTGTATATACAGTCACGTGAATAGAGCAAAAAAATTACGAAGTAGA
AATATTGTGTAGCGCGTTAGGGCTATAGCCCTATTAGTTTGTGCACCACACGACTTACAATTTTTT
TTTTTTTCTTTCTTAGAATCCTTGAGGCACTGACACTGTACTCTCTCTCTCTCTCTCTCTCTCG
TAGGTAGTGAATAATTTCCACTAGTCTTCCCATAAACCCACCTAGGTTCTTTCTTTTGGAAACCACT
GAGCAGTAAATCAATTTACTTGACGAAGAAGTCTATACATAAATATAAACTTGTCCTCCCTCCCTCC
CTTTTTTTTAACTAACTAAGAAGAAAAAATTAATAAATGTCTGACGTTGAACAGAACAAATGT
TTGAAGAAGTTGTTGTTGAAGAACAATCCGGTGCCATCACCATGGAAGATGCTTTAAAGTTGTTT
TAAGAATCTTTTAGTCCATGATGGTTTAGCTAGAGGTTTGAAGAAGCTTCTAAAGCTTTATCTTA
AAGAGAAGCTCAATTAATGTTGTTTGTGTGACTGTTTACTGAAGAATCAATCATCAATTTGGTTG
AAGCTTTATGTAATGAACAGAGAAGAAAAATCCCATTTGATTAAAGTTTCCGATGCTAAATTTATGG
GTGAATGGGCTGTTTATGTCAATTAGATAGAGATGGTAATGCTAGAAAAAGTTGTTGGTGCCTCTT
GTGTTGTTGTTCAAAAAGTGGGCTGCTGATTCTGATGAAGAACAATCTTGTGGAACACTTTTCTC
AACAATA

YOR369C_homolog 143aa (SEQ ID NO 448)
MSDVEQEIVVEVVVEQSGAIIIEDALKVVLRTSLVHDGLARGLREASKALSKREAQLCVLCSVS
TEESTIKLVEALCNEPEKIFLIKVSADAKLGEWAGLCQLDRDGNARKRVVVGASCVVKNWGDSD
RNILLEHFSQ

YPL047W_homolog 881bp public: 1..811, PathoSeq: 812..881; CDS:
501..878 (SEQ ID NO 449)
AAAAATTCCAATCTTGAATTTTCATCTTCAACGTCATAAACTTGTTCTGTTTGAATTTATCGTCTC
CATTTACGTTGTCATTTTCATTTGTCATTTGTCATTAATACGGTTACGATTTTGTGTTTCCGCTTGAAG
TCTTTGACTCTAGCTGTTCTACTGTCAATACCTTGGCTTGGTTGTCTTACTGTTGAGCGATGAG
ACAAACTTTTGTATTGATGCAACTGAACAAAAAATACGACAGACACACACACACACACAC
ACACAATTTTCAGCTCCTTCAAGCTGCTTTTTTTTGAAGAAGAAAAAACAATTTGGCCCTAAA

FIG. 2 - 57

TTCTGTTGATAAACTCGAGCAGCATCCGCAACAGCAGATTCTCTCAAGAAGACCTAAACGAGGTAA
 TGTTTTAAATTCACAGGACATCAATGCACCCTCCAAGACTATGTCTTGGGATTTCAGTTTAAATGA
 ACCAAATAAATAAGATGACGGTAAATCACACAACCACTTCCAAATATAGTGATCATGAAATTCGCTAT
 AGCTGAAGATGCTCAACCGCAGCAATTAATGAAGCAGAAAAACATGCTCAAGAAGCTCATCGACA
 AGCCAAAAAGATTTGCTCAAGAAAGTTTCTGGGTATAGATCACATAGATTTCATATCCATTAAAGAAAGG
 TGGTAGTGTGGTAAATCTAACACCAACGGCAACGCAATGACGAAGATGATGATGAGGTTGAAGA
 AGCATGTTGATAAGAAATTTGGCAAAATGATGTTTCTGTGGATGGACCGTTGCATGTGCCAGAACACA
 TTTTCGAAGAAGAAATTTGAAAGCAAAAAACGGTGAAGAAACCAATTCATTGGAAACAATCTATACAA
 ATGTTGTGCAATTCAGAGAAATTTTACCAATCCAGCAACATTGAAACAAATGAAAAAAATAGACAGC
 ACCGTTGGAAGTGTAAAGATGCTCAACCCAAACCAACTTTAAATTGATGTGTTTATCTCTTTTTCAGA
 TTTTATTTGCCATTACCACTTATTAACACGGTCATTTTGTATAACGTCGACTATGACACAAGAGATGTT
 GAAAAACTTTCTTGAGTCGTTGACATATAATAAACAAATGGAAAAAGTTATCGTGTAGAAAAATGTTT
 CATTTGATGAGTTGGGATGGAAGTATTTGTGTGAATTTTGGCAACAATAAAACAGTTAAAGAAAT
 GGATATATCAACAACAGCTATCAAGCCAGATACCCAGACACAAGCATTCGTGGTAATATGAACCTG
 GGACTTATTTTATTCGATCATTAATTTTGTGTGGTGAATAGAAGAATTTGGTTATCAATGGATGTAA
 ACTATCCGATGCAATATTTGAAAGTTTCATCAATCAACCGGTTAAGAAGTCAACCTATTCGATTAGG
 TATTGCTGGTATTGATTTGAATGTTAAAAATTCAGAAATGGTCACATCGTGGTTAACTGATGGTAA
 TTCTCAATGTGTTGGTGTGATATTGCTTTTAAATGATTTGAGCAAGGGACAAATTCAGTCCATTCAT
 TAATCGGTTTAAACACTGGCAAGTCAACAATTTTGTGTTTTCATTGAAATTCACAAAGTTTACT
 GAACATTTGAAGAAATCTTGACTTGATCAAGTCATTAATTAATGTTTAAAAACATTCAGATTTTTAGA
 TTTTAAAGTTCCATACCTAATATCTTCCGAAAAATTAATPACCATTTGGCAACAATCATTCGCCAGCAT
 TCCATAATCTCGAAGAATACATTTTGATCTTAATGAATTAACCGCACAGCTATTTGGGTCATTGGC
 GGGGTTTACTGAAAAATGCCCAATTAAGTCTGTCGTTTATGGGTAAATAGAAAAATTTGTCACTA
 TACGTCAGCAGCTACATTTATACGGAGCAGTTAAACAATCCCAAGACCTTTGTTGCTCTGATTTTGA
 CTACGATTTAATTAACCTGATCAATTTATCAACGCTATTGCGCTTTTATTTGATGAGAAAACTTGAATA
 CACTTTGAAGCCATCTCATGGCGCAATATTGAAAGCAATCCAGAAAAACAGAGGATTTGATGTA
 TGATGGATCGTTTAAATGGAAACAGCTGAAAAATTTATAGTTGAAATAGAAAAAGGTTAAGAAAGA
 GGATATCAAAATGCAAGAAATTTATATCCGATTCAGTATTGGAAGAAACAGATTCGATTTCGTAAGGA
 TATTCACAAACCATTTGATACATTATTCGAACAAGAAATTTAGGTAAATTTATCATTTGAAGGTAA
 AGAGAAATTTAGTTCGATTTTGTTTATTAGATTTCGCTTTTGAAGAAATTTGGTTGTTATGGTTGAGGA
 ACATGCCAACGGATTATTTAACAACCAACGACCTCCACGGACGATCTCAGAAGTAGAGCCATGTC
 GCCATCGGTCACTGTGATACAATCCATGAAAGTGCAATGAGTTGATTACTGTCTGGACCAATTTT
 ATCACCACATGTCAATAGGAAAGCAGAACAAAGCTCGTATTTCCAGTGTTTGCAATTAATGATAA
 TTTGACCCCTCATCAAGTTGTCGTTGAGTCAATGATGAAGGTAGAGATGTTCCCAATAGATAAAAT
 GACGAGCAGCAGCTTTTGTATTCGATCAATTAGTCAAACTCTGTCGATGCAAAAAGACAGAAAT
 TGAAGCAAGGGAGCTTCATAAATTTGGATTCTTTATTCAACAAAAAGAGAGACAAAAACAACACA
 ACAACAAGCAACCAACCAAGCACTCACACCAGCACCAACCGGCCAGCTGATCCACAAAGAAAA
 CCAGCTGCGCTGCCACAACAGGAAAAATATGAAGATTTACCGATATTTAAATACATTTACCTGACG
 ACCAGATTTGAGAGATGCTATAATGCGAGCTAAGGGAGTAGCAATGTTATCGAATTAATTTGATGCT
 AATTAAATATCATCGTGTTTAAATTCGATGCACCATTCGACAAAAACCATTCATCAATTTGAACAAAC
 AATCTTTCAGCAAAATAGTTGAGGATGAAGTTGAAGTTTCTGATAATGCCTCTATTGATCTTACTAA
 TGGTGACGATTTTACATCAACTTGGTGACGGTAAACATAATGGTAATGGTAGCGTTGATCCCTGGT
 TAGTGAAGTTTATGACAAGTTGTTTAAATGATGCTGAACGAGTCAGACTGAATAGAGATATATAA

YPL137C_homolog 1364aa (SEQ ID NO 452)

MTSNSPPLGSGTNDQRLPQSGVSSIPTNKLPLPNAEDFATGVNSGVDVWDLFRGSKSLGKKMMANN
 NANKDERKNSHGNIKNSEKTTAKPNETHESNGEKLEFNVPKSVMPTKHTSSGNPKPATNGQISNV
 TFSQSPKLTQTSNSTANDIPPIPSPKPEKASKNLKIGRSRSSASTVSPSTTASTTTNPNDGP
 KSQPKRRSSSNFVTPSLTSDLAYDDPALVQSLNNSNSNSNSPNVSRNSKKGGLFSSLSKFR
 SSSASQSPQSHSSSTPSTTTNGGNSNSAAPKSSSHSPKFNPSLVGPVSKHNRRAEDLVSLTNVL
 PAGSGIPIKRPSPISGNSIFKDSFLDDASSPSSSLNSDGLKFFRRRSVSTPSTHASTPVSIL
 NKNPNRRRVPIEETSEVRLRRVTFVDKLHDPQQQIPSRPRKGRNVLPQDINAPPRLCLGISV
 NEFPNNKDGKSHNHSKYSDHEIALAEDAQRRAIEAEKHAQEAHQAKKIAQEVSGYRSRHFISIK
 EGGSVNSNTNGNDEDDEVEEAVDKKLANDVSDGLHVHEQHFEIEIESKTEKISLETLY

FIG. 2 - 59

TRCCHLREILPIPATLKQLKNKPTAPLEVLKMLNPKPTLIDVLSFSDFIATPINTIVFDNVTMTTE
MLKNFLGSLTYNKQLEKLSLRNVSIDELGWKYLCEFLATNKTVKKLDISQORIKPDPFDTISIRGNM
NWDLFIRSLILRGGIEELVINGCKLSDAIFEKFINQAVKKSTYRLGIAGIDLNVKSKSEMTVSWLTD
GNSQCVGVDFIANDLSKQQLRPFINAFNTGKVNINLVFSLNNTSNIETSDLIKSLINVKTLRFL
LDLSSIPNIPFKIITHLDKYLPRYPNLRIRHFDLNLTAQAIISGLAGCLSKMPQLVHVSLGNGRNL
STTSAATLYGAVKQSKTLFALDDLYDLIPDQLSQRIAPFYLMRNLLEYTLKPSHGGNIENSPKPEDL
MYDGSLLMETAEKLLVEIEKGKKEDIKMORIISDSVLERTSRIRKDIHKTIDTLPQERNLKGKLSFE
GRENLRVFCLLDSSLEKLVVMVEEHANGLLLTPTTSTDLLRSRAMSPSVTVDITHESANELITAGP
ILSPHVNRKAEQSSYFPVFANNDNLTPHQVVVESNDEGRDVPIDKMTGRPVILRSISQTSVHAKEQ
LIEBEGELHKPGFFIQQKERQKQQQQQQQQNSHHQHPAQSIQENQSPSPQOQGYEDLPILMTLP
SGPELRDAIMAAKGVANVELIDRINNHRVKIDAPSTKHHEHLNKNPSDKVVEDEVEVDNASIDS
TNGDDLHLQLGDGKHNGTVDPMVSEVYDKLLNDAERVRNRI

YPL175W_homolog 1859bp public: 1..393/395..1859, PathoSeq:

394;CDS: 501..1856 (SEQ ID NO 453)

ACGGAATAATGTTATGCGAACAGAGTAACCTGGGATTATCAACAAGCATCAGTCAATTTCAAAAACT
CGGCTGCTTCTTTCGCTAGTGATGCATTGTACAATAGAAATTAATAAAAAAGAAAGGTAGAAATAG
AATTCAATGTAGGTGATGATCACTTCTTGAGAGTCTCTATTACGATATATAAAAAACATAGACCAAAA
TTATAATGAAGTAAAAACATGTAACCTGTGTAATTTTATCAAGTCAAAGGTATTGATTAAATATTG
TAGAGTTGTGAGCATTTAAAAATAGAAGGAACCGATAACCTAAAAGTTTCTCCAGGTGTCGAA
GCTTAGGAGGAATAAAATCTGAGTAGAAGAACTTTCGTTTATATCAGTTTTCGACAGAAAAAAGG
AAAACAAAACAAAATAACACCAACAAACGAAATTACACAAGCACATCTCAACACCACTCTGTGGAG
CACCATAACCTGAGAAATGCAAACTTGTAAATAAAATATGGGATACAATATAGCAATGGTAAACAG
ATTTTCTTTACCTCAACCTGGAGGAGTAGAGTTTCATGTGTATCATTTTATCAGAAAACTCATTG
AATFAGGACATCACTGAGTGTATCATAACTATAATTATTCATCAAGAAATGGTGACGAGTATTAA
CGAATGTTGTGAAGGTGTTATTATGTACCCTTTGGGTGATCTATAGAAGCTCAGTTTTCCTCACTG
TATTTCTGTGCTTCCCAATATTGAGGAATATCTTCATACGAGAAAAACATTGAGATTATTCACGGAC
ATGGTTCTCTCAGCACATTATGCCACGAAGCTATATTACATGCGCGAACAATGGGATTAAAAACAG
TCTTCACTGATCATCTCACTTTTGGATTGTCCGAGATTGGATCAATTATGGGGAATAAAGCATATAA
AGTTCACTTTCAGTGATGTTGGCCATGTTATCTGTGTCAGTCAACCTGTAAAGAAAAACAGGTTT
TAAAGAGGATCAATAGACCCATAAAAAGTGAGTGTGATACCGAATGCAGTTATTCTGAAAAGATTCA
AGCCCAAAATCGCATTTGTGTTAAACAAGAACTATACTAAAGAGATCACCATTTGGGTGATCAGAGAT
TGTTTCCAAATAAAGGAGCCGATCTATTAAACGGCTGTTATCCCCAAAATTTGCGAGTTGAAACCAA
AAGTGAATTTCTAATTGCTGGTGACGGCCCCAAGTTTGTAGATTAGAAACAAATGAGAGAAAAGT
ACTTTCTTCAGGAAAGGGTTACATTAGTAGGCGCTATAAAACACGAAGAAGTAAAGAGATTGAATGG
TCCAAGGTGACATATACTTATCATCTTCAATTAAACAGAGCGGTTTGGTACAGTTATTGTGGAAGCTG
CATCATCTGGGTATATGTTGTGCACTACAAAAGTTGGAGGCATACCCGAAGCTTACCAAAACGAAA
TGACAAGCTTGTCTGAACCGGAAGAAAACCTCACTTATTGATGCTGCTATAGATGCTATAAATAAAA
TTGAAAGTAAATGAAATCGATACCTCAAAATTTTCACGATGCGGTTGCAAAAGATGTACAGTTGGAATG
ATATTGCAAGAAGAACAGAAAATGTTTATAATTCACTTGATTAGACAACTAAACGAGTCTTTTAC
TTACCGGATTACAAAGATACATTGTTGTGGTATAATAGCAGGCAAACTTTATGCTTTATGTGTAA
TAGTGGATATTTTATTTTCTGTGATCTAGAAATGGTGTATCCCGCTGATCATATCGATAAGCAAA
CAAAATGGCACTGCTATCAAGGAAGAAGACGAGCTGGAAGAAGAAACATTTATTTTCCGAAACA
AAGTAAATTAG

YPL175W_homolog 452aa (SEQ ID NO 454)

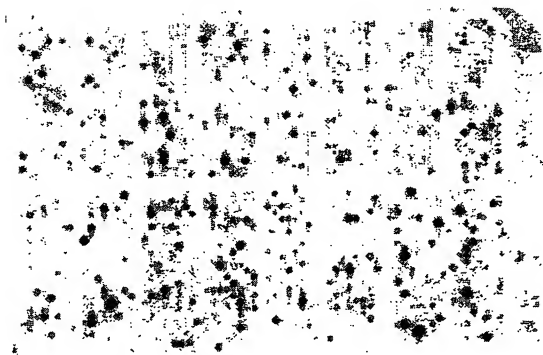
MGYNIAMVDFDFYPQPGVEFHVHLSQKLIELGHSVVIITHNYSRRNGVRVLTNGLKVYVPLVW
IYRSSVFPKTVSCFPLILRNIFIRENIEIHHGHSFSTLCHEAILHGRTMGLKTVPTDRSLVPGFAEI
GSIMGKALKFTFSVDVGHVICSHTCKENTVLRGSIDPIKVSVPINAPVIAISKDFPKPSHCVNKNVTK
EITTVIRLTLFPNKGADLLTAVIPKICQLKPKVKFLIADGPKFLDEQMRREKYPLOERVTLVGAI
KHEEVEDVMVQGDILYHPSLTFEAGFTVIVEAASCGLYVVTTKVGGIPELVNEMTSFAEPENSLI
DAIDAINKIESNEIDTSKFHDAVAKMYSWNDIARRTENVNLSLDLKLNESLHRLQRYCCGII
AGKLYALCVIVDIFVIFVLENLVYFADHIDKATKWPSAKKEDESEEBETIFPNKVN

FIG. 2 - 60

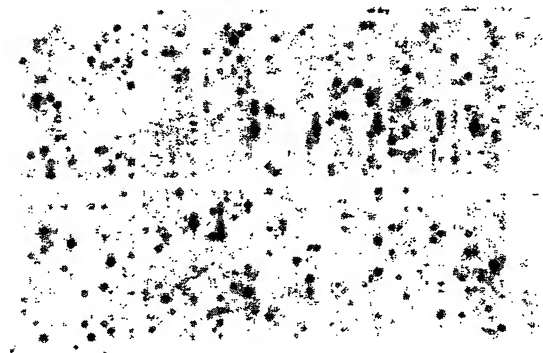
YPL218W_homolog 1231bp PathoSeq: 1..407, public: 408..1231; exon
 1: 501..518, intron 1: 519..676, exon 2: 677-1228 (SEQ ID NO 455)
 GATACAATTCACGACCTCTAATTTCCCTTAGTGATAGGTTAATCATGAAATATATAAAATGCTAGA
 AATAATTGAATAATGATATAAATATAATGTTGTGAAACTTGTGGAAAAATTTGACAGCCTAGTAAC
 TCAAGTGTGTGTACACTCTTGTATTATTATTATTATATCGTTTACAAAGTAGATTCTCATTTTGA
 ACAGCAAACTACTGTCGTTAATAGGAATCAGAGGCAGAAAAGAAAGAGAGAGAAAAAAGGACA
 CATTTACACGTACACCCCTTAACTTGAAGGAAAAAACAACAAAGAGAGACAAAGAAAGACAAAA
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 AAGTTTATTAGAAATTGAAGAAATTGAGTCAAGTTCCATTGTATTTTGGGTAATAAGATTGATGT
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FIG. 2 - 61

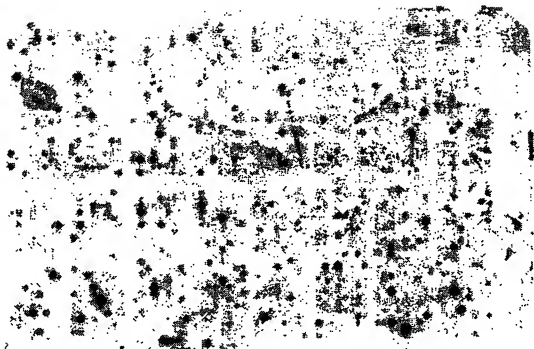


Filter I

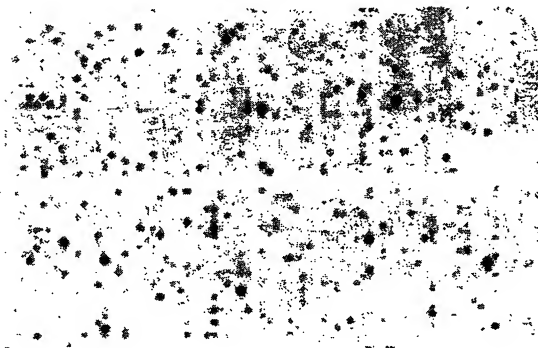


Filter II

FIG. 3A



Filter I



Filter II

FIG. 3B

SEQUENCE LISTING

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<120> Cell death related drug targets in yeast and fungi

<130> JAN-02-RC/CAND

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<170> PatentIn Ver. 2.1

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<213> *Saccharomyces cerevisiae*

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Arg Lys Asn Gly Met Asn Val Asn Phe Tyr Lys Tyr Ser Leu Leu Asp

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40

45

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Asn Trp Asn
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<213> *Saccharomyces cerevisiae*

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20

25

30

Ile Arg Gly Gly Leu Ala Tyr Asn Asp Phe Leu Ile Leu Pro Gly Leu

35

40

45

Val Asp Phe Ala Ser Ser Glu Val Ser Leu Gln Thr Lys Leu Thr Arg

50

55

60

Asn Ile Thr Leu Asn Ile Pro Leu Val Ser Ser Pro Met Asp Thr Val

65

70

75

80

Thr Glu Ser Glu Met Ala Thr Phe Met Ala Leu Leu Asp Gly Ile Gly

85

90

95

Phe Ile His His Asn Cys Thr Pro Glu Asp Gln Ala Asp Met Val Arg

100

105

110

Arg Val Lys Asn Tyr Glu Asn Gly Phe Ile Asn Asn Pro Ile Val Ile

115

120

125

Ser Pro Thr Thr Thr Val Gly Glu Ala Lys Ser Met Lys Glu Lys Tyr

130

135

140

Gly Phe Ala Gly Phe Pro Val Thr Ala Asp Gly Lys Arg Asn Ala Lys

145

150

155

160

Leu Val Gly Ala Ile Thr Ser Arg Asp Ile Gln Phe Val Glu Asp Asn

165

170

175

Ser Leu Leu Val Gln Asp Val Met Thr Lys Asn Pro Val Thr Gly Ala

180

185

190

Gln Gly Ile Thr Leu Ser Glu Gly Asn Glu Ile Leu Lys Lys Ile Lys

195

200

205

Lys Gly Arg Leu Leu Val Val Asp Glu Lys Gly Asn Leu Val Ser Met

210

215

220

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 Asn Met Ile Lys Trp Ile Lys Glu Thr Phe Pro Asp Leu Glu Ile Ile
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 Ala Gly Asn Val Val Thr Lys Glu Gln Ala Ala Asn Leu Ile Ala Ala
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 Gly Ala Asp Gly Leu Arg Ile Gly Met Gly Thr Gly Ser Ile Cys Ile
 325 330 335
 Thr Gln Lys Val Met Ala Cys Gly Arg Pro Gln Gly Thr Ala Val Tyr
 340 345 350
 Asn Val Cys Glu Phe Ala Asn Gln Phe Gly Val Pro Cys Met Ala Asp
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<213> *Saccharomyces cerevisiae*

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<213> *Saccharomyces cerevisiae*

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Val Trp Ser Ser Cys Phe Gln Val Ala Phe Ile Phe Ser Leu Trp Tyr
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Phe Ile Leu Ser Ile Tyr Thr Phe Phe Tyr Ser Lys Lys Ile Lys Gln
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Ile Ile Ser Tyr Glu Pro Ser Tyr Phe Val Phe Ser Tyr Arg Ala Ile
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<212> PRT

<213> *Saccharomyces cerevisiae*

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 35 40 45
 Gln Thr Glu Thr Gly Glu Asn Ser Ala Lys Asn Ala Glu Gln Asn Val
 50 55 60
 Ser Ser Thr Asn Leu Asn Asn Ala Pro Thr Asn Gly Ala Leu Asp Asp
 65 70 75 80
 Asp Val Ile Pro Asn Ala Ile Val Ile Lys Asn Ile Pro Phe Ala Ile
 85 90 95
 Lys Lys Glu Gln Leu Leu Asp Ile Ile Glu Glu Met Asp Leu Pro Leu
 100 105 110
 Pro Tyr Ala Phe Asn Tyr His Phe Asp Asn Gly Ile Phe Arg Gly Leu
 115 120 125
 Ala Phe Ala Asn Phe Thr Thr Pro Glu Glu Thr Thr Gln Val Ile Thr
 130 135 140
 Ser Leu Asn Gly Lys Glu Ile Ser Gly Arg Lys Leu Lys Val Glu Tyr
 145 150 155 160
 Lys Lys Met Leu Pro Gln Ala Glu Arg Glu Arg Ile Glu Arg Glu Lys
 165 170 175
 Arg Glu Lys Arg Gly Gln Leu Glu Glu Gln His Arg Ser Ser Ser Asn
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 Leu Ser Leu Asp Ser Leu Ser Lys Met Ser Gly Ser Gly Asn Asn Asn
 195 200 205
 Thr Ser Asn Asn Gln Leu Phe Ser Thr Leu Met Asn Gly Ile Asn Ala
 210 215 220
 Asn Ser Met Met Asn Ser Pro Met Asn Asn Thr Ile Asn Asn Asn Ser
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      290                      295                      300

Thr Leu Glu Ile Tyr Ser Gln Leu Leu Leu Phe Lys Asp Arg Glu Lys
      305                      310                      315                      320

Tyr Tyr Tyr Glu Leu Ala Tyr Pro Met Gly Ile Ser Ala Ser His Lys
      325                      330                      335

Arg Ile Ile Asn Val Leu Cys Ser Tyr Leu Gly Leu Val Glu Val Tyr
      340                      345                      350

Asp Pro Arg Phe Ile Ile Ile Arg Arg Lys Ile Leu Asp His Ala Asn
      355                      360                      365

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Leu Gln Pro Asn Ser Thr Gly Gly Ser Met Asn Arg Ser Gln Ser Tyr
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Thr Ser Leu Leu Gln Ala His Ala Ala Ala Ala Asn Ser Ile Ser
      405                      410                      415

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      420                      425                      430

Asn Gly Asn Gly Asn Asn Val Ile Ile Asn Asn Asn Ser Ala Ser Ser
      435                      440                      445

Thr Pro Lys Ile Ser Ser Gln Gly Gln Phe Ser Met Gln Pro Thr Leu
      450                      455                      460

Thr Ser Pro Lys Met Asn Ile His His Ser Ser Gln Tyr Asn Ser Ala
      465                      470                      475                      480

Asp Gln Pro Gln Gln Pro Gln Pro Gln Thr Gln Gln Asn Val Gln Ser
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Ala Ala Gln Gln Gln Gln Ser Phe Leu Arg Gln Gln Ala Thr Leu Thr
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Ser Gln Ile Pro Ile Asn Ser Gln Thr Leu Ser Gln Ala Gln Pro Pro
    545                                550                                555                                560

Ala Gln Ser Gln Thr Gln Gln Arg Val Pro Val Ala Tyr Gln Asn Ala
    565                                570                                575

Ser Leu Ser Ser Gln Gln Leu Tyr Asn Leu Asn Gly Pro Ser Ser Ala
    580                                585                                590

Asn Ser Gln Ser Gln Leu Leu Pro Gln His Thr Asn Gly Ser Val His
    595                                600                                605

Ser Asn Phe Ser Tyr Gln Ser Tyr His Asp Glu Ser Met Leu Ser Ala
    610                                615                                620

His Asn Leu Asn Ser Ala Asp Leu Ile Tyr Lys Ser Leu Ser His Ser
    625                                630                                635                                640

Gly Leu Asp Asp Gly Leu Glu Gln Gly Leu Asn Arg Ser Leu Ser Gly
    645                                650                                655

Leu Asp Leu Gln Asn Gln Asn Lys Lys Asn Leu Trp
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<210> 9

<211> 3674

<212> DNA

<213> *Saccharomyces cerevisiae*

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<211> 1057

<212> PRT

<213> *Saccharomyces cerevisiae*

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 20 25 30

Phe Pro Ser Lys Lys Gln Arg Ile Ser His His Asp Asp Ser His Gln
 35 40 45

Ile Asn His Arg Pro Val Thr Ser Cys Thr His Cys Arg Gln His Lys
 50 55 60

Ile Lys Cys Asp Ala Ser Gln Asn Phe Pro His Pro Cys Ser Arg Cys
 65 70 75 80

Glu Lys Ile Gly Leu His Cys Glu Ile Asn Pro Gln Phe Arg Pro Lys
 85 90 95

Lys Gly Ser Gln Leu Gln Leu Leu Arg Gln Asp Val Asp Glu Ile Lys
 100 105 110

Ser Lys Leu Asp Thr Leu Leu Ala Asn Asp Ser Val Phe Val His Leu
 115 120 125

Leu Gln Gln Ile Pro Met Gly Asn Ser Leu Leu Asn Lys Leu Asn Leu
 130 135 140

His Pro Thr Pro Thr Pro Gly Thr Ile Ile Pro Asn Pro Asp Ser Ser
 145 150 155 160

Pro Ser Ser Gly Ser Pro Thr Ser Ser Ala Ala Gln Arg Asp Ser Lys
 165 170 175

Val Ser Val Gln Thr Tyr Leu Ser Arg Glu Pro Gln Leu Leu Gln Ala
 180 185 190

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Asn Gln Gly Ser Asn Thr Asn Lys Phe Lys Ala Asn Asn Glu Ala Ser
195                      200                      205

Ser His Met Thr Leu Arg Ala Ser Ser Leu Ala Gln Asp Ser Lys Gly
210                      215                      220

Leu Val Ala Thr Glu Pro Asn Lys Leu Pro Pro Leu Leu Asn Asp Ser
225                      230                      235                      240

Ala Leu Pro Asn Asn Ser Lys Glu Ser Leu Pro Pro Ala Leu Gln Met
245                      250                      255

Ala Phe Tyr Lys Asn Asn Ser Ala Gly Asn Thr Pro Asn Gly Pro Phe
260                      265                      270

Ser Pro Ile Gln Lys Thr Tyr Ser Pro His Thr Thr Ser Thr Thr Val
275                      280                      285

Thr Thr Thr Thr Asn Gln Pro Pro Phe Ala Ala Thr Ser His Val Ala
290                      295                      300

Thr Asn Asn Asn Ala Asp Arg Thr Lys Thr Pro Val Val Ala Thr Thr
305                      310                      315                      320

Thr Thr Met Pro Leu Leu Pro Ser Pro His Ala Asn Val Asp Glu Phe
325                      330                      335

Val Leu Gly Asp Ile Ser Ile Ser Ile Glu Lys Ala Asn Arg Leu His
340                      345                      350

His Ile Phe Val Thr Arg Tyr Leu Pro Tyr Phe Pro Ile Met Tyr Ser
355                      360                      365

Asn Asn Ala Thr Glu Leu Tyr Ser Gln Ser Gln Leu Leu Phe Trp Thr
370                      375                      380

Val Met Leu Thr Ala Cys Leu Ser Asp Pro Glu Pro Thr Met Tyr Cys
385                      390                      395                      400

Lys Leu Ser Ser Leu Ile Lys Gln Leu Ala Ile Glu Thr Cys Trp Ile
405                      410                      415

Arg Thr Pro Arg Ser Thr His Ile Ser Gln Ala Leu Leu Ile Leu Cys
420                      425                      430

Ile Trp Pro Leu Pro Asn Gln Lys Val Leu Asp Asp Cys Ser Tyr Arg
435                      440                      445

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Gly Glu Phe Ile Ser Glu Phe Thr Arg Thr Gln Thr Ser Met Pro Asn
 465 470 475 480

Ala Glu Lys Trp Arg Thr Arg Thr Trp Leu Gly Ile Phe Phe Ala Glu
 485 490 495

Leu Cys Trp Ala Ser Ile Leu Gly Leu Pro Pro Thr Ser Gln Thr Asp
 500 505 510

Tyr Leu Leu Glu Lys Ala Leu Ser Cys Gly Asp Glu Glu Ser Glu Glu
 515 520 525

Asp Asn Asn Asp Ser Ile Asp Asn Asn Asn Asn Asp Lys Arg Asn Lys
 530 535 540

Lys Asp Glu Pro His Val Glu Ser Lys Tyr Lys Leu Pro Gly Ser Phe
 545 550 555 560

Arg Arg Leu Leu Ser Leu Ala Asn Phe Gln Ala Lys Leu Ser His Ile
 565 570 575

Ile Gly Ser Ser Thr Ser Ser Pro Asp Gly Leu Leu Glu Pro Lys Tyr
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Arg Ala Glu Thr Leu Ser Ile Leu Gly Lys Glu Leu Asp Leu Leu Ala
 595 600 605

Lys Thr Leu Asn Phe Gln Ser Asp Asp Thr Val Asn Ile Tyr Phe Leu
 610 615 620

Tyr Val Lys Leu Thr Val Cys Cys Phe Ala Phe Leu Pro Glu Thr Pro
 625 630 635 640

Pro Thr Asp Gln Ile Pro Tyr Val Thr Glu Ala Tyr Leu Thr Ala Thr
 645 650 655

Lys Ile Val Thr Leu Leu Asn Asn Leu Leu Glu Thr His Gln Leu Ile
 660 665 670

Glu Leu Pro Ile Tyr Ile Arg Gln Ala Ala Thr Phe Ser Ala Leu Ile
 675 680 685

Leu Phe Lys Leu Gln Leu Thr Pro Leu Leu Pro Asp Lys Tyr Phe Asp
 690 695 700

Ser Ala Arg Gln Ser Val Val Thr Ile His Arg Leu Tyr Arg Asn Gln
 705 710 715 720
 Leu Thr Ala Trp Ala Thr Ser Val Glu Asn Asp Ile Ser Arg Thr Ala
 725 730 735
 Ser Met Leu Glu Lys Leu Asn Phe Val Leu Ile Met His Pro Glu Val
 740 745 750
 Phe Val Glu Glu Asp Gly Ile Ile Ser Arg Met Arg Ser His Leu Thr
 755 760 765
 Gly Ser Leu Phe Tyr Asp Leu Val Trp Cys Val His Glu Ala Arg Arg
 770 775 780
 Arg Glu Met Asp Pro Glu Tyr Asn Lys Gln Ala Leu Glu Lys Ala Ala
 785 790 795 800
 Lys Lys Arg Lys Phe Ser Ser Asn Gly Ile Tyr Asn Gly Thr Ser Ser
 805 810 815
 Thr Gly Gly Ile Thr Asp Arg Lys Leu Tyr Pro Leu Pro Leu Tyr Asn
 820 825 830
 His Ile Ser Arg Asp Asp Phe Glu Thr Val Thr Lys Thr Thr Pro Ser
 835 840 845
 Gly Thr Thr Val Thr Thr Leu Val Pro Thr Lys Asn Ala Leu Lys Gln
 850 855 860
 Ala Glu Lys Leu Ala Lys Thr Asn Asn Gly Asp Ser Asp Gly Ser Ile
 865 870 875 880
 Met Glu Ile Asn Gly Ile Pro Leu Ser Met Leu Gly Glu Thr Gly Ser
 885 890 895
 Val Lys Phe Gln Ser Leu Phe Ala Asn Thr Ser Asn Ser Asn Asp Tyr
 900 905 910
 Asn Asn Asn Arg Thr Leu Leu Asp Ala Ser Asn Asp Ile Ser Ile Pro
 915 920 925
 Ser Asn Ser Ile Tyr Pro Val Ala Ser Val Pro Ala Ser Asn Asn Asn
 930 935 940
 Pro Gln Ser Thr Lys Val Asp Tyr Tyr Ser Asn Gly Pro Ser Val Ile
 945 950 955 960

Pro Asp Leu Ser Met Lys Arg Ser Val Ser Thr Pro Val Asn His Phe
 965 970 975

Pro Ala Ser Val Pro Gly Leu Arg Asn His Pro Val Gly Asn Leu Ser
 980 985 990

Asn Asn Val Thr Leu Gly Ile Asp His Pro Ile Pro Arg Glu His Ser
 995 1000 1005

Asn Leu Gln Asn Val Thr Met Asn Tyr Asn Asn Gln Phe Ser Asn Ala
 1010 1015 1020

Asn Ala Ile Gly Arg Ser Gln Ser Ser Met Ser His Ser Arg Thr Pro
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Leu Phe Arg Ser Ile Tyr Asp Ser Trp Ile Pro Arg Pro Thr Pro Val
 1045 1050 1055

Leu

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<211> 854

<212> DNA

<213> *Saccharomyces cerevisiae*

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 acccaattgg tgatgaagaa caatctatta atgacacccat ttccaaatta aaagtgttca 180
 aattatgaaa acaactcata taaatcacgta caaatttttc tctactcgaa gtgatataga 240
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<210> 12

<211> 117

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 12

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Glu Ser Glu Arg Ile Ala Asp Arg Phe Lys Asn Arg Ile Pro Val Ile
 20 25 30

Cys Glu Lys Ala Glu Lys Ser Asp Ile Pro Glu Ile Asp Lys Arg Lys
 35 40 45

Tyr Leu Val Pro Ala Asp Leu Thr Val Gly Gln Phe Val Tyr Val Ile
 50 55 60

Arg Lys Arg Ile Met Leu Pro Pro Glu Lys Ala Ile Phe Ile Phe Val
 65 70 75 80

Asn Asp Thr Leu Pro Pro Thr Ala Ala Leu Met Ser Ala Ile Tyr Gln
 85 90 95

Glu His Lys Asp Lys Asp Gly Phe Leu Tyr Val Thr Tyr Ser Gly Glu
 100 105 110

Asn Thr Phe Gly Arg
 115

<210> 13

<211> 1145

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 13

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<210> 14

<211> 214

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 14

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Tyr Ala Pro Arg Arg Gln Leu Ala Asn Thr Pro Ala Lys Asp Ser Thr
 35 40 45

Gly Lys Glu Val Ala Arg Pro Asn Asn Tyr Ala Gly Ala Leu Tyr Asp
 50 55 60

Pro Arg Asp Glu Thr Leu Asp Asp Trp Phe Asp Asn Asp Leu Ser Leu
 65 70 75 80

Phe Pro Ser Gly Phe Gly Phe Pro Arg Ser Val Ala Val Pro Val Asp
 85 90 95

Ile Leu Asp His Asp Asn Asn Tyr Glu Leu Lys Val Val Val Pro Gly
 100 105 110

Val Lys Ser Lys Lys Asp Ile Asp Ile Glu Tyr His Gln Asn Lys Asn
 115 120 125

Gln Ile Leu Val Ser Gly Glu Ile Pro Ser Thr Leu Asn Glu Glu Ser
 130 135 140

Lys Asp Lys Val Lys Val Lys Glu Ser Ser Ser Gly Lys Phe Lys Arg
 145 150 155 160

Val Ile Thr Leu Pro Asp Tyr Pro Gly Val Asp Ala Asp Asn Ile Lys
 165 170 175

Ala Asp Tyr Ala Asn Gly Val Leu Thr Leu Thr Val Pro Lys Leu Lys
 180 185 190

Pro Gln Lys Asp Gly Lys Asn His Val Lys Lys Ile Glu Val Ser Ser
 195 200 205

Gln Glu Ser Trp Gly Asn
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 <211> 3377
 <212> DNA
 <213> *Saccharomyces cerevisiae*

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<210> 16

<211> 958

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 16

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Thr Gln Met Gln Ile Pro Lys Tyr Glu Asn Lys Pro Phe Lys Pro Pro
    35                40                45

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Arg Arg Val Gly Ser Asn Lys Tyr Thr Gln Leu Lys Pro Thr Ala Thr
    50                55                60

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Ala Val Thr Thr Ala Pro Ile Ser Lys Ala Lys Val Thr Val Asn Leu

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Asn Asn Leu Ser	Ser Asn Glu Asn Thr	Arg Tyr Phe Thr	Ile Met Tyr			
	100	105	110			
Arg Lys Pro Thr	Thr Lys Lys His Lys	Thr Trp Ser Gly Asp	Gly Tyr			
	115	120	125			
Ala Thr Leu Lys	Ala Ser Ser Asp Lys	Leu Cys Phe Tyr	Asn Glu Ala			
	130	135	140			
Gly Lys Phe Leu	Gly Ser Ser Met Leu	Pro Ser Asp Ser Asp	Ser Leu			
	145	150	155		160	
Phe Glu Thr Leu	Phe Lys Ala Gly Ser	Asn Glu Val Gln Leu	Asp Tyr			
	165	170	175			
Glu Leu Lys Glu	Asn Ala Glu Ile Arg	Ser Ala Lys Glu Ala	Leu Ser			
	180	185	190			
Gln Asn Met Gly	Asn Pro Ser Pro Pro	Thr Thr Ser Thr Thr	Glu Thr			
	195	200	205			
Val Pro Ser Thr	Lys Asn Asp Gly Gly	Lys Tyr Gln Met Pro	Leu Ser			
	210	215	220			
Gln Leu Phe Ser	Leu Asn Thr Val Lys	Arg Phe Lys Ser Val	Thr Lys			
	225	230	235		240	
Gln Thr Asn Glu	His Met Thr Thr Val	Pro Lys Thr Ser Gln	Asn Ser			
	245	250	255			
Lys Ala Lys Lys	Tyr Tyr Pro Val Phe	Asp Val Asn Lys Ile	Asp Asn			
	260	265	270			
Pro Ile Val Met	Asn Lys Asn Ala Ala	Ala Glu Val Asp Val	Ile Val			
	275	280	285			
Asp Pro Leu Leu	Gly Lys Phe Leu Arg	Pro His Gln Arg Glu	Gly Val			
	290	295	300			
Lys Phe Met Tyr	Asp Cys Leu Met Gly	Leu Ala Arg Pro Thr	Ile Glu			
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Asn Pro Asp Ile	Asp Cys Thr Thr Lys	Ser Leu Val Leu Glu	Asn Asp			

325

Ser Asp Ile Ser Gly Cys Leu Leu Ala Asp Asp Met Gly Leu Gly Lys
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Thr Leu Met Ser Ile Thr Leu Ile Trp Thr Leu Ile Arg Gln Thr Pro
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Phe Ala Ser Lys Val Ser Cys Ser Gln Ser Gly Ile Pro Leu Thr Gly
370 375 380

Leu Cys Lys Lys Ile Leu Val Val Cys Pro Val Thr Leu Ile Gly Asn
385 390 395 400

Trp Lys Arg Glu Phe Gly Lys Trp Leu Asn Leu Ser Arg Ile Gly Val
405 410 415

Leu Thr Leu Ser Ser Arg Asn Ser Pro Asp Met Asp Lys Met Ala Val
420 425 430

Arg Asn Phe Leu Lys Val Gln Arg Thr Tyr Gln Val Leu Ile Ile Gly
435 440 445

Tyr Glu Lys Leu Leu Ser Val Ser Glu Glu Leu Glu Lys Asn Lys His
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Leu Ile Asp Met Leu Val Cys Asp Glu Gly His Arg Leu Lys Asn Gly
465 470 475 480

Ala Ser Lys Ile Leu Asn Thr Leu Lys Ser Leu Asp Ile Arg Arg Lys
485 490 495

Leu Leu Leu Thr Gly Thr Pro Ile Gln Asn Asp Leu Asn Glu Phe Phe
500 505 510

Thr Ile Ile Asp Phe Ile Asn Pro Gly Ile Leu Gly Ser Phe Ala Ser
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Phe Lys Arg Arg Phe Ile Ile Pro Ile Thr Arg Ala Arg Asp Thr Ala
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Asn Arg Tyr Asn Glu Glu Leu Leu Glu Lys Gly Glu Glu Arg Ser Lys
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Glu Met Ile Glu Ile Thr Lys Arg Phe Ile Leu Arg Arg Thr Asn Ala
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Ile Leu Glu Lys Tyr Leu Pro Pro Lys Thr Asp Ile Ile Leu Phe Cys

580

585

590

Lys Pro Tyr Ser Gln Gln Ile Leu Ala Phe Lys Asp Ile Leu Gln Gly
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Ala Arg Leu Asp Phe Gly Gln Leu Thr Phe Ser Ser Ser Leu Gly Leu
610 615 620

Ile Thr Leu Leu Lys Lys Val Cys Asn Ser Pro Gly Leu Val Gly Ser
625 630 635 640

Asp Pro Tyr Tyr Lys Ser His Ile Lys Asp Thr Gln Ser Gln Asp Ser
645 650 655

Tyr Ser Arg Ser Leu Asn Ser Gly Lys Leu Lys Val Leu Met Thr Leu
660 665 670

Leu Glu Gly Ile Arg Lys Gly Thr Lys Glu Lys Val Val Val Val Ser
675 680 685

Asn Tyr Thr Gln Thr Leu Asp Ile Ile Glu Asn Leu Met Asn Met Ala
690 695 700

Gly Met Ser His Cys Arg Leu Asp Gly Ser Ile Pro Ala Lys Gln Arg
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Asp Ser Ile Val Thr Ser Phe Asn Arg Asn Pro Ala Ile Phe Gly Phe
725 730 735

Leu Leu Ser Ala Lys Ser Gly Gly Val Gly Leu Asn Leu Val Gly Arg
740 745 750

Ser Arg Leu Ile Leu Phe Asp Asn Asp Trp Asn Pro Ser Val Asp Leu
755 760 765

Gln Ala Met Ser Arg Ile His Arg Asp Gly Gln Lys Lys Pro Cys Phe
770 775 780

Ile Tyr Arg Leu Val Thr Thr Gly Cys Ile Asp Glu Lys Ile Leu Gln
785 790 795 800

Arg Gln Leu Met Lys Asn Ser Leu Ser Gln Lys Phe Leu Gly Asp Ser
805 810 815

Glu Met Arg Asn Lys Glu Ser Ser Asn Asp Asp Leu Phe Asn Lys Glu
820 825 830

Asp Leu Lys Asp Leu Phe Ser Val His Thr Asp Thr Lys Ser Asn Thr

835

840

845

His Asp Leu Ile Cys Ser Cys Asp Gly Leu Gly Glu Glu Ile Glu Tyr
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Pro Glu Thr Asn Gln Gln Gln Asn Thr Val Glu Leu Arg Lys Arg Ser
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Thr Thr Thr Trp Thr Ser Ala Leu Asp Leu Gln Lys Lys Met Asn Glu
885 890 895

Ala Ala Thr Asn Asp Asp Ala Lys Lys Ser Gln Tyr Ile Arg Gln Cys
900 905 910

Leu Val His Tyr Lys His Ile Asp Pro Ala Arg Gln Asp Glu Leu Phe
915 920 925

Asp Glu Val Ile Thr Asp Ser Phe Thr Glu Leu Lys Asp Ser Ile Thr
930 935 940

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<210> 17

<211> 3341

<212> DNA

<213> *Saccharomyces cerevisiae*

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<210> 18

<211> 946

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 18

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 35 40 45
 Ser Tyr Ala Phe Ile Arg Ile His Gln Asp Asn Ala Lys Pro Leu Phe
 50 55 60
 Ser Phe Leu Gln Asn Leu Asp Phe Ile Glu Ser Ile Ile Pro Tyr His
 65 70 75 80
 Asp Thr Glu Leu Ser Asp Asp Leu His Lys Leu Ile Ser Ile Ser Lys
 85 90 95
 Ser Lys Ile Leu Glu Ala Pro Lys Gln Tyr Glu Leu Tyr Asn Leu Ser
 100 105 110
 Asn Leu Thr Asn Asn Pro Lys Gln Ser Leu Tyr Phe Ala Phe Leu Gln
 115 120 125
 Asn Tyr Ile Lys Trp Leu Ile Pro Phe Ser Phe Phe Gly Leu Ser Ile
 130 135 140
 Arg Phe Leu Ser Asn Phe Thr Tyr Glu Phe Asn Ser Thr Tyr Ser Leu
 145 150 155 160
 Phe Ala Ile Leu Trp Thr Leu Ser Phe Thr Ala Phe Trp Leu Tyr Lys
 165 170 175
 Tyr Glu Pro Phe Trp Ser Asp Arg Leu Ser Lys Tyr Ser Ser Phe Ser
 180 185 190
 Thr Ile Glu Phe Leu Gln Asp Lys Gln Lys Ala Gln Lys Lys Ala Ser
 195 200 205
 Ser Val Ile Met Leu Lys Lys Cys Cys Phe Ile Pro Val Ala Leu Leu
 210 215 220
 Phe Gly Ala Ile Leu Leu Ser Phe Gln Leu Tyr Cys Phe Ala Leu Glu
 225 230 235 240
 Ile Phe Tyr Lys Gln Ile Tyr Asn Gly Pro Met Ile Ser Ile Leu Ser
 245 250 255
 Phe Leu Pro Thr Ile Leu Ile Cys Thr Phe Thr Pro Val Leu Thr Val

260	265	270
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290	295	300
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Tyr Leu Pro Met Gly His Leu Leu Thr Ala Glu Ile Arg Thr Lys Val		
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Phe Asn Ala Phe Ser Ile Leu Ala Arg Leu Pro Thr His Asp Ser Asp		
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Leu Val Ser Ile Ala Gln Gln Lys Ile Asn Gly Pro Asn Pro Asn Phe		
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Val Lys Ala Glu Ser Glu Ile Gly Lys Ala Gln Leu Ser Ser Ser Asp		
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Gly Tyr Leu Val Met Phe Ser Thr Ile Trp Pro Leu Ala Pro Phe Ile		
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Cys Leu Ile Val Asn Leu Ile Val Tyr Gln Val Asp Leu Arg Lys Ala		
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Val Leu Tyr Ser Lys Pro Glu Tyr Phe Pro Phe Pro Ile Tyr Asp Lys		
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 595 600 605
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 610 615 620
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 625 630 635 640
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 675 680 685
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770 775 780
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 Lys Ile Ala Val Thr Gly Gly Glu Asn Asn Glu Asn Thr Gln Ala Lys
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 820 825 830
 Pro Val Val Asn Ala Ala Val Asn Asp Asn Gln Ser Lys Val Ser Val
 835 840 845
 Ala Thr Glu Gln Thr Lys Lys Thr Glu Val Ser Thr Lys Asn Gly Pro
 850 855 860
 Ser Arg Ser Ile Ser Thr Lys Glu Thr Lys Asp Ser Ala Arg Pro Ser
 865 870 875 880
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 900 905 910
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 Lys Leu
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<210> 19
 <211> 1904
 <212> DNA
 <213> *Saccharomyces cerevisiae*

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<210> 20

<211> 467

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 20

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Thr Gln Lys Asp Ile Phe Pro Phe Leu Gly Gly Ala Gly Pro Tyr Tyr
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Ser Phe Pro Gly Asp Tyr Gly Ile Ser Arg Asp Leu Pro Glu Gly Cys
      50                      55                      60

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Glu Met Lys Gln Leu Gln Met Val Gly Arg His Gly Glu Arg Tyr Pro

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325

330

335

His Asp Thr Asp Ile Leu Asn Phe Leu Thr Thr Ala Gly Ile Ile Asp
 340 345 350

Asp Lys Asn Asn Leu Thr Ala Glu Tyr Val Pro Phe Met Gly Asn Thr
 355 360 365

Phe His Arg Ser Trp Tyr Val Pro Gln Gly Ala Arg Val Tyr Thr Glu
 370 375 380

Lys Phe Gln Cys Ser Asn Asp Thr Tyr Val Arg Tyr Val Ile Asn Asp
 385 390 395 400

Ala Val Val Pro Ile Glu Thr Cys Ser Thr Gly Pro Gly Phe Ser Cys
 405 410 415

Glu Ile Asn Asp Phe Tyr Asp Tyr Ala Glu Lys Arg Val Ala Gly Thr
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Asp Phe Leu Lys Val Cys Asn Val Ser Ser Val Ser Asn Ser Thr Glu
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Leu Arg Gln
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<210> 21

<211> 1563

<212> DNA

<213> *Saccharomyces cerevisiae*

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<210> 22

<211> 236

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 22

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 35 40 45
 Val Phe Lys Ile Ser Gly Gly Asn Asp Lys Gln Gly Phe Pro Met Lys
 50 55 60
 Gln Gly Val Leu Leu Pro Thr Arg Ile Lys Leu Leu Leu Thr Lys Asn
 65 70 75 80
 Val Ser Cys Tyr Arg Pro Arg Arg Asp Gly Glu Arg Lys Arg Lys Ser
 85 90 95
 Val Arg Gly Ala Ile Val Gly Pro Asp Leu Ala Val Leu Ala Leu Val
 100 105 110
 Ile Val Lys Lys Gly Glu Gln Glu Leu Glu Gly Leu Thr Asp Thr Thr
 115 120 125

```

Val Pro Lys Arg Leu Gly Pro Lys Arg Ala Asn Asn Ile Arg Lys Phe
130                      135                      140

Phe Gly Leu Ser Lys Glu Asp Asp Val Arg Asp Phe Val Ile Arg Arg
145                      150                      155                      160

Glu Val Thr Lys Gly Glu Lys Thr Tyr Thr Lys Ala Pro Lys Ile Gln
165                      170                      175

Arg Leu Val Thr Pro Gln Arg Leu Gln Arg Lys Arg His Gln Arg Ala
180                      185                      190

Leu Lys Val Arg Asn Ala Gln Ala Gln Arg Glu Ala Ala Glu Tyr
195                      200                      205

Ala Gln Leu Leu Ala Lys Arg Leu Ser Glu Arg Lys Ala Glu Lys Ala
210                      215                      220

Glu Ile Arg Lys Arg Arg Ala Ser Ser Leu Lys Ala
225                      230                      235

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<210> 23

<211> 893

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 23

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agtgtattac caacttgcgc atgcaaggat atcacactcc tgtttctgccc tcatgtcttt 180
taaaacgctt ccacgggaca tgggttctaa ttatggagaa gatcaagctt tgaatatggcc 240
cgtttacaca ttttgatata accgtagacg gcgtctcggt tcaagacgcy tgtggttgc 300
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acgtcacttg gcttgatata ctgcacgctt tattctgcaa attcaggctt caaatctgaa 480
cggcgtggag ccaccaaggy atggagctgg caaaggaacg taatggccca catcaaaaac 540
atcatggcca atgtcaaaat cactgtactt ctccaaacac tgtacgacaa aacaaaacaa 600
acaaactctt gttagtaaaa aagaaaggya aactagtaat atggagacac atcgtaaaaa 660
aaatgttgca catagccttg gttgttcttt ggagccatta tccagaacag caggacatg 720
gcactaacca ctatgaatac accaacaaca gtatagctaa atggagcgcg cagagagtta 780
gtagaagaga aaggaagaaa agggaagcgy agagaagaga ttatgacaca tacaactac 840
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<210> 24

<211> 130

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 24

Met Glu Leu Ala Lys Glu Arg Asn Gly Pro His Gln Lys His His Gly
 1 5 10 15

Gln Cys Gln Asn His Cys Thr Ser Pro Asn Thr Val Arg Gln Asn Lys
 20 25 30

Thr Asn Lys Leu Leu Val Lys Lys Gly Lys Leu Val Ile Trp
 35 40 45

Arg His Ile Val Lys Lys Met Leu His Ile Arg Leu Val Val Leu Trp
 50 55 60

Ser His Tyr Pro Glu Gln His Gly His Gly Thr Asn His Tyr Glu Tyr
 65 70 75 80

Thr Asn Asn Ser Ile Ala Lys Leu Asp Ala Gln Arg Val Ser Arg Arg
 85 90 95

Arg Arg Lys Lys Arg Glu Ala Glu Arg Arg Asp Tyr Asp Thr Tyr Lys
 100 105 110

Leu Leu Ile Thr Leu Cys Ser Leu Leu Phe Val Gly Pro Leu Phe Leu
 115 120 125

Lys Val
 130

<210> 25

<211> 1429

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 25

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 caccacgatg gtgacgaaa tctctaggag tagcatacca cagcgatatt atttagtagt 120
 aggcggttta ttatctttgt ccctttatac tgttgtgttt cttgcttatt gcttcagtag 180
 gcagcgata gtataaccag aaaaaagtga aaaataaact aaaaaagcac tatgagatga 240
 acggtaaaaa tccaccagag atttgctcac taataatcct gtaccatgtc catcaacctt 300
 cattccgcac ccgagtatga tccatcttat aagctgaccc agttgacacc agagttactg 360
 gatataatac aggatccggt tcaaaatcac cagttaaggt ttaagtcatg ggacaaagac 420
 aagtcggaag ttgtactgtg ttgcgcagac aagacttggg tgctgcaagc agcgcaaac 480
 ttcaaacaca gtttacttaa tgagagaatt tgttcctgaa caacctatta ctttcgacga 540


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aacgctcttg tttggactgt ccaagccgta catggacgtc gtgggattcg ccaagactga 600
atcagaattt gagaccagag agacacatgg cgaattgaac tgaattcac taccaatata 660
caacggagaa ctggatttct cgcacaaat catgaagagg tcatctacaa aggttatcgg 720
gaccttgaa gaactactgt agaactcacc atgtttctcg ctagaaggta tatcaaatg 780
gcataagatt ggtggatctg tgaaagacgg tgtgtgtgt attctttcac aagacttctc 840
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gctaaggaaa tatgtttctg gaataagcat gccaatgat gagtctctca tcaagtggaa 1140
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tttcaagcct accgataaga ctgtccagta tatagcgaaa agcacactac caatggaccc 1260
caaagaacgg tttaaagtcc tgtttaggct acagtcacag tgggacttgg aggatataca 1320
gcctctaatt gaagaactaa attcaagagg tatgaaaata gacagtttca tcatgaagta 1380
tgcccgctg aaaaagactg gcaaaaagac cgtggtcacg agcaggtag 1429

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<210> 26

<211> 309

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 26

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Met Arg Glu Phe Val Pro Glu Gln Pro Ile Thr Phe Asp Glu Thr Leu
  1                      5                      10                      15

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Leu Phe Gly Leu Ser Lys Pro Tyr Met Asp Val Val Gly Phe Ala Lys
      20                      25                      30

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Thr Glu Ser Glu Phe Glu Thr Arg Glu Thr His Gly Glu Leu Asn Leu
      35                      40                      45

```

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Asn Ser Val Pro Ile Tyr Asn Gly Glu Leu Asp Phe Ser Asp Lys Ile
      50                      55                      60

```

```

Met Lys Arg Ser Ser Thr Lys Val Ile Gly Thr Leu Glu Glu Leu Leu
      65                      70                      75                      80

```

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Glu Asn Ser Pro Cys Ser Ala Leu Glu Gly Ile Ser Lys Trp His Lys
      85                      90                      95

```

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Ile Gly Gly Ser Val Lys Asp Gly Val Leu Cys Ile Leu Ser Gln Asp
      100                      105                      110

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Phe Leu Phe Lys Ala Leu His Val Leu Leu Met Ser Ala Met Ala Glu
      115                      120                      125

```

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Ser Leu Asp Leu Gln His Leu Asn Val Glu Asp Thr His His Ala Val

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130	135	140
Gly Lys Asp Ile Glu Asp Glu Phe Asn Pro Tyr Thr Arg Glu Ile Ile		
145	150	155 160
Glu Thr Val Leu Asn Lys Phe Ala Val Gln Glu Gln Glu Ala Glu Asn		
165	170	175
Asn Thr Trp Arg Leu Arg Ile Pro Phe Ile Ala Gln Trp Tyr Gly Ile		
180	185	190
Gln Ala Leu Arg Lys Tyr Val Ser Gly Ile Ser Met Pro Ile Asp Glu		
195	200	205
Phe Leu Ile Lys Trp Lys Ser Leu Phe Pro Pro Phe Phe Pro Cys Asp		
210	215	220
Ile Asp Ile Asp Met Leu Arg Gly Tyr His Phe Lys Pro Thr Asp Lys		
225	230	235 240
Thr Val Gln Tyr Ile Ala Lys Ser Thr Leu Pro Met Asp Pro Lys Glu		
245	250	255
Arg Phe Lys Val Leu Phe Arg Leu Gln Ser Gln Trp Asp Leu Glu Asp		
260	265	270
Ile Lys Pro Leu Ile Glu Glu Leu Asn Ser Arg Gly Met Lys Ile Asp		
275	280	285
Ser Phe Ile Met Lys Tyr Ala Arg Arg Lys Arg Leu Gly Lys Lys Thr		
290	295	300
Val Val Thr Ser Arg		
305		

<210> 27
 <211> 1952
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 27
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 attacgggag acaacgctga ggaggagttg gaaaggtaca tccgtgctat ggtagagag 180
 cagatgctgg gccagggctc catggcgggt tccggggacg aaccagattc caagagaaga 240
 aaataacgac ccagcaca aa ggcctctaca gcttgctaaa agaaattgaa cgcgacgcta 300

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catgaactac ttctttctct tacatagttc ttcccttat gtatcttttc tgtacattaa 360
tagacgttct tacaaggtaa aatttcacgc cgttttttaa tagaatgaaa aaaacgttgt 420
agagtgaaga aaaagcaaca aatatacagt tcacaaggca gcttcgtata gtaatacagc 480
acgaaaaaca gctcatagaa atggtaacac agaccaatcc gggtccgtgt acatatccaa 540
cggatgctta tatccccagc tatctgccgc atgataaggt ctccaatctg gcagatttga 600
aaaaattgat agaaatggat tccagactag atttgtatct gacaagaagg aggtctggata 660
cgctccatcaa ttacctaca aacaccaaga ccaaggacca tcccccaat aaagagatgc 720
tgaggattta cgtctacaac actacggaaa gcagccctcg cagcgattct ggcaccccag 780
cggactcagg caagactaca tggacactga gaataagaag taagctcttg cacgagtcgc 840
caaacggaaa gcaccattt agtgagtttt tgggaaggtgt cgcggtcgac tttaaaagac 900
tgaaacgcgt gggcatgggc aagaagagga aacgcgattc gtcattgagc ctctctttga 960
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actacgatga aaacaacgtt gtggagtttg atggtatcga catcaagagg caaggcaagg 1140
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actcgcccaa cttagctacc ttgataggtg tgcaaacggg ctccgttaat gacgcggttt 1260
attcgatcta caagtacatt ttgatcaaca atctgttttg tacggaacaa acagaggctc 1320
aagatgggtc caacgatgcc gaagacagca gtaacgagaa taacaataaa aacggtgctg 1380
gtgacgatct tggcgtcgag ggaagtactc caaaggataa gcccgaaattg ggtgaagtga 1440
agctagattc actcttaca aaaggtatttg atacaaacgc cgcgcacctc ccttgatga 1500
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caattgatct ttccaaagat accacctatg gtgctacca cttggatgta gatgtgtcgc 1620
acattctcca ccagcctcaa cccagccaa atttacaata agaggaagaa acagatgctg 1680
aagcacagc aaaactcgt gaatcacaa agctgcctt gcagttgaac tctagtgtc 1740
aaaaatacca gtttttccac gaactgtctt tgcattcaag agaaacgctg actcactact 1800
tatggtcttc caagcaaac gagcttgtgc tgcaggcgca ccaatactc aatgaagatg 1860
ctgcaagaac gagtgacata tacagtaaca acaacaatga caggtcacta atgggcaata 1920
tctcactact gtactccaa ggaagactat aa 1952

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<210> 28
<211> 483
<212> PRT
<213> Saccharomyces cerevisiae

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<400> 28
Met Val Thr Gln Thr Asn Pro Val Pro Val Thr Tyr Pro Thr Asp Ala
  1              5              10             15

Tyr Ile Pro Thr Tyr Leu Pro Asp Asp Lys Val Ser Asn Leu Ala Asp
  20              25             30

Leu Lys Lys Leu Ile Glu Met Asp Ser Arg Leu Asp Leu Tyr Leu Thr
  35              40             45

Arg Arg Arg Leu Asp Thr Ser Ile Asn Leu Pro Thr Asn Thr Lys Thr
  50              55             60

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Lys Asp His Pro Pro Asn Lys Glu Met Leu Arg Ile Tyr Val Tyr Asn
 65 70 75 80
 Thr Thr Glu Ser Ser Pro Arg Ser Asp Ser Gly Thr Pro Ala Asp Ser
 85 90 95
 Gly Lys Thr Thr Trp Thr Leu Arg Ile Glu Gly Lys Leu Leu His Glu
 100 105 110
 Ser Ala Asn Gly Lys His Pro Phe Ser Glu Phe Leu Glu Gly Val Ala
 115 120 125
 Val Asp Phe Lys Arg Leu Lys Pro Leu Gly Met Gly Lys Lys Arg Lys
 130 135 140
 Arg Asp Ser Ser Leu Ser Leu Pro Leu Asn Leu Gln Gln Pro Glu Tyr
 145 150 155 160
 Asn Asp Gln Asp Ser Thr Met Gly Asp Asn Asp Asn Gly Glu Asp Glu
 165 170 175
 Asp Ser Ala Glu Ala Glu Ser Arg Glu Glu Ile Val Asp Ala Leu Glu
 180 185 190
 Trp Asn Tyr Asp Glu Asn Asn Val Val Glu Phe Asp Gly Ile Asp Ile
 195 200 205
 Lys Arg Gln Gly Lys Asp Asn Leu Arg Cys Ser Ile Thr Ile Gln Leu
 210 215 220
 Arg Gly Val Asp Gly Gly Lys Val Gln Tyr Ser Pro Asn Leu Ala Thr
 225 230 235 240
 Leu Ile Gly Met Gln Thr Gly Ser Val Asn Asp Ala Val Tyr Ser Ile
 245 250 255
 Tyr Lys Tyr Ile Leu Ile Asn Asn Leu Phe Val Thr Glu Gln Thr Glu
 260 265 270
 Ala Gln Asp Gly Ser Asn Asp Ala Glu Asp Ser Ser Asn Glu Asn Asn
 275 280 285
 Asn Lys Asn Gly Ala Gly Asp Asp Asp Gly Val Glu Gly Ser Thr Pro
 290 295 300
 Lys Asp Lys Pro Glu Leu Gly Glu Val Lys Leu Asp Ser Leu Leu Gln
 305 310 315 320

Lys Val Leu Asp Thr Asn Ala Ala His Leu Pro Leu Met Asn Val Val
 325 330 335
 Gln Thr Val Asn Lys Leu Val Ser Pro Leu Pro Pro Ile Ile Leu Asp
 340 345 350
 Tyr Thr Ile Asp Leu Ser Lys Asp Thr Thr Tyr Gly Ala Thr Thr Leu
 355 360 365
 Asp Val Asp Val Ser His Ile Leu His Gln Pro Gln Pro Gln Pro Asn
 370 375 380
 Leu Gln Lys Glu Glu Glu Thr Asp Ala Glu Asp Thr Ala Lys Leu Arg
 385 390 395 400
 Glu Ile Thr Lys Leu Ala Leu Gln Leu Asn Ser Ser Ala Gln Lys Tyr
 405 410 415
 Gln Phe Phe His Glu Leu Ser Leu His Pro Arg Glu Thr Leu Thr His
 420 425 430
 Tyr Leu Trp Ser Ser Lys Gln Asn Glu Leu Val Leu Gln Gly Asp Gln
 435 440 445
 Tyr Phe Asn Glu Asp Ala Ala Arg Thr Ser Asp Ile Tyr Ser Asn Asn
 450 455 460
 Asn Asn Asp Arg Ser Leu Met Gly Asn Ile Ser Leu Leu Tyr Ser Gln
 465 470 475 480
 Gly Arg Leu

<210> 29
 <211> 911
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 29
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 gtcgtcttttg acgaaggaga cgaaaacctc ttctaaaacg ttgggagaga gataattaca 180
 tggccagaac aatactgcaa cgtgcataata gtcttagtc tgtgcttgca catccacggc 240
 agccgcagtg gacgcaactg tggaaggaca cctgtgtgcc ctttttgcgt gctttcttct 300
 ctaactgtgc acgaggcacc ctgcagatgc aagtgtctacc gttgttagtt tcgttctttt 360
 gaatgcagcg cagacagcac agttttttcat acccggtttt gcgccatttg gcaattagca 420

attatcagc atacttttcc ttatcaacc aatcgtaaag gtctttggag atggccttc 480
 tctttagta cagagtatat atgtatctag agcgctgggt gtggagttgc attatctccc 540
 agagctgctc attggacttt gctgcgagct tagacgactt gtcccttttg gcatctctga 600
 gttggatttc gaaatctgtg agggttggct tgattttttc gaaccggtca ggtgcaggct 660
 tggatcttct ggtctttatg cgcggcatgt cgtttttgtg ggtgagcttt gctagtcttg 720
 acggctgtag aggtgtttac attgatgatg agtccctaag aaaatttttc ttttttttc 780
 agtatttcac ttcccggtgt gaacgacaaa tgtactatgc gttcaagagc caacgcagta 840
 tcatcgtaaa agttctctacc acaacgcgtg tgattgatct tgtactgggt gtaaatgtgc 900
 taagtctgtg a 911

<210> 30

<211> 136

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 30

Met Tyr Leu Glu Arg Trp Trp Trp Ser Cys Ile Ile Ser Gln Ser Cys
 1 5 10 15

Ser Leu Asp Phe Ala Ala Ser Leu Asp Asp Leu Ser Phe Trp Ala Ser
 20 25 30

Leu Ser Trp Ile Ser Lys Ser Val Arg Val Gly Leu Ile Phe Ser Asn
 35 40 45

Pro Ser Gly Ala Gly Leu Asp Leu Leu Val Phe Met Arg Gly Met Ser
 50 55 60

Phe Cys Glu Val Ser Phe Ala Ser Leu Asp Gly Cys Arg Gly Val Tyr
 65 70 75 80

Ile Asp Asp Glu Ser Leu Arg Lys Phe Phe Phe Phe Phe Gln Tyr Phe
 85 90 95

Thr Phe Arg Cys Glu Arg Gln Met Tyr Tyr Ala Phe Lys Ser Gln Arg
 100 105 110

Ser Ile Ile Val Lys Val Pro Thr Thr Thr Arg Val Ile Asp Leu Val
 115 120 125

Leu Val Val Asn Val Leu Ser Leu
 130 135

<210> 31

<211> 1448

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 31

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 ttttcacctt caaggaacta ctttttatag ccaccctaag taaacaaca ttatgcttagc 180
 atccctaagt cttatcgatg gtgtgtgctg ctatttttat cctattgttc ctggcatcgc 240
 ttttttacct aaggtaccaa ggcaagagaa aagaccgcgc aaattttcaa ttcgagacat 300
 agggtaata cgaatatgt taaggtctag tttccaaaa atgaagaaaa tgtgattaga 360
 catccctggg aaattaggtt taaatagggc gggcgctaca ggggttttcc taacaatttt 420
 caatgataat agtggcatca tcatcgctat atccagtgtt ggtatggact agaacagaaa 480
 gcaatttcca gcaagacaat atgactacga cggtagccaa gatatttcgc tttcacgagt 540
 tttcagacgt ggcagaggcc gtagctgacc atgtagtcca cgcgcaagac ggtgcattgg 600
 ctccaaagaa cgagagagaa cactctgttc ccaacatcag catgaatgca ctggatatga 660
 cgagagagcc ctcttgcaaa agcacagcat ctgccgcgga agggaaaagt ggtagcagtg 720
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 gagactggga catttacttt gcagacgaga gacttgtacc cttcagctcg aatgaaagca 900
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 aggacaactc acgtgagaaa ctgcatggg tgggtccgct ggagaaacgt cctagtgggc 1200
 cctcgaccag aatttcgctg actatacctg taatctgcca ttctcacag gttacttttc 1260
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 gcctacctag cagttatgtc aacgaaggtg ctgctggtcg tgtatcatg tttgttgacg 1380
 acgatgctct tacggagctc ctgctcacca aaaaaaagta taaattccac caaggtttgt 1440
 ctatttaa 1448

<210> 32

<211> 315

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 32

Met Thr Thr Thr Val Pro Lys Ile Phe Ala Phe His Glu Phe Ser Asp
 1 5 10 15
 Val Ala Glu Ala Val Ala Asp His Val Val His Ala Gln Asp Gly Ala
 20 25 30
 Leu Ala Pro Lys Asn Glu Arg Lys His Ser Val Pro Asn Ile Ser Met
 35 40 45
 Asn Ala Leu Asp Met Thr Arg Glu Ala Ser Cys Lys Ser Thr Ala Ser
 50 55 60

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Ala Ala Glu Gly Lys Ser Gly Ser Ser Gly Ser Gly Ser Ser
 65              70              75              80

Lys Pro Lys Lys Glu Lys Arg Phe Lys Ile Ala Leu Ser Gly Gly Ser
              85              90              95

Leu Ile Glu Val Leu His Glu Gly Leu Leu Lys Arg Asp Asp Val Arg
      100              105              110

Trp Gly Asp Trp Asp Ile Tyr Phe Ala Asp Glu Arg Leu Val Pro Phe
      115              120              125

Ser Ser Asn Glu Ser Asn Tyr Gly Cys Ala Lys Arg Lys Ile Leu Asp
      130              135              140

Leu Ile Asp Thr Ala Lys Tyr Gly Thr Pro Lys Val Tyr His Ile Asp
      145              150              155              160

Glu Ser Leu Ile Asp Asp Pro Gln Glu Cys Val Asp Asn Tyr Glu Lys
      165              170              175

Val Leu Ile Arg Gly Phe Ala Gly Arg Asp Ser Val Lys Leu Pro Met
      180              185              190

Phe Asp Leu Phe Leu Leu Gly Cys Ala Pro Asp Gly His Ile Ala Ser
      195              200              205

Leu Phe Pro Asn Phe Gln Asp Asn Leu Arg Glu Lys Leu Ala Trp Val
      210              215              220

Val Pro Val Glu Asn Ala Pro Ser Gly Pro Ser Thr Arg Ile Ser Leu
      225              230              235              240

Thr Ile Pro Val Ile Cys His Ser His Arg Val Thr Phe Val Val Glu
      245              250              255

Gly Ala Thr Lys Ala Pro Ile Ile Lys Thr Ile Met Glu Arg Pro Glu
      260              265              270

Lys Gly Leu Pro Ser Ser Ile Val Asn Glu Gly Ala Ala Gly Arg Val
      275              280              285

Ser Trp Phe Val Asp Asp Asp Ala Leu Thr Asp Val Leu Val Thr Lys
      290              295              300

Lys Lys Tyr Lys Phe His Gln Gly Leu Ser Ile
      305              310              315

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<210> 33
 <211> 1196
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 33
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 ctacgtacc gattagtgtt gttgactttt ccgcaagatc cttttctccc tctttggacc 180
 tagtcacccc tccacacaag attcgcctctt aagtagtggt gcaggctgtt cgcttttaag 240
 catagtgttt aatgtcgaag gctttataga tcccaaatac tacgccttga gaaattgaat 300
 gcactagcac ttagttaact ttctggaacg cgcatagcgc gtcccggggc gcctgaggcg 360
 gagcggttgc gaaatcgga aaacattata ctgggaaga tcactatcta ttctctaaat 420
 gaacttttaa gcaaattatc gtaagataga aaagacgaaa ccttagcaac ctagcgggtt 480
 aatatagaaa caattttatt atgatacctt ccaataagag aatgctaga attttaagca 540
 ttacaacgct attattgttg ttagtggttt tcgtagcgca aaatgcgaac ttcttgacgg 600
 tagagataaa agaggaaact tctaaagcat ttagtactaa tatggacaat atggctggaag 660
 gatcttcacg ggaatatgct gctatgccga cttctaccac gaataagggg agctctgaag 720
 tagacgaaga aattaatgaa ataaaacaga aggtgggact ccaacagccc atagcatcgg 780
 ttgatgatag ttgttcggcc attaaaaacg ataaagggtc gcgaataacc aaagctttta 840
 atgttcaaaa agaatactcc ctcatactag acttgctccc gattataata tttagtaaaa 900
 gcacctgttc atatagcaag ggcatgaagg aactgcttga aatgagtat cagtttatcc 960
 caaactacta tattatagaa cttgacaaac atggacatgg ggaagagctg caagaatata 1020
 tcaagtgtgt gaccggtaga ggaactgttc caaacctttt gggtaatgga gtatcaagag 1080
 gaggtaatga agaaatcaag aaactgcaca ctcaagggaa acttttagaa tcattacaag 1140
 tctggagtga tggtaaatc tcggttgagc aacgtgaaaa accttccaat aattga 1196

<210> 34
 <211> 231
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 34
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 Leu Leu Leu Leu Val Phe Phe Val Ala Gln Asn Ala Asn Phe Leu
 20 25 30
 Thr Val Glu Ile Lys Glu Glu Thr Ser Lys Ala Phe Ser Thr Asn Met
 35 40 45
 Asp Asn Met Ala Gly Gly Ser Ser Arg Glu Tyr Ala Ala Met Pro Thr
 50 55 60

Ser Thr Thr Asn Lys Gly Ser Ser Glu Val Asp Glu Glu Ile Asn Glu
 65 70 75 80
 Ile Lys Gln Lys Val Gly Leu Gln Gln Pro Ile Ala Ser Val Asp Asp
 85 90 95
 Ser Leu Ser Ala Ile Lys Asn Asp Lys Gly Ser Arg Ile Thr Lys Ala
 100 105 110
 Phe Asn Val Gln Lys Glu Tyr Ser Leu Ile Leu Asp Leu Ser Pro Ile
 115 120 125
 Ile Ile Phe Ser Lys Ser Thr Cys Ser Tyr Ser Lys Gly Met Lys Glu
 130 135 140
 Leu Leu Glu Asn Glu Tyr Gln Phe Ile Pro Asn Tyr Tyr Ile Ile Glu
 145 150 155 160
 Leu Asp Lys His Gly His Gly Glu Glu Leu Gln Glu Tyr Ile Lys Leu
 165 170 175
 Val Thr Gly Arg Gly Thr Val Pro Asn Leu Leu Val Asn Gly Val Ser
 180 185 190
 Arg Gly Gly Asn Glu Glu Ile Lys Lys Leu His Thr Gln Gly Lys Leu
 195 200 205
 Leu Glu Ser Leu Gln Val Trp Ser Asp Gly Lys Phe Ser Val Glu Gln
 210 215 220
 Arg Glu Lys Pro Ser Asn Asn
 225 230

<210> 35
 <211> 1889
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 35
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 caataaccagg tacgactcct gatccaataa ttgaggcgca gaacgataat gatagtagtg 180
 atagtagcgg catagatttg atagccttct taagaaatgg accattataa agtttttcta 240
 tcgcatgtt tgaaaatgga aagtaaggaa cgtaatacaa attgacaagt agccgacatg 300
 aatgacgctc acttctctta tatatgttag gtagtatatg cattatagaa ttatttcatt 360

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gaagcaatgt gattccctga taagtaagct tttttctgt ctggcggcga accattagag 420
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tataatggaa taggaaactt atgcaaagaa ataataaggtt aagaaatttg ttacagctg 540
cagtaataat ggctcgacaa ctcaaaagga atgcattatc tgcagggtctt gcttttgagc 600
gtaatgcaac ctcaaatgag tttgatgaac atttgcaaaa tgaggttgaa agagagaggg 660
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atcgtttcaa tacaattacg aaaatgcttc aaaataatct cggatttgtt gtgaacccat 1200
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agtatccaga atgggctctg agaagatag 1889

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<210> 36

<211> 462

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 36

Met Gln Arg Asn Asn Arg Leu Arg Asn Leu Phe Thr Val Pro Val Ile
1 5 10 15

Met Ala Arg Gln Leu Lys Arg Asn Ala Leu Ser Ala Gly Leu Ala Phe
20 25 30

Ala Gly Asn Ala Thr Ser Asn Glu Phe Asp Glu His Leu Gln Asn Glu
35 40 45

Val Glu Arg Glu Arg Glu Ile Gln Lys Lys Lys Lys Ile Lys Arg Thr
50 55 60

Gln Ser Lys Lys Ser Pro Asp Leu Ile Asn Lys Ser Thr Phe Gln Ser
65 70 75 80

Arg Thr Ile Gly Ser Lys Lys Glu Lys His Arg Gln Leu Asp Pro Glu
 85 90 95
 Tyr Glu Ile Val Ile Asp Gly Pro Leu Arg Lys Ile Lys Pro Tyr His
 100 105 110
 Phe Thr Tyr Arg Thr Phe Cys Lys Glu Arg Trp Arg Asp Lys Lys Leu
 115 120 125
 Val Asp Val Phe Ile Ser Glu Phe Arg Asp Arg Glu Ser Glu Tyr Tyr
 130 135 140
 Lys Arg Thr Ile Glu Asn Gly Asp Val His Ile Asn Asp Glu Thr Ala
 145 150 155 160
 Asp Leu Ser Thr Val Ile Arg Asn Gly Asp Leu Ile Thr His Gln Val
 165 170 175
 His Arg His Glu Pro Pro Val Thr Ser Arg Pro Ile Lys Val Ile Phe
 180 185 190
 Glu Asp Asp Asn Ile Met Val Ile Asp Lys Pro Ser Gly Ile Pro Val
 195 200 205
 His Pro Thr Gly Arg Tyr Arg Phe Asn Thr Ile Thr Lys Met Leu Gln
 210 215 220
 Asn Asn Leu Gly Phe Val Val Asn Pro Cys Asn Arg Leu Asp Arg Leu
 225 230 235 240
 Thr Ser Gly Leu Met Phe Leu Ala Lys Thr Pro Lys Gly Ala Asp Asn
 245 250 255
 Ile Gly Asp Gln Leu Lys Ala Arg Glu Val Thr Lys Glu Tyr Val Ala
 260 265 270
 Lys Val Val Gly Glu Phe Pro Glu Thr Glu Val Ile Val Glu Lys Pro
 275 280 285
 Leu Lys Leu Ile Glu Pro Arg Leu Ala Leu Asn Ala Val Cys Gln Met
 290 295 300
 Asp Glu Lys Gly Ala Lys His Ala Lys Thr Val Phe Asn Arg Ile Ser
 305 310 315 320
 Tyr Asp Gly Lys Thr Ser Ile Val Lys Cys Lys Pro Leu Thr Gly Arg
 325 330 335

Ser His Gln Ile Arg Val His Leu Gln Tyr Leu Gly His Pro Ile Ala
340 345 350

Asn Asp Pro Ile Tyr Ser Asn Asp Glu Val Trp Gly Asn Asn Leu Gly
355 360 365

Lys Gly Gly Gln Ala Asp Phe Asp Ile Val Ile Thr Lys Leu Asp Glu
370 375 380

Ile Gly Lys Arg Lys Pro Ala Lys Ser Trp Phe His Ser Asn Gly Gly
385 390 395 400

Tyr Gly Glu Val Leu Arg Gln Glu Lys Cys Ser Ile Cys Glu Ser Asp
405 410 415

Leu Tyr Thr Asp Pro Gly Pro Asn Asp Leu Asp Leu Trp Leu His Ala
420 425 430

Tyr Leu Tyr Glu Ser Thr Glu Thr Glu Glu Gly Thr Glu Lys Lys Lys
435 440 445

Trp Cys Tyr Lys Thr Glu Tyr Pro Glu Trp Ala Leu Arg Arg
450 455 460

<210> 37

<211> 1364

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 37

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ctgtatttca gaaaaaacac ccatacatgt tgaaaaataa tgcattgtga aaaaaagtgg 180
ttgaaaaaat tatgcgatct aggaaaaact gaattttcct taggttgtgc ctccctctct 240
agaaggatgc tgtggccttt gacctgggag gaaattctct ctgtttccct ctgactgagg 300
gaaacagaaac tggtagcagt tcgttcgggc caggccgcgt gaggctatgc caccgaatat 360
tatcctagcg cagagagtaa cactggcaca gtcaaaagta aatgccatgt aaaatgtata 420
ggttacgcag tagactattt aatatatacc tttttattta gcagtgtttc gaaaaatata 480
gcaagagaaat aagcaacaag atgtctgcgc tccaagtgtt ccaagtatgt taaataattt 540
aaacgatgtc acgaatttgt gagggatatt gaaaccatgc agtgagataa tttcaattta 600
agaacacatc cactggaata agacgggtgg ggcagcact agatgcgaat catagtttta 660
gaacaacgga tcaccatttc acacgtttaa gaccgagtag aaataaccaa taaattgtgt 720
gggaaaatat tatacttaat ttctctgtgg agtaaagtaa tgagcgtctt ttgcggtctt 780
attttatcat tcgctccctt tgcaatgaat tttgaacaga atgctccaaa gaggaagtgc 840
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 aaccattatt gttgggttgg ttggacaagt tctccaacat cgatatcaga gtttagtgca 1140
 ctgggtgggtg tcatgtttct caagtctacg ccatacagaca agctattgct aagggtttag 1200
 tcgcttacca ccaaaagtac gttgacgaac aatccaagaa cgaattgaag aaggccttca 1260
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<210> 38

<211> 143

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 38

Met Ser Ala Val Pro Ser Val Gln Thr Phe Gly Lys Lys Lys Ser Ala
 1 5 10 15

Thr Ala Val Ala His Val Lys Ala Gly Lys Gly Leu Ile Lys Val Asn
 20 25 30

Gly Ser Pro Ile Thr Leu Val Glu Pro Glu Ile Leu Arg Phe Lys Val
 35 40 45

Tyr Glu Pro Leu Leu Leu Val Gly Leu Asp Lys Phe Ser Asn Ile Asp
 50 55 60

Ile Arg Val Arg Val Thr Gly Gly Gly His Val Ser Gln Val Tyr Ala
 65 70 75 80

Ile Arg Gln Ala Ile Ala Lys Gly Leu Val Ala Tyr His Gln Lys Tyr
 85 90 95

Val Asp Glu Gln Ser Lys Asn Glu Leu Lys Lys Ala Phe Thr Ser Tyr
 100 105 110

Asp Arg Thr Leu Leu Ile Ala Asp Ser Arg Arg Pro Glu Pro Lys Lys
 115 120 125

Phe Gly Gly Lys Gly Ala Arg Ser Arg Phe Gln Lys Ser Tyr Arg
 130 135 140

<210> 39

<211> 1088

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 39

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 acgcatggag gcttctacaa aacagcgtgc cgttttgatg gcatgagcag gggcgcaaa 180
 ggaaacacgc gtaaatcgcg caagaccttg ttggccacgt agcctcaaa gttgaattga 240
 cacttgctca cagaacttga aaagtacaaa aggaggtcac ataaaacagt aagcttgaga 300
 agctttaaga tatggtgcga atcggttacg aatattcctt gcagaaataa tggcgggtcc 360
 gttctcttct gaagaagtta ccgccttact gaagcattgc tgcacgatcg tgtaattgta 420
 tgtgtgttcg actggaaagc ggagaacatt atgaagtaaa aggacaatca gcacgccttc 480
 cagactttta agaaacattg atggagccat tgatatcggc accgtacctt acaacaacaa 540
 aaatgtctgc tctgtctacg cttgatgtcg cctgtatttt ttgcaagatt attaaaagta 600
 tgtcacatta ctaataaaga gcttacactc acaccaatga tggcgatagt ctctatgtag 660
 tacatacata taaagcagaa tactaacat cgatccgcta tgcaacaggc gaaattccat 720
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 aatccctac cgatgctatg ccgattgcca agagactggc caaggcaatg aagttggaca 900
 cttataatgt gttgcagaat aatggtaaaa ttgcgcatac agaagtcgac cacgtccact 960
 tccatttgat tcctaagaga gatgagaaaa gtgggtttgat tgtaggttg gacgcccacg 1020
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<210> 40

<211> 158

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 40

Met Glu Pro Leu Ile Ser Ala Pro Tyr Leu Thr Thr Thr Lys Met Ser
 1 5 10 15

Ala Pro Ala Thr Leu Asp Ala Ala Cys Ile Phe Cys Lys Ile Ile Lys
 20 25 30

Ser Glu Ile Pro Ser Phe Lys Leu Ile Glu Thr Lys Tyr Ser Tyr Ala
 35 40 45

Phe Leu Asp Ile Gln Pro Thr Ala Glu Gly His Ala Leu Ile Ile Pro
 50 55 60

Lys Tyr His Gly Ala Lys Leu His Asp Ile Pro Asp Glu Phe Leu Thr
 65 70 75 80

Asp Ala Met Pro Ile Ala Lys Arg Leu Ala Lys Ala Met Lys Leu Asp
 85 90 95

Thr Tyr Asn Val Leu Gln Asn Asn Gly Lys Ile Ala His Gln Glu Val
100 105 110

Asp His Val His Phe His Leu Ile Pro Lys Arg Asp Glu Lys Ser Gly
115 120 125

Leu Ile Val Gly Trp Pro Ala Gln Glu Thr Asp Phe Asp Lys Leu Gly
130 135 140

Lys Leu His Lys Glu Leu Leu Ala Lys Leu Glu Gly Ser Asp
145 150 155

<210> 41

<211> 578

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 41

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ttcagaatgc tttctttatt tcacgacggt taccacaccc gtacaccctt atctcatttc 180
accagtacct ttcttatta gattcatctt attttatttt aggattttta ggtcattgta 240
cgacgcgtgt cgcaccatgg aaaaggtgtc gcagctgcga tgctatccat ttaccgcgta 300
tcattgctgg cagaaatccc atcttctctt gctggggtga tttatatata tggagagtta 360
acgaatgtaa tatttctgaa tgtaaataa ttgttatccg tcattattgt ttcacttctc 420
tctttgaaat ttcgcttggt ttctgttttc atcttatatt ttacttcaat cctaagatag 480
tcatatcgac ttaattccaa atgagagcta agtggagaaa gaagagaact agaagactta 540
agagaaagag acggaaggtg agagccagat ccaaataa 578

<210> 42

<211> 25

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 42

Met Arg Ala Lys Trp Arg Lys Lys Arg Thr Arg Arg Leu Lys Arg Lys
1 5 10 15

Arg Arg Lys Val Arg Ala Arg Ser Lys
20 25

<210> 43

<211> 1268

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 43

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tactatatga aaaaaagaaa agaggccctg ctttgaaccc gtacatttta ttctataata 240
ttgcatctgt ggtttgcctg acggcagcga gtccaacaca aagtctggca tatgctacga 300
attttccacc atggattcag cacccaaaaa tttgaatttt ttttcatgtc gattgtgaaa 360
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attgaaaaatc tactcacatc tcttttttgg gggtttggtg gtacagtggg aacacgataa 480
agaaccaaata aggactaaaa atgggtatgta gagatgaata tacatgaaac ggacgtgata 540
taatgtgcta tggaaagaaa aagtcctcct taatgtctgc aggataaata atcaagtggg 600
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ctcaccagct acaacttggg aacagaaatt tataagttta tggcacttgt taaaattggt 720
tggaaagttt cgaattata atattggtct tcagaaacct ggaaccacat gtgaactatt 780
ttttttggat aatgcattgc acagagcgta ttagtgata cgagaatcta aaaatttgaa 840
actggctcat aaaaacagga acttttacta acagttatga tttttgttcc cacttttctt 900
atcaataggc cggcgttata gttacgaac taagaacca atccaaggaa caattagcct 960
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acgaacaaca aagagaagct gttagacaat tatacaaggg taagaagtac caaccaaagg 1140
acttgagagc caagaagacc agagctttga gaagagcttt gaccaaatcc gaagcttccc 1200
aagttaccga aaagcaaaa aagaagcaaa tcgctttccc acaagaaaag tacgctatca 1260
aggcttaa 1268

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<210> 44

<211> 120

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 44

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Met Ala Gly Val Lys Ala Tyr Glu Leu Arg Thr Lys Ser Lys Glu Gln
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Leu Ala Ser Gln Leu Val Asp Leu Lys Lys Glu Leu Ala Glu Leu Lys
      20              25              30

Val Gln Lys Leu Ser Arg Pro Ser Leu Pro Lys Ile Lys Thr Val Arg
      35              40              45

Lys Ser Ile Ala Cys Val Leu Thr Val Ile Asn Glu Gln Gln Arg Glu
      50              55              60

Ala Val Arg Gln Leu Tyr Lys Gly Lys Lys Tyr Gln Pro Lys Asp Leu
      65              70              75              80

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Arg Ala Lys Lys Thr Arg Ala Leu Arg Arg Ala Leu Thr Lys Phe Glu
85 90 95

Ala Ser Gln Val Thr Glu Lys Gln Arg Lys Lys Gln Ile Ala Phe Pro
100 105 110

Gln Arg Lys Tyr Ala Ile Lys Ala
115 120

<210> 45

<211> 2660

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 45

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tgtgtgtaga acaacatcca gatggagtca caaatgaata tcaagggcct cgtagcgatg 180
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gatgcccgat ggaaaagtgt aaagtgaata atttttcaac acatacaagt ttaataagtt 420
ggttttgatg caaatagcat tactaaagaa gagcgctagg ataattgtgc attgctattg 480
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cagatacccc caaggatcaa tgcgcattg caaatatagc atttcaaatt gtgaatgctg 600
aaacattagt atgccattat gggaccaatt ctttaccgag cattgaagta aacgggacga 660
caaagagttt ggagagtga atggtgcaat tggacaagga tattcatgac gttattggta 720
acgcagactt tgttctgttt tccctgtatt caacatggca tatccgtgtt accttaccac 780
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aagcaatctc caacaacaat tgtaatacta aaagtattag tattaatgca gccaaaata 960
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ctaacaacac gccagcagct ttaacatata atagagctca ttttctgcga attacgccat 1860
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cggatcattt ttccgggaaat aataatatag ccccaaatata tcgttataat aataatatta 1980
acaataacaa caataatatt aacaatatga ccaataatag atataacatt aataacaaca 2040
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atagttcaat acgttggtag                                     2660

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<210> 46

<211> 719

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 46

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Met His Tyr Val Val Leu Glu Leu Gln Val Ala His Leu Pro Asp Thr
  1                      5                      10                     15

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Pro Lys Asp Gln Cys Arg Ile Ala Asn Ile Ala Phe Gln Ile Val Asn
      20                      25                     30

```

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Ala Glu Thr Leu Val Cys His Tyr Gly Thr Asn Ser Leu Pro Ser Ile
      35                      40                     45

```

```

Glu Val Asn Gly Thr Thr Lys Ser Leu Glu Ser Ala Met Val Gln Leu
      50                      55                     60

```

```

Asp Lys Asp Ile His Asp Val Ile Gly Asn Asp Asp Phe Val Leu Val
      65                      70                     75                     80

```

```

Ser Leu Tyr Ser Thr Trp His Ile Arg Val Thr Leu Pro Arg Gln Ala
      85                      90                     95

```

```

Arg Asp Asp Gly Phe Ile Leu Thr Ser Tyr Leu Gln His Pro Lys Val
      100                     105                    110

```

```

Phe Asp Leu Trp Lys Glu Phe Asp Arg Trp Cys Val Asn His Pro Glu
      115                     120                    125

```

```

Ile Leu Gly Gln Lys Lys Ala Ile Ser Asn Asn Asn Cys Asn Thr Lys

```

130	135	140
Ser Ile Ser Ile Asn Ala Ala Lys Asn Thr Lys Asp Leu Asp Glu Ile		
145	150	155 160
Val Arg Ile Leu Glu Val Ser Ile Pro Thr Glu Glu Ala Gly Ser Val		
	165	170 175
Pro Glu Ile Tyr Ser Leu Leu Lys Arg Thr Thr Asp Ile Leu Ile Gln		
	180	185 190
Leu His Lys Lys Cys Thr Ser Pro Glu Asp Met Glu Ser Val Leu Thr		
	195	200 205
Lys Pro Tyr Asp Ser His Thr Asp Ile Arg Ala Phe Leu Gln Glu Lys		
	210	215 220
Ser Lys Ile Leu Tyr Met Asn Asn Leu Pro Pro Asp Thr Thr Gln Ser		
	225	230 235 240
Glu Leu Glu Ser Trp Phe Thr Gln Tyr Gly Val Arg Pro Val Gly Phe		
	245	250 255
Trp Thr Val Lys Asn Ile Val Glu Asp Thr Ser Asn Val Asn Asn Asn		
	260	265 270
Trp Ser Leu Asn Asn Ser Pro Tyr Val Glu Asp Gln Asp Ser Ile Ser		
	275	280 285
Gly Phe Val Val Phe Gln Thr His Glu Glu Ala Thr Glu Val Leu Ala		
	290	295 300
Leu Asn Gly Arg Ser Ile Leu Ser Asn Leu Ala Asn Thr Lys Gln Pro		
	305	310 315 320
Arg Val Val Glu His Val Leu Glu Leu Gln Pro Ser Ser Thr Gly Val		
	325	330 335
Leu Asp Lys Ala Gln Glu Ile Leu Ser Pro Phe Pro Gln Ser Lys Asn		
	340	345 350
Lys Pro Arg Pro Gly Asp Trp Asn Cys Pro Ser Cys Gly Phe Ser Asn		
	355	360 365
Phe Gln Arg Arg Thr Ala Cys Phe Arg Cys Ser Phe Pro Ala Pro Ser		
	370	375 380
Asn Ser Gln Ile His Thr Ala Asn Ser Asn Asn Asn Val Asn Ser Ser		